

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 27, 2002, 20:25:35 ; Search time 3172 Seconds
(without alignments)
5994.168 Million cell updates/sec

Title: US-09-837-961-8
Perfect score: 6244

Sequence: 1 MNNIQQCVPYCNLNPEV.....IGETGTFIVDSVLLMEE 1174

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-O=/cgn2.1/USPNC_spool/US09837961/runat_25112002.142416.5933/app_query.fasta.1.1351
-DB=EST -QFWT=fastap -SUFFIX=ist -MINMATCH=0.1 -LOOCL=0 -LOOEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -List=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09837961 -CGN_1.1.2735 -runat_25112002.142416.5933 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	122	2.0	1192	12	BG425459
2	115	1.8	1457	11	AK009951 Mus muscu
3	111	1.8	993	12	BG164308
4	111	1.8	1438	12	BE896304
5	110.5	1.8	638	12	BG641200
6	109.5	1.8	1699	12	BE971314
7	108.5	1.7	1284	11	AK011138
8	108	1.7	3750	11	AK019545
9	107.5	1.7	616	13	BI637532
10	107.5	1.7	629	13	BI635059
11	107.5	1.7	649	13	BI639112
12	107.5	1.7	699	13	BI372337
13	107.5	1.7	970	10	BE561336
14	107.5	1.7	1382	10	BE541010
15	106	1.7	580	12	BG385276
16	106	1.7	2914	11	BC022105
17	104.5	1.7	671	13	BI234068
18	104.5	1.7	1309	12	BG491756
19	104.5	1.7	1615	11	BC020373
20	104	1.7	1130	12	BG331892
21	104	1.7	2282	11	AK012926
22	104	1.7	2874	11	BC020549
23	103	1.6	2685	11	AK016554
24	102.5	1.6	575	9	AA596165
25	102.5	1.6	1214	14	BQ926267
26	102	1.6	917	14	BQ924785
27	101.5	1.6	772	12	BF968812
28	101.5	1.6	999	10	BE542913
29	101.5	1.6	1097	17	CNS06LC5
30	101.5	1.6	2072	11	AK005502
31	101	1.6	854	17	CNS0729V
32	101	1.6	1170	12	BF568423
33	101	1.6	1576	14	BM906297
34	100.5	1.6	543	13	BI343429
35	100.5	1.6	612	9	AI405242
36	100.5	1.6	651	17	BH390224
37	100.5	1.6	682	13	BI228162
38	100.5	1.6	689	9	AI777237
39	100.5	1.6	689	13	BI486958
40	100.5	1.6	935	14	BQ215157
41	100.5	1.6	2361	11	BC014239
42	100.5	1.6	2944	11	AK004769
43	100	1.6	1137	17	CNS06QJF
44	100	1.6	1383	12	BG615889
45	99.5	1.6	688	9	AV086490

ALIGNMENTS

RESULT 1
BG425459

LOCUS 602447303F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4585728 5',
DEFINITION mRNA sequence.

ACCESSION BG425459
VERSION BG425459.1 GI:13331965

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1192)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DIP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1313 row: f column: 01
High quality sequence stop: 626.
Location/Qualifiers
1. .1192
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4585728"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(S). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source

BASE COUNT 248 a 407 c 310 g 227 t
ORIGIN
Alignment Scores:
Pred. No.: 0.0069 Length: 1192
Score: 122.00 Matches: 75
Percent Similarity: 33.77% Conservative: 28
Best Local Similarity: 24.59% Mismatches: 98
Query Match: 1.95% Indels: 104
DB: 12 Gaps: 15
US-09-837-961-8 (1-1174) x BG425459 (1-1192)

Qy 358 ThrLeuSerAspProValPheVal-----Arg 366
Db 127 AGCGTCCCGAGCGCTGTTCCTCCATCGTCGGCTGCCCGACAGACACCGAGCGGTGAT 186
Qy 367 GlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly----- 380
Db 187 GGTGGCATGGCCAGAGAGGACTCTCTGCGGCGACGAGGCGCCAGAGCAATGCGTGCCA 246
Qy 381 -----ValAlaPheGlnGlnThrGlyThrAsnHisThr 391
Db 247 TCCTGACCTGAAGTACCCATTGAGCATGCGTCACCAACTGGGACG----- 297
Qy 392 ArgThrPheArgAsnSerGlyThrIleAspSer----- 402
Db 298 ---ACATGGAGAGATCTGGCACCAACACTTCTACAGAGCTGGCGCTGGCCGGAGGA 354
Qy 403 -----LeuAspGluIleProGlnAspAsnSerGlyAlaProTrpAsnAsp 418
Db 355 GCACCATGCTGCTGACGAGTCCCTGAAACCCCAAGGCCAACAGAGAAAGATGAC 414
Qy 419 TyrSerHisVal-----LeuAsnHisValThrPheValArg---TrpProGlyGluIle 435
Db 415 TCAGATTATGCTGAGACTTCAACACCCCGCCATGTACGTGGCCATCCAGGCGCTGCT 474
Qy 436 SerGlySerAspSerTrpArgAlaProMet---PheSerTrpThrHisArgSerAlaThr 454
Db 475 GTTCTCTACGCTTGGCGCGCACCACTGCGCATGTCTGACACTCTGGAGACGGGGTCA 534
Qy 455 ProThrAsnThrIleAspProGluArgIleThrGlnIleProLeuValIleAlaHisThr 474
Db 535 CCC-----ACACGGTCCCATCTACGAGGCT---ACG 564

Qy 475 LeuGlnSerGlyThrThrValValArgGlyProGlyPheThrGlyGlyAspIleLeuArg 494
Db 565 CTCTCCCCACGCACAAATCCTGCTGTGGACCTGGTGGACGGGACCTGAC-----CGA 618
Qy 495 ArgThrSerGlyGlyProPheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGln 514
Db 619 CTAACTCATGCAGATCCTCAGTCAGCCGAGGTTTACAGCTTCACCCACACACTGGCGGAG 678
Qy 515 ArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrVal 534
Db 679 CGGGGACAATCCGTGGCGGA----- 699
Qy 535 AlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeu 554
Db 700 -----CAATTCAGGAGAGAGCTGTGCTTACACACTGCGCTTGCCTTG 735
Qy 555 ThrPhe-----GlnSerPheSerTyrAlaThrIleAsnThrAla 567
Db 736 ACTTTCGACCTGGACATGTGCCACGCCCATCCCTCTACTCGAGAAACAAC----- 789
Qy 568 PheThrPheProMetSerGlnSerSerPheThrValGly----- 580
Db 790 TAGCAGCTAGCCAGATGCCAGTTCTCACTCACCTTGGCCACTGACAGGATCCGAGTGCC 849
Qy 581 AlaAspThr-----PheSerSerGlyAsnGluValTyrIle 592
Db 850 CGAGACACTGTTCCAGGCGTTCATACGTGCGACTTGTTCATCATTTGCGGCCATCAGACGA 909
Qy 593 AspArgPheGluLeu 597
Db 910 CCACGCTTCTCAGTA 924
RESULT 2
AK009951
LOCUS
DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310057B22:homolog to DNA DOUBLE-STRAND BREAK REPAIR AND V(D)J RECOMBINATION PROTEIN XRCC4, full insert sequence.
ACCESSION AK009951.1 GI:12845062
VERSION AK009951
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone:lib-RIKEN full-length enriched mouse cDNA library clone:2310057B22.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159
REFERENCE 3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
JOURNAL MEDLINE


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Db 478 -----GAAATGAAGGCTCTCTGAGAGACTGG----- 504
Qy 700 ThrileGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPhe 719
Db 505 -----AATGATGTT-----CAAGGCCGATTT 525
Qy 720 AspGluCysTyrProThrTyr-----LeuTyrGlnLys----- 730
Db 526 GAGAAATGCTGAGTGCCAAAGAGCCCTTGAGGCTGATTCTATCAAGATTTATCTTG 585
Qy 731 ---IleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuLeuArgGlyTyrIleGlu 749
Db 586 GTGTCGAATGAGAAAGAACAAAGATCGGAGCTTGCAATAATG-----CTAAAT 636
Qy 750 AspSerGlnAspLeuGlu 755
Db 637 GAAGTCACAGCTGGAG 654

RESULT 3
LOCUS BGI164308 993 bp mRNA linear EST 06-FEB-2001
DEFINITION 6023341347F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:449226 5',
mRNA sequence.
ACCESSION BGI164308
VERSION BGI164308.1 GI:12671011
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10232 row: n column: 11
High quality sequence start: 24
High quality sequence stop: 389.
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Location/Qualifiers
1..993
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/db_xref="taxon:9606"
/clone="IMAGE:449226"
/clone_lib="NIH_MGC_89"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dt primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 231 a 308 c 305 g 149 t
ORIGIN

Alignment Scores:
Pred. No.: 0.105 Length: 993
Score: 111.00 Matches: 60
Percent Similarity: 33.73% Conservative: 25
Best Local Similarity: 23.81% Mismatches: 78
Query Match: 1.78% Indels: 90
DB: 12 Gaps: 11

US-09-837-961-8 (1-1174) x BGI164308 (1-993)
Qy 316 TrpGlyGly-HisLeuValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSe 335

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Db 346 TCGGGAGGATCATTTAGGATCTCTCAAGGAAACGAGGACCAAGGTGCCCTTCTGTGAG 405
Qy 335 rTyrGlyValPheAsn-ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProp 355
Db 406 ACATCTCTGCTCTCTCTCCATCC-----CCAT 432
Qy 355 heTyrArgThrLeuSerAspProValPheValArgGlyGlyPheGlyAsnProHisTyrV 375
Db 433 CTACAGATGATTAAAG-----AAGCCTCAGATGA 462
Qy 375 alLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly----- 387
Db 463 GCATGCGCGCGCTGCTGAGCGCAAGGCACAGGATGACATGGTGGCAGGCC 522
Qy 388 -----ThrAsnHisThr- 391
Db 523 CATTGACTTTGTGCTCTCAATGCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 582
Qy 392 ----ArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluLeuProGlnA 410
Db 583 GCATCGCACCTTGGCAGTACGCGGATGTAGATCGGCGGATGATGATGATGATGATGATGAT 640
Qy 410 spAsnSerGlyAlaProTyrAsnAspTyrSerHisValLeuAsnHisValThrPheValA 430
Db 641 -----GCCACCGCTGAACAT----- 658
Qy 430 rgTrpProGlyGluLeuSerGlySerAspSerTrpArgAlaProMetPheSerTrp---T 449
Db 659 -----TCGGGGAACGAGGCTGGAAGAAACCCCACTGGACTGGGCC 701
Qy 449 hrHisArgSerAlaThrProThrAsnThrIleAspProGluArg---lleThrGlnIleP 468
Db 702 CCCACCGAGCGGACGCGGACCATGACCCGCGGCGGCGGCTGTGAGACCCCTTC 761
Qy 468 roLeuValLysAlaHisThrLeuGlnSerGlyThrValValArgGlyProGlyPheT 488
Db 762 CACAATCCGTCACCATACA-----C 782
Qy 488 hrGlyGlyAspIleLeuArgThrSerGlyGlyProPheAlaTyrThrIleValAsnI 508
Db 783 CCAGCAGACATCTACTACTACTAACGAAACGGGACACCC---CGGGGAGGGCGGCCACAG 839
Qy 508 leAsnGlyGlnLeuProGlnArg-----TyrArgAlaArgIleArgTyrA 523
Db 840 TCGGAGCGCGGACGCGGCGGACACATGCGACCGCGGAAACGCGGACCAAAAGTGA 899
Qy 523 laSerThrAsnLeuArgIleTyrValThr 533
Db 900 CCCAAACACGAGCTACGACAAACACAGCACA 931

RESULT 4
LOCUS BE896304 1438 bp mRNA linear EST 20-OCT-2000
DEFINITION 601439143F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924083 5',
mRNA sequence.
ACCESSION BE896304
VERSION BE896304.1 GI:10360572
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM9761 row: e column: 12
 High quality sequence stop: 299.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3924083"
 /clone_lib="NIH_MGC_72"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SpORF6; Site1: NotI; Site2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."
 Technology: 2
 BASE COUNT 429 a 477 c 311 g 221 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.197 Length: 1438
 Score: 111.00 Matches: 103
 Percent Similarity: 32.21% Conservative: 31
 Best Local Similarity: 24.76% Mismatches: 123
 Query Match: 1.78% Indels: 159
 DB: 23 Gaps: 23

US-09-837-961-8 (1-1174) x BE896304 (1-1438)

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Qy 177 GlyGlnGlyTrp-----Gly 181
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Db 150 GGTCAAGAGTGGAGCTGTGAGGCTATTGCAGTAATCCAGAAACGAAAGGTGACAAATGSC 209

Qy 182 LeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArgTyr 201
|||||
Db 210 TTAGCTTCAGTGTAGTGTGCGACACACTGGACATAATAGACCTA-----TTC 260

Qy 202 ThrLysHisCysLeu-----AspThrTyrAsnGlnGlyLeuGluAsn 215
|||||
Db 261 ACGAACAATATTGATCTTAGACTCTAAGTAAAGACAGTACATACGA---CTCCGACAG 317

Qy 216 LeuArgGlyThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThr 235
|||||
Db 318 CTCAGGACACATTAACTCGCAACAAACAGCAGCA-----ACTTACAGGACTGACCTTACT 371

Qy 236 LeuThrValLeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIle 255
|||||
Db 372 CACTCGGCTTGCAAACTGCTACA-----ACTGGACTCCACCCGCTG 413

Qy 256 GlnThrSerSerGlnLeuThrArgGluIleTyrThrSerSerValIle----- 271
|||||
Db 414 CTGCTCTTACGTGACGCGCGGAGGAGCTGGAGCTGGTGCATCGGTGAGTACGCC 473

Qy 272 -----GluAspSerProValSerAlaAsnIleProAsnGlyPhe----- 284
|||||
Db 474 AATTCGCACACAGCGCAATAATCCAAAGAATATCCACAGAACACTTCCAGCAAGCAAACT 533

Qy 285 -----AsnArgAlaGluPheGlyValArgProHisLeuMetAsp 298
|||||
Db 534 GTTACCAATTACTCTCCCTCTCGCATCAGCTCGGCTCCAGCTCCCATCTCTCTCAATCA 593

Qy 299 -----PheMetAsnSerLeuPhe-ValThrAlaGluThrVa 310
|||||
Db 594 ACGTGGCATTCGCTCACAACACTCTTCGCTATACCTATCCCGTCTCTTCGGAGGCGT 653

Qy 310 lArgSerGlnThrVal-----Trp-----GlyG1 318
|||||
Db 654 CCGGCACTACACGCTGGACACTTCAGGGTGTGGTGTGACCTCGGAGTCTCAATGGTAG 713

Qy 318 yHis-----LeuValSerSerAr 324
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Db 714 GCATCACAACTACCCCTACTCTCTCTGACACAGAAATTCCTTCGCTCACTTAGCGCAGC 773

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Qy 324 gAsnThrAlaGlyAsnArgIleAsnPheProSer-TyrGlyValPheAsnProGlyGlyA 344
|||||
Db 774 CACTTGTGGCTGGAAGACTACATACACAGAGCTGGAGCTCGGAGCCAGCAGCGG 833

Qy 344 laileTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSerAspProValP 364
|||||
Db 834 CA-----AGGCAGCGGATCACAGCTCAACAGCTCATAACTCCACTAAACT 878

Qy 364 heValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGlyValAlaPheG 384
|||||
Db 879 TCGCAGG-----CTACCGCAC-----CCTGGGATCACCTCA 911

Qy 384 IngInThrGlyThrAsnHisThrArg----- 392
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Db 912 CACAGGAGCAGCACACACCCGCGGCGCGCAGCAGCAGCATGAGAGTAACCT 971

Qy 393 -----ThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIleP 407
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Db 972 CCATCCAGAGGCGCACACTACACCAACGAGGGAACC-----ACCCAGCAACTCGA 1025

Qy 407 roProGlnAspAsnSerGlyAlaProTrpAsn-----AspTyrSerHisValLeuAsnH 425
|||||
Db 1026 CGCCACAA-----AACGGCGCCGCCACAAATAGAGAGACAGCAGCAACCCCAAAACC 1079

Qy 425 lsValThrPheValArgTrp-ProGlyGluIleSerGlySerAspSerTrpArgAlaPro 444
|||||
Db 1080 AC-----GACAGCAGGCTCCCGAATTA----- 1103

Qy 445 MetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIle 464
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Db 1104 -----CGACACCGCTAAGCCGACGCGGCGGCAACCGCCGCCACCCAGCGG--- 1148

Qy 465 ThrGlnIleProLeuValIleHisThrLeuGlnSerGlyThrValValArgGly 484
|||||
Db 1149 -----ACCCAGGCGGCGCAG 1163

Qy 485 ProGlyPheThrGlyAspIleLeuArgArgThrSerGly 498
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Db 1164 CCACAGCTCACGGCGGC-----AGACGCGCATGCGGC 1196

RESULT 5
BG641200 638 bp mRNA linear EST 23-APR-2001
LOCUS SD12481.Sprime SD Drosophila melanogaster Schneider L2 cell culture
DEFINITION POT2 Drosophila melanogaster cDNA clone SD12481 5, mRNA sequence.
ACCESSION BG641200
VERSION BG641200.1 GI:13773126
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 638)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/WHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003553: arm:3L [8822534,9109551]
estimated-cyto:66E3-67A1: 04/13/2001
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FEATURES
source

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Alignment Scores:
Pred. No.: 0.0566 Length: 638
Score: 110.50 Matches: 50
Percent Similarity: 34.27% Conservatives: 35
Best Local Similarity: 20.16% Mismatches: 96
Query Match: 1.77% Indels: 67
DB: 12 Gaps: 11

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Db 28 TATCGGTAGAACAAGACAGACAGATTTCCGAGATGTATCAAAATCCTTGACATACGTCGG 87
Qy 950 IlePhe-----GluGluLeuLysGlyA-gillePheThrAlaPhePheLeuTyr 965
Db 88 ATCTTTGGCCCTTTTGGGGCTCAATTGCGGAAGCTGTAGTGTGATCAGTTTGGGATATAT 147
Qy 966 AspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnVal 985
Db 148 GGTGTTTCCACGATTACCACACGACGAAAGAGTAGTAATGCGGAGTTCGCTGCATGAACATC 207
Qy 986 ----LysGlyHisValAspValGluGluInAsnAsnHisArgSerValLeuValVal 1003
Db 208 ATCCCGAAGACTCGGTGGACTGTGAGCAGAG----- 240
Qy 1004 ProGluTrpGluAlaGluValserGlnGluValArgValCysProGlyArgGlyTyrIle 1023
Db 241 -----ATGGACTCTGCTACGGC 258
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Qy 1039 ThrIleHisGluIleGluAsnThrAspGluLeuLysPheSerAsnGlyValGluGlu 1058
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Db 421 GGAGCACACACACACACTCAATCC-----TCCATCCGGATACGATGAG 465
Qy 1099 ValProAlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAsp-----Gly 1115
Db 466 TACCG-----TTGAGTACGATTCAAAGCCAGCAGAGTACCTACGTTTGATCTGGAGT 519
Qy 1116 ArgArgAspAsnProCysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAla 1135
Db 520 GAGCGTGATAACAATCTGGAG-----TATACC----- 546
Qy 1136 GlyTyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGluIle 1155
Db 547 -----TTCAACTATACCAACGACCTGCGTACGTCAGTGGTCCCAACATC 588
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RESULT 6

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BE971314
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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BE971314 1699 bp mRNA linear EST 04-OCT-2000
601651647F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3935051 5',
mRNA sequence.
BE971314
BE971314.1 GI:10584650
EST.
human.

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1699)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM776 row: n column: 12
High quality sequence stop: 66.
Location/Qualifiers
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(Clontech); Site_1: SfiI (ggccgctcgcc); Site_2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATCTAGGCGGAGCGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

```

```

FEATURES
source

```

```

BASE COUNT 556 a 516 c 273 g 353 t 1 others
ORIGIN

```

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Alignment Scores:

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Score: 109.50 Matches: 86
Percent Similarity: 33.01% Conservatives: 50
Best Local Similarity: 20.87% Mismatches: 178
Query Match: 1.75% Indels: 100
DB: 12 Gaps: 16

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US-09-837-961-8 (1-1174) x BE971314 (1-1699)

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Qy 206 LeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsnThrArgGlnTrpAla 225
Db 212 TTCTCTTATATGTCGCGACATTTCTTCA-----TCCATCCACTCCAAAGCTTGGTCT 265
Qy 226 ArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAspIle---ValAlaLeu 244
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    |||
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Db 418 TTCACACTACCAAGGTCGTTATACGCAAGATGGGA-----TCTCGC 462
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LOCUS AK011138 1284 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2600001J17:homolog to ARSENITE RELATED GENE

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AK011138 GI:12847071
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Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA,
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clone:2600001J17.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
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Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
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Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5 (bases 1 to 1284)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hangaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koyas,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
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Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
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LOCUS BI637532 616 bp mRNA linear EST 10-SEP-2001
DEFINITION SD19571.5prime SD Drosophila melanogaster Schneider L2 cell culture
pOT2 Drosophila melanogaster cDNA clone SD19571 5, mRNA sequence.
ACCESSION BI637532
VERSION BI637532.1 GI:15539742
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 616)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE BDGP/HMMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003553: arm:3L [8822534,9109551]
estimated-cyto:66E3-67A1: 05/19/2001
Plate: SD.195 row: F column: 11
High quality sequence stop: 532.
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fractionated cDNAs were directly ligated into pOT2.
Plasmid cDNA library."
BASE COUNT 161 a 153 c 153 g 149 t
ORIGIN
Alignment Scores: 0.122 Length: 616
Pred. No.: 107.50 Matches: 54
Score: 36.73% Conservative: 36
Percent Similarity: 22.04% Mismatches: 94
Best Local Similarity: 1.72% Indels: 61
Query Match: 13 Gaps: 14
US-09-837-961-8 (1-1174) x BI637532 (1-616)
QY 930 HisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsnValAsp 949
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REFERENCE 1 (bases 1 to 649)
AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
          Lewis,S. and Rubin,G.M.
TITLE     BDGP/HMMI Drosophila EST Project
JOURNAL   Unpublished (2001)
COMMENT   Contact: Stapleton, M.
          BDGP
          Lawrence Berkeley National Lab
          One Cyclotron Rd, Berkeley, CA 94720, USA
          Fax: 510 486 6798
          Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
          hit genomic AE003553: arm:3L [8822534,9109551]
          estimated-cyto:66E3-67A1: 05/19/2001
          Plate: SD.215 row: F column: 3
          High quality sequence stop: 587.
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            /note="Vector: pot2; Site:1: EcoRI; Site:2: XhoI; Sized
            fractionated cDNAs were directly ligated into pot2.
            Plasmid cDNA library."
BASE COUNT 171 a 164 c 159 g 155 t
ORIGIN
Alignment Scores:
Pred. No.: 0.133 Length: 649
Score: 107.50 Matches: 54
Percent Similarity: 36.73% Conservative: 36
Best Local Similarity: 22.04% Mismatches: 94
Query Match: 1.72% Indels: 61
DB: 13 Gaps: 14
US-09-837-961-8 (1-1174) x BI639112 (1-649)
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QY 966 AspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnVal 985
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Db 540 AACATCTGGAG-----TATACC----- 557
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Db 609 CGGGATCTCTGGTC 623
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BI372337
LOCUS      BI372337 699 bp mRNA linear EST 01-AUG-2001
DEFINITION Drosophila melanogaster cDNA clone RE59277 5, mRNA sequence.
ACCESSION  BI372337
VERSION    BI372337.1 GI:15068365
KEYWORDS   EST.
SOURCE     fruit fly.
ORGANISM   Drosophila melanogaster
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            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 699)
AUTHORS   Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson
          ,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
          ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,
          Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
          Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
          ,G.M.
TITLE      BDGP/HMMI RE Drosophila EST Project
JOURNAL    Unpublished (2001)
COMMENT    Contact: Stapleton, M.
          BDGP
          Lawrence Berkeley National Lab
          One Cyclotron Rd, Berkeley, CA 94720, USA
          Fax: 510 486 6798
          Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
          hit genomic AE003553: arm:3L [8822534,9109551]
          estimated-cyto:66E3-67A1: 05/16/2001
          Plate: RE.592 row: G column: 5
          High quality sequence stop: 630.
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            /dev_stage="0-24 hours mixed stage embryonic"
            /lab_host="DH5-alpha Tona"
            /note="Organ: embryo; Vector: pflc1; Site:1: XhoI; Site:2:
            BamHI. Library was kindly generated by Piero Carninci at
            the RIKEN. The library was normalized and excised using
            Cre recombinase. Plasmid cDNA library."
BASE COUNT 182 a 171 c 179 g 167 t
ORIGIN
Alignment Scores:
Pred. No.: 0.151 Length: 699
Score: 107.50 Matches: 54
Percent Similarity: 36.73% Conservative: 36
Best Local Similarity: 22.04% Mismatches: 94
Query Match: 1.72% Indels: 61

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Db 616 CATTGAACCTAGAGAGAAATTCATCTCCTACCAGAGGAGCAATCCAGGGAATGAGACCC 675
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Db 676 CTTTCGTCAAGGGTCGAGGT-----CARACATCTT 705
QY 412 erGlyAlaProTrpAsnAspTyrSerHisValLeuAsn-----HisV 426
Db 706 CCGCGCCTCCCTATCGTCCAGTTCAGTGTGCGAGGTACCGGTGGCTTCCTGGCATC 765
QY 426 alThrPheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetp 446
Db 766 TTTCAGAGCCCGCTGCGCGGTTCCTCTCCGCACTGGAAGC-----CCCGCA 816
QY 446 heSerTrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrG 466
Db 817 TTTCCTGGTGACCTGTGGGCGACGCCACTTTCG-----GGCCGGGCATATGGCCC 870
QY 466 lntleProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgly 484
Db 871 AATGGCCCTGGGTGCGGCGCGTCCGCGAGAGAGTGTCTACGCTGGCAACGGGG 926

RESULT 14
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LOCUS 601064356F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450877 5',
DEFINITION mRNA sequence.
ACCESSION BE541010
VERSION BE541010.1 GI:9769754
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1382)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8429 row: p column: 14
High quality sequence stop: 210.

FEATURES
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT 353 a 387 c 387 g 255 t
ORIGIN

Alignment Scores:
Pred. No.: 0.482 Length: 1382
Score: 107.50 Matches: 103
Percent Similarity: 30.67% Conservative: 39
Best Local Similarity: 22.25% Mismatches: 128
Query Match: 1.72% Indels: 193
DB: 10 Gaps: 25

US-09-837-961-8 (1-1174) x BE541010 (1-1382)

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QY 180 TrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsn----- 192
Db 128 TGGGGAAACCCACGTGCGGGGTGCGTGCACCATGGACACCATCCCGTCTTGAAGAAG 187
QY 193 ---ArgLeuIleAsnLeuIleHisArgTyrThrLysHisCysLeuAspThrTyrAsnGln 211
Db 188 GAACGGGTACTGGAGTCCGACCGA-----CACTGCTGCTGTACGGGGCCCC 238
QY 212 GlyLeuGlnAsnLeuArgGlyThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArg 231
Db 239 GGG-----TCTAAGCGCGGTACGGGAGCAAGTCCAGTCTCGCGCAACACACTGGCGG 292
QY 232 ArgAspLeuThrLeuThrValLeuAspIleValAlaLeuPhePro-AsnTyrAspValar 251
Db 293 CAAGGCTTACCA-----CGCGAGGGGCCAGGATTACAGGTTCT 331
QY 251 gThrTyrProIleGlnThrSer-----SerGlnLeuThrArgGluIleTyrTh 267
Db 332 CCGGTTCCCGCTTACGGGCGTGTAAAGCCCGTGGGGGCTTCCCGCTTAAAGCTTT-- 389
QY 267 rSerSerValIleGluAspSerProValSerAlaAsnIlePro-----AsnGl 283
Db 390 -----CCAGAGGTGTTCACCCCGCGCGCGGTGGAGAGG 427
QY 283 yPhe---AsnArgAlaGluPheGly-----Valar 292
Db 428 ATTCCCAACAGGGCAGCAGCGGCGCAGACAGTATTATACGGATGGCGTTAAAGCGTTAG 487
QY 292 gProProHisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSe 312
Db 488 GCGGCGCGCAA----- 497
QY 312 rGlnThrValTrpGlyGlyHisLeuValSerSerArgAsnThrAlaGlyAsnArgIleAs 332
Db 498 -----TGGGGGCGCCACGCGCCAGCGGCAAGAAAGACCCACAGACGAG 547
QY 332 nPheProSerTyrGly----- 337
Db 548 CCGCGCCACAGAGGGGAGGGAATATCCAGTTACTCCAGACGACTGGTGAGAAAGC 607
QY 338 -----ValPheAsnProGlyGlyAlaI 345
Db 608 GCAAAATGTCCTATTTAAAGCCTAACAGCTACAGAGTTCATCCGGCGGCGACAT 667
QY 345 eTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSerAspPro----- 362
Db 668 TACCAAAAACGATGTGGACCT-----CTGGTTTCGGAGGTATACAGCA 712
QY 363 -----ValPheValArgGlyGly-----PheGl 370
Db 713 AGTGCAACACGGCGGCACACACCTAGTGTATACAGAGCGGGCCACCATACATCTTGG 772
QY 370 yAsnProHisTyrValLeuGly---LeuArgGlyValAlaPheGln-----GlnThrGl 387
Db 773 GCGATTAAACCATATCTTAGCGAGCTTTATGGGAGAGACTCGCGCATTTAGACTGCGG 832
QY 387 yThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIle-P 407
Db 833 CGAGCAACATACCCGCAACA-----AACAAATATTATTCAGAAAGCGTTTTCATACCTTACC 886
QY 407 roProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValT 427
Db 887 CACCACAGGACCATGGAGGAGCCCCA-----CCACAT----- 918
QY 427 hrPheValArgTrpProGlyGluIleSerGlySerAspSerTrpArg----- 442
Db 919 -----TCATCCCAACAGTGTGGCGCCCTTTTGGCAGC 952
QY 443 -----AlaProMetPheSerTrpThrHisArg-SerAlaThr 454
Db 953 AGCCACGGGAAAAAATCTTCCCGCCCGCGGATTTGTGTGGCGCGCAGACATAGCCACACC 1012

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 18:30:04 ; Search time 93 seconds

(without alignments)
2601.068 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNIQOCVPYCNLNPEV.....IGTEGTFIVDSVELLMEE 1174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
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2	4373	70.0	1180	2	Q9S5V8
3	4328	69.3	1176	2	Q45736
4	4312	69.1	1176	2	Q9RC30
5	4209.5	67.4	1189	2	Q9L877
6	4192.5	67.1	1155	2	Q9F296
7	4186.5	67.0	1155	2	Q93721
8	4184	67.0	1176	2	Q9S514
9	4169	66.8	1171	2	Q06894
10	4151.5	66.5	1177	2	Q45735
11	4145.5	66.4	1177	2	Q03743
12	4144	66.4	1178	2	Q9R826
13	4142	66.3	1178	2	Q45768
14	4136	66.2	1160	2	Q93TF9
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16	3545.5	56.8	1118	2	Q9AM82

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Q9FDC0 bacillus th
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Q8RQJ6 bacillus th
Q93N14 bacillus th
Q45740 bacillus th

ALIGNMENTS

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ID Q45749
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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTS00349A;
RA Lambert B.;
RT "NO INFORMATION";
RL Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z22512; CAA80235.1; -.
DR HSP; P02965; ICIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1174 AA; 133350 MW; 8C7F122F9446F15C CRC64;

Query Match 86.6%; Score 5406; DB 2; Length 1174;
Best Local Similarity 86.5%; Pred. No. 0;
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QY 121 NAQLREDVRIRFANTDDALITAINNFTLSFEIPLLSYVQAANLHLSLLRDAYSFGGOW 180
Db 121 NAQLREDVRIRFANTDDALITAINNFTLSFEIPLLSYVQAANLHLSLLRDAYSFGGOW 180

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Db 241 IVALFPNDVRYPIQTSQSLTREIYTSVIEDSPVSNINPENGFNRAEFGVRPPLMDFM 300
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Db 301 NSLFTVATVRSQTVWGHLVSSRNAGNRINFPYGVNPGGAIWIADDEPRPFRYRLS 360
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Db 361 DPVFRVGGFGNPHYVGLRGVAFQGTGNHRTFNSGTIDSLDEIPQDNGAPNDYS 420
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QY 721 ECPYTYLYQKIDSKLPYTRYQLRGVIEDSDLEIYLIRYNKAKHETVNLGTGSLMPLS 780
Db 720 ECPYTYLYQKIDSKLPYTRYQLRGVIEDSDLEIYLIRYNKSHHEIVNPGTGSMLPLS 779
QY 781 VQSPIRKCGPNRCAPHLNPNLDLSCRGCKEKAHSHHFSLDIDYGDCTDLNEDLDVWV 840
Db 780 VENQIGPCGPNRCAPHLNPNLDLSCRGCKEKAHSHHFSLDIDYGDCTDLNEDLDVWV 839
QY 841 IFKIKTODGHARLGNLEFLEKPLVGEALARYKAEKKRDKREKLETNIVYKEAKES 900
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QY 961 AFPLYDARNVTKNGDFNNGLSCHWNKGVHDVBEQNNHRSVLVPEWEAEVSVQVRVCPGR 1020
Db 960 AISLYDARNVTKNGDFNNGLSCHWNKGVHDVBEQNNHRSVLVPEWEAEVSVQVRVCPGR 1019
QY 1021 GYLIRVTAKEGEGCVTTHETENNDELKFSNCVVEEYVPNNVTCNDYTANO--EY 1078
Db 1020 GYLIRVTAKEGEGCVTTHETENNDELKFSNCVVEEYVPNNVTCNENYMQVGE 1078
QY 1079 GGAYTSNRNRYDETYGSSSVADYASVEEYKSTYDGRDRNPNCESNRGYDTPPLPAGVY 1138
Db 1079 TDACNVNRNGYEDAYGNPSTPVHYTTPYEETVYDERRNPCEANKGYNYTPLPGVYV 1138
QY 1139 TKELEYFPETDVKWIEGTETGTFIVDSVLELLMEE 1174
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RESULT 2
Q9S5V8 PRELIMINARY; PRT; 1180 AA.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BtT84A1 crystal protein.
GN BtT84A1.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
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SEQUENCE FROM N.A.
RC STRAIN-T84A1;
RA Nagamatsu Y.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RC STRAIN-T84A1;
RA Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
RT "Nucleotide Sequence of the lepidoptera-toxic Protein Gene of Bacillus
thuringiensis subsp. dendrolimus T84A1.";
RL J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
[3]
SEQUENCE FROM N.A.
RC STRAIN-T84A1;
RA Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
RT "A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
thuringiensis.";
RL Agric. Biol. Chem. 48:611-619(1984).
DR EMBL; AB026261; BAA77213.1; -.
DR HSP; P02965; ICIY
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DC562D CRC64;

Query Match 70.0%; Score 4373; DB 2; Length 1180;
Best Local Similarity 71.9%; Pred. No. 2.6e-288;
Matches 856; Conservative 85; Mismatches 222; Indels 28; Gaps 11;

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Db 1 MDNNPNINECIPYNCLSNPEVEVLGGERIEFTGYTPIIDISLTLQTLSEFVPGVGVAFGL 60
QY 59 FDLIWTGITSDSWLSFLQIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLI 118
Db 61 VDIITWIGTSGSDAFVLQIEQLINQRIEFAFNQALISLGLSNLYQIYAESFEWEAD 120
QY 119 PNAQLREDVRIRFANTDDALITAINNFTLTSPEIPLLSVVQVQANLHLSLRDAVSFGQ 178
Db 121 PTNPALREEMRIQFNDMSALTALPLFAYQYQVPLLSVYQVQANLHLSLRDAVSFGQ 180
QY 179 GWGLDIATVNNHYNRLNLHRYTHKCHDLYNOCLENLRCNTNRQARPNQFRDLTLTVID 238
Db 181 RWGFDAAATINSRYNDLRLIGNTYDAVRNTGLRWGPDSDRWVRYNQFRDLTLTVID 240
QY 239 LDIVALPNVDVRYPIQTSQSLTREIYTSVIEDSPVSNINPENG----NRAEFGVRPP 294
Db 241 LDIVALFNSDSSRYPRTVTSQTLREIYTNFVLE-----NFDGSRFGMAQRIBQNIQRP 294
QY 295 HLMDFMNSLFTVATVRSQTVWGHLVSSR--NTAGNRINFPSPVGVNPGGAI--WIAD 350
Db 295 HLMDLNRIIYTDVHRGFNYWSHQITASPVGSGFEFAFPLFG--NAGNAAPVVLVSL 352
QY 351 DRRPFRVTLSDPVFVR-----GGFGNPHYVGLRGVAFQGTGNHRTFNSGTIDSLD 404
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Db 470 ITQIPLTKSTNLGSGTSVVKGPQGTGDIILRRISPGQISTLRVNITAPLSQRYVRIRYA 529
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QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAVNALFTSINQIGIKTDVTDYHIDQVSN 643
Db 590 FNSGNEVYIDRIEVPVPAEYFVPAEYDLERAKAVNELFTSSNQIGLKTVDYDIDQVSN 649
QY 644 LVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 703
Db 650 LVECLSEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 709
QY 704 GDDVFKENYVTLPGTFDECPTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 763
Db 710 GDDVFKENYVTLGTFDECPTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 769
QY 764 KHETVNVLGTGSLWPLSVQSPIRKCGPNRCAPHELNWPDLDSCRDGCKCAHSHHFS 823
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Db 830 DIDVGCDDLNEGLDWWVIFIKITQDGHARLGNLEFLBEKPLVGEALARKVRAEKKWRDK 889
QY 884 EKLEFETNVIYKEAKESVDALFVNSQYDQLOADNMIAMIHAADKRVHIREAYLPESVI 943
Db 890 EKLEWETNVIYKEAKESVDALFVNSQYDQLOADNMIAMIHAADKRVHIREAYLPESVI 949
QY 944 PGVNVDIFELKGRIFTAFFLYDARNVKNKGDFNGLSCNVKGVHVDVEGNHRSVLV 1003
Db 950 PGVNAALFELEGRIFTAFSLYDARNVKNKGDFNGLSCNVKGVHVDVEGNHRSVLV 1009
QY 1004 PEWEAEVSQEVRCVPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVEEYVP 1063
Db 1010 PEWEAEVSQEVRCVPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVEEYVP 1069
QY 1064 NTVTCNDYTANOQEBYGAYSRNREGYDETGSNSVPAADVASVYEEKSYTDGRDNPCES 1123
Db 1070 NTVTCNDYTANOQEBYGAYSRNREGYDETGSNSVPAADVASVYEEKSYTDGRDNPCES 1129
QY 1124 NRGYGDYPLPAGVYKVELEFPETDKVWTEIGETGTFIVDSVELLLEE 1174
Db 1130 NRGYGDYPLPAGVYKVELEFPETDKVWTEIGETGTFIVDSVELLLEE 1180

RESULT 3
ID Q45736 PRELIMINARY; PRT; 1176 AA.
AC Q45736;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Insecticidal crystal protein.
GN CryIA(A).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FU-2-7;
RA Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
RT "Cloning and nucleotide sequencing of two insecticidal delta-endotoxin
RL genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
RN Agric. Biol. Chem. 51:455-463(1987).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FU-2-7;
RX MEDLINE=94289859; PubMed=7764972;
RA Udayasuriyan V., Nakamura A., Mori H., Masaki H., Uozumi T.;
RT "Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain
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RT FU-2-7 and analysis of chimaeric CryIA(a) proteins for toxicity.";
RL Biosci. Biotechnol. Biochem. 58:830-835(1994).
DR EMBL; D17518; BAA04468.1; -.
DR HSP; P02963; IC1Y.
DR Interpro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
FT CONFLICT 77 77 L -> P (IN REF. 1).
FT CONFLICT 965 965 S -> F (IN REF. 1).
SQ SEQUENCE 1176 AA; 133075 MW; AA4135B4A289F85 CRC64;
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Query Match 69.3%; Score 4328; DB 2; Length 1176;

Best Local Similarity 71.4%; Pred. No. 2.9e-285;

Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;

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QY 1 MENNIO-NOCVPYNCLANPEVEIILNEER-STGRPLDLSISLTLRFLSEFVPGVGVAFGL 58
Db 1 MDNPNFNECIPYNCLSNPEVEILGGERIETGYTPDISLTOFLSERFVPGAGFVLGL 60
QY 59 FDLTWGFTTSDWSLFLQLEOLLEORLETLEARNKAITTLRGLADSYEITYEALREWEAN 118
Db 61 VDIITWIFGFSQWDAFLVQLEQLINQRIEERFARQAISRLEGLSNLQIYAESFREHAD 120
QY 119 PNNAQLREDVRIRFANTDDALITAINNFTLTSTFPIPLSVYVQAANLHLSLLRDVAFSG 178
Db 121 PTNPALREEMRIQFDMNSALTTPILLAYQYQVPLSVYVQAANLHLSVLRDVSFVGQ 180
QY 179 GWGLDIATVNNHYNRLNLHRYTKHCLDIYNOGLENRGTNTQWARFNQFRDLILTV 238
Db 181 RWGPDATINSRYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDWVRYNQFRELTIV 240
QY 239 LDIVALPNVDVRYPTQTSQLTREIYTSVIEDSPVSANIPNGF---NRAEFGVRRP 294
Db 241 LDIVALSNDSRXYPRTVTSQLTREIYTNVLE-----NFDGSRGMAORIQNIRP 294
QY 295 HLMDFMNSLFVTAETVRSQTVWGHLYSSR--NTAGNRINFPYSYGVNPGGAI--WIADE 350
Db 295 HLMDLNSITITVDHRGFNVYSGHQITASPVGSGPEFAFLFG--NAGNAAPVLVSL 352
QY 351 DPRFYFTLSDPVVR-----GGFGNPHYVLGLRGVAPQQTGCTNHTRT-FRNSGTIDSLD 404
Db 353 TGLGIFRTLSPYRRRIILGSGPNQNELFVLDGTETFSASLTTLNPLSTIYRQGRDVTSLD 412
QY 405 EIPQDQSGAPWNDYSHVLNHVTVVRWPGETSGS-DSWRAPWFSWTHESATPTIDPER 463
Db 413 VIPQDQSNVPPRAGFSRLSHVTML---SQAGAVYVLRFTFSQWHSRAEFNIIIPSSQ 469
QY 464 ITQIPLVKAHTLQSGTIVYVRGFTGDIILRRISPGQISTLRVNITAPLSQRYVRIRYA 529
Db 470 ITQIPLTKSTNLGSGTSVVKGPQGTGDIILRRISPGQISTLRVNITAPLSQRYVRIRYA 529
QY 524 STTNLRIVYVAGERIFAGQFNKMTMDGDLTFCQSFYATINTAFTFPMQSSSTVAGDT 583
Db 530 STTNLFQHTSIDGRPINQGNFSAATMSSGNLQSGSFRTVGTFFPNFSGSSVFTLSAHV 589
QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAVNALFTSINQIGIKTDVTDYHIDQVSN 643
Db 590 FNSGNEVYIDRIEVPVPAEYFVPAEYDLERAKAVNELFTSSNQIGLKTVDYDIDQVSN 649
QY 644 LVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 703
Db 650 LVECLSEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQ 709
QY 704 GDDVFKENYVTLPGTFDECPTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 763
Db 710 GDDVFKENYVTLGTFDECPTYLYQKIDESKLPYTRYQLRGVIEDSODLEIYLIRYA 769
QY 764 KHETVNVLGTGSLWPLSVQSPIRKCGPNRCAPHELNWPDLDSCRDGCKCAHSHHFS 823
Db 770 KHETVNPGTGLWPLSAQSPIGKCGPNRCAPHELNWPDLDSCRDGCKCAHSHHFS 829
QY 824 DIDVGCDDLNEGLDWWVIFIKITQDGHARLGNLEFLBEKPLVGEALARKVRAEKKWRDK 883
Db 830 DIDVGCDDLNEGLDWWVIFIKITQDGHARLGNLEFLBEKPLVGEALARKVRAEKKWRDK 889
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QY 884 EKLEETNIVYKEAKESVDALFVNSQYDQADTAMTHAADKRVHRIRREAYLPESLVI 943
DB 890 EKLEETNIVYKEAKESVDALFVNSQYDQADTAMTHAADKRVHRIRREAYLPESLVI 949
QY 944 PGVNDVIFELKGRIFTAFFLYDARNVKNQDFNNGLSQWNVKGVHVDVEEQNNHRSVLV 1003
DB 950 PGVNAAFEELEGRISTAFSLYDARNVKNQDFNNGLSQWNVKGVHVDVEEQNNHRSVLV 1009
QY 1004 PEWEAEVSEVRCVPCRGYILVYATYKEGYGEGCVTHIEIENNTDELKFSNCVEEYTPN 1063
DB 1010 PEWEAEVSEVRCVPCRGYILVYATYKEGYGEGCVTHIEIENNTDELKFSNCVEEYTPN 1069
QY 1064 NTVTCNDYTAQEEYGGAYTSNRNGYDETYGSSVPADYASVYEKSYTDGRDNPCEP 1123
DB 1070 NTVTCNDYTAQEEYGGAYTSNRNGYDETYGSSVPADYASVYEKSYTDGRDNPCEP 1125
QY 1124 NRGYDYTPLPAGYVTKLEYFPPETDKVWIEIGETGTFIVDSVELLME 1174
DB 1126 NRGYDYTPLPAGYVTKLEYFPPETDKVWIEIGETGTFIVDSVELLME 1176

RESULT 4
Q9RC30 PRELIMINARY: PRT: 1176 AA.
AC Q9RC30;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 135 kDa insecticidal protein.
OS Bacillus thuringiensis (subsp. kurstaki).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=29339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-1-02;
RA Hou B.K., Chen Z.H.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF154676; AAD5382.1; -
DR HSSP: P02965; 1CIY.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1176 AA; 133010 MW; FCEE069D0B81D8C4 CRC64;

Query Match 69.1%; Score 4312; DB 2; Length 1176;
Best Local Similarity 71.2%; Pred. No. 3.6e-284;
Matches 848; Conservative 85; Mismatches 226; Indels 32; Gaps 12;

QY 1 MERNIO-NOCVPVNCNNPVEILNEER-STGRPLDLSLDRFLLSSEFPVGVGVAFL 58
DB 1 MDNPNINECIPYNCLNPNPEVLGGRIETGTPDLSLQFLLSSEFPVGVGVAFL 60
QY 59 FDLWGFTPSDMSFLQIEQIEORIEYLRNRAITTLRGLADSYEYIEALREWEAN 118
DB 61 VDIWIGFGPSQWDTFLVQIEQLINRIERFARNQALSLEGLSNLYQIYAFREWEAD 120
QY 119 PNNQALREDFRISFANTDDALITAINFTLSFEIPLLSYVQAAHLHLSLRLDAYSFG 178
DB 121 PTPNALREEMKRIOFNDKNSALTAPILLAVQNYOVLPSVYVQAAHLHLSLRDXSVFG 180
QY 179 GWGLDIATVNNHYNRLNHRHTKCHLDYTNQGLENRGNTLRQWAFNRQFRDLTLTV 238
DB 181 RWGFDATINSRYNDLFLIGNYTDYAVRYNTGLERVWGPDSRDVRYNQFRDLTLTV 240
QY 239 LDIVALFNVDRYPTIOTSQTREYTSVIEDSPVSANINPGF----NRAEFGVRPP 294
DB 241 LDIVALFNSDRYPTIRTSQTREYTSVIEDSPVSANINPGF----NFDGSRGMAQRIEQNIQ 294
QY 295 HLMDFMNSLFVTAETVRSQTVGWGHLYSSR--NTAGNRINPSPGVFNPGGAI--WIAE 350
DB 295 HLMDFMNSLTIYDVHGFNWSGHQITASPVGFGPEFAFLFG--NAGNAAPPVIVSL 352

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QY 351 DPRPFYTLSDPVEVR-----GQFGNPHYVLGRGVAFOQTGTHNHT-FRNSETIDSLD 404
DB 353 TGLGIFRTLSPLRYRRIILGSGPNNQBELFVLDGTETEFASILTTLNLPSTIYRQRTVDSLD 412
QY 405 EIPQDNGSPWINDYSHVNLHVTEVRWPGELSGS-OSWRAPMFSWTHRSATPNTIDPER 463
DB 413 VIPQDNSVPPRAGFSHRLGHVTML---SOAGAVYFLRAPTFMQHRSFAENNIIPSSQ 469
QY 464 ITQIPLVKAHTLQSGTWRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIRYA 523
DB 470 ITQIPLKSTNLGSGTSVYKPGFTGGDILRTSPGOISTLRVNTAPLSQRYEVIRYA 529
QY 524 STTNLRIVTVAGSRIIPAGOFNKTMDGTBLTFQSPYATINATFTFPMQSQSFTVADT 593
DB 530 STTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFTVGTFTTFPNSGSSVFTLSAHV 589
QY 584 FSSGNEVYIDREFELIPYATATFEAYDLERAKAVNALFTSINOIGIKTDTVDTHIDOVN 643
DB 590 FNSGNEVYIDREFVPAEVTEAYDLERAKAVNELFTSSNQLGLKTDVTHIDOVN 649
QY 644 LVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITQIR 703
DB 650 LVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITQIR 709
QY 704 GDDVFKENYVTLPGTFDECYPTLYLQKIDSKLAPYTRYQLRGVIEDSQDLEYLIRYNA 763
DB 710 GDDVFKENYVTLPGTFDECYPTLYLQKIDSKLAPYTRYQLRGVIEDSQDLEYLIRYNA 769
QY 764 KHEVNVLTGSLWPLSVOSPIRKGEPNRCAPHLNPNLDCCSRGDKCAHSHHFS 823
DB 770 KHEVNVLTGSLWPLSAQSPIGKGEPNRCAPHLNPNLDCCSRGDKCAHSHHFS 829
QY 824 DIDVGTDLNEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVKAQKWDKR 883
DB 830 DIDVGTDLNEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVKAQKWDKR 889
QY 884 EKLEETNIVYKEAKESVDALFVNSQYDQADTAMTHAADKRVHRIRREAYLPESLVI 943
DB 890 EKLEETNIVYKEAKESVDALFVNSQYDQADTAMTHAADKRVHRIRREAYLPESLVI 949
QY 944 PGVNDVIFELKGRIFTAFFLYDARNVKNQDFNNGLSQWNVKGVHVDVEEQNNHRSVLV 1003
DB 950 PGVNAAFEELEGRIFTAFSLYDARNVKNQDFNNGLSQWNVKGVHVDVEEQNNHRSVLV 1009
QY 1004 PEWEAEVSEVRCVPCRGYILVYATYKEGYGEGCVTHIEIENNTDELKFSNCVEEYTPN 1063
DB 1010 PEWEAEVSEVRCVPCRGYILVYATYKEGYGEGCVTHIEIENNTDELKFSNCVEEYTPN 1069
QY 1064 NTVTCNDYTAQEEYGGAYTSNRNGYDETYGSSVPADYASVYEKSYTDGRDNPCEP 1123
DB 1070 NTVTCNDYTAQEEYGGAYTSNRNGYDETYGSSVPADYASVYEKSYTDGRDNPCEP 1125
QY 1124 NRGYDYTPLPAGYVTKLEYFPPETDKVWIEIGETGTFIVDSVELLME 1174
DB 1126 NRGYDYTPLPAGYVTKLEYFPPETDKVWIEIGETGTFIVDSVELLME 1176

RESULT 5
Q9L877 PRELIMINARY: PRT: 1189 AA.
AC Q9L877;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Toxin CryIcA6.
GN CRXIC6.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2-F;

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RA Yu J., Pang Y., Li J.;
RT "Cloning and sequence analysis of the cryIcA6 gene from *Bacillus*
RT *thuringiensis*, strain A2-P.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF215647; AAF37224.1;
DR HSP: P02965; ICIY.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1189 AA; 134685 MW; 98F8C1D978DF9451 CRC64;

Query Match 67.4%; Score 4209.5; DB 2; Length 1189;
Best Local Similarity 68.6%; Pred. No. 3.4e-277;
Matches 830; Conservative 99; Mismatches 224; Indels 57; Gaps 17;
QY 1 MENNIOQCVPYCNLNNPEVEILNEER-STGRPLDLSLTRELLSFEVPGVAGFLP 59
Db 1 MEENNQOCIPYCNLSNPEVEILLGERISTGSSIDLSLVQLVSNFVPGGFLVGLI 60
QY 60 DLWGFITPDSWLSFLQIEQLIQRITLERNRAITTLRGLADSYEIIYIALREWEANP 119
Db 61 DFVWGIQVPSQWDAFLQIEQLINERAEFARNAAIANLEGUNNFNIYVEAFKEWEDP 120
QY 120 NNAQLREDVRIRFANTDALTAINNETLTSTFEPLSLSVYVQAAHLSSLRDVSGQG 179
Db 121 NNPAIRTRVIDRFRILDGLRDPISFRISGFVEPLLSVYAAQAANHLAIURDSVIFGER 180
QY 180 WGLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGTNTROWARENOPRRDLTLVL 239
Db 181 WGVTTINVENYRILRHIDYADHCANTYNRGLNLPKSYQDWITTYNRRLDITLVL 240
QY 240 DIVALFNYDRTYPIQTSSTLREIYTSVIEDSP---VSANIPGNFNRAE-FCVRPPH 295
Db 241 DIAAFFPNYDNRRYPIQVPGQLTREYTDPLINFPQLSVAQLPT-PNVMESSAIRNPH 299
QY 296 LMDPNSLFTVTAE--TVRSQTWGHVLSRNTAGRNINFPESYGVNPGGAIWADEDP- 352
Db 300 LFDILNLTITFDVSGRNFYWGHRVYISSLIGGNITSPIYG-----REANQEP 351
QY 353 -----RPEYRTLSDPV--FVRGFGFNPHYVL-GLRGVAFQGTGTHHPTFRNSGTDSL 403
Db 352 RSFTFNGVGFVTLNPNYLRLLQQWPAPPFNLRGVEGVF-STPTN-SFTYRGRTVDLSL 409
QY 404 DEIPPQDSGAPWNDYSHLVNHTVFRWPGISGSDSWRAP-----MFSWTHRSATPTN 457
Db 410 TELPEDNSVPPREGYSHRCHAFVQRSG-----TFPLTGVVFSWTHRSATLTN 460
QY 458 TIDPERITQPLVKAHQLQSGTTVVYRGPGFTGGILLRTSGGPAYTIVNGLQLPQYR 517
Db 461 TIDPERINQPLVGRFVWGTSTVITGPGFTGGDLIRNTFGDFVSLQVNSIPITQYR 520
QY 518 ARIRYASTNLRIVV-TVAGERIEFAGQ-----FNKMTMDTGDTLTFQSFYATINTAFTF 570
Db 521 LRFRYASSRDARVILVTCASGTGGVGGQVSVNMPLOKTMIEIGENLTSRTFRYTDSPNPSF 580
QY 571 PMSOSSTV-----GADTFSSGNEVIDRELIPVTAFAEYDLERAQKAVNALFTSI 624
Db 581 RANPDITIGISRRPLFGAGSISG-ELYIDKTEIILADATPEAESDLERAQKAVNALFTSS 639
QY 625 NOIGIKTDVTDYHIDQVSNLVDCSLDERCLDEKSELSEKVKHAKLSLDERNLLQDPNFKG 684
Db 640 NOIGLKTVDVTDYHIDQVSNLVDCSLDEFCLDEKSELSEKVKHAKLSLDERNLLQDPNFRG 699
QY 685 INRQLDRGWRGSTDITIQRGDDVFENKENVTLPGTFDECYPTLYOKIDESKLKPYRYOL 744
Db 700 INRPDRGWRGSTDITIOGGDDVFKENVTLPGTVDECYPTLYQKIDESKLKATRYEL 759
QY 745 RGYIEDSODLEIYLIRYNAKHETVNVLTGSLWPLSVSPKRCGCEPNRCAPHLEWNPDL 804
Db 760 RGYIEDSODLEIYLIRYNAKHEIVNVPGTGSILWPLSAQSPGCKGCEPNRCAPHLEWNPDL 819
QY 805 DCSRDGEKCAHHSHHFLSDIDVGCSTDLNEDLDVWVFIKTIQDGHARLGNLEFLKPL 864
Db 820 DCSRDGEKCAHHSHHFLSDIDVGCSTDLNEDLDVWVFIKTIQDGHARLGNLEFLKPL 879

QY 865 VGEALARVKRAEKKWRDKREKLELETRNIVYKEAKESVDALFVNSQYDQLQADTNIAIHA 924
Db 880 LGEALARVKRAEKKWRDKREKLOLETRNIVYKEAKESVDALFVNSQYDRLQVDTNIAIHA 939
QY 925 ADKRVRHIREAYLPESLVPGVNVDIIFELGRIFTAFFLYDARNVIKNGDFNNGSLCWN 984
Db 940 ADKRVRHIREAYLPESLVPGVNAAIPEELGRIFTAYSLYDARNVIKNGDFNNGSLCWN 999
QY 985 VKGHVDYEEQNHRSLVLPWEAEVSOEVRVCPGRGIVILVATYKKEGYGCGCTIHEIE 1044
Db 1000 VKGHVDYEEQNHRSLVLPWEAEVSOEVRVCPGRGIVILVATYKKEGYGCGCTIHEIE 1059
QY 1045 NNTDELAFSCNVEEVPNNVTCTNDYTANOEYGGAYTSNRGVDYETSGNSSVPADYA 1104
Db 1060 DNTDELAFSCNVEEVPNNVTCTNNTIGTQEEYEGYSSRNQGYDEAFGNPSPADYA 1119
QY 1105 SVYEKSYTDGRRDNPCESNRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETGTIV 1164
Db 1120 SVYEKSYTDGRRDNPCESNRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETGTIV 1179
QY 1165 DSVELLIMEE 1174
Db 1180 DSVELVIMEE 1189
RESULT 6
Q9F296 PRELIMINARY; PRT; 1155 AA.
ID Q9F296 AC Q9F296;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Delta endotoxin.
OS *Bacillus thuringiensis*.
OC Bacteria; Firmicutes; *Bacillus*/Clostridium group; Bacillales;
OC Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Meza-Basso L.A., Theoduloz C.;
RT "Cloning and expression of a delta endotoxin gene from a Chilean
RT native *Bacillus thuringiensis* strain."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U94191; AAG16877.1; -
DR HSP: P02965; ICIY.
DR InterPro: IPR001178; Endotoxin.
DR Pfam: PF00555; endotoxin; 1.
SQ SEQUENCE 1155 AA; 130557 MW; 5D69E3E2F527749D CRC64;

Query Match 67.1%; Score 4192.5; DB 2; Length 1155;
Best Local Similarity 69.7%; Pred. No. 4.7e-276;
Matches 827; Conservative 85; Mismatches 230; Indels 45; Gaps 9;

QY 1 MENNIO-QVCVPYCNLNNPEVEILNEER-STGRPLDLSLTRELLSFEVPGVAGFLP 58
Db 1 MDNPNNECIPYCNLSNPEVEILGGERIETGYTPIDISLITQFLISEFVPGAGFLGL 60
QY 59 FDLWGFITPDSWLSFLQIEQLIQRITLERNRAITTLRGLADSYEIIYIALREWEAN 118
Db 61 VDIWGFIPGSQWDAFLVQIEQLINQRITLERNRAITTLRGLADSYEIIYIALREWEAN 120
QY 119 PNNALREDVRIRFANTDALTAINNETLTSTFEPLSLSVYVQAAHLSSLRDVSGQG 178
Db 121 PTNPALEEMRIQFNDMNSALTALPLFAVONYQVPLSLSVYVQAAHLSSLRDVSGQG 180
QY 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDYNQGLNLRGTNTROWARENOPRRDLTLVL 238
Db 181 RWGFDAAITNSRYNDLRELIGNYTDHVRWYNTGLERWVGPDSDRWIRYNGFRRELITV 240
QY 239 LDIVALFPNVDRYPIQTSSTLREIYTSVIEDSPSVANIPGNFNA-----BFGVRPP 294
Db 241 LDIVSLFPNYSRTYPIRTVSQLTREIYTNVLE-----NFDGSRGSAQIGSIRSP 294

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QY 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPFSGYVF--NPGGAIWADIAD 351
D 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPFSGYVF--NPGGAIWADIAD 351
QY 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407
D 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407
QY 355 GCGVYTLSTLRYFPNFGINNOQLSLVDGTGFAYGTSNLPSSAVYRKSGTVDLSDEIP 414
D 355 GCGVYTLSTLRYFPNFGINNOQLSLVDGTGFAYGTSNLPSSAVYRKSGTVDLSDEIP 414
QY 408 PQNSGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467
D 408 PQNSGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467
QY 415 PQNNVPPRQGFSLHSHVMSFSGSNSSVSIIRAPMSWTHRSATPTNTIDPERITQI 474
D 415 PQNNVPPRQGFSLHSHVMSFSGSNSSVSIIRAPMSWTHRSATPTNTIDPERITQI 474
QY 468 PLVKAHTLQSGTVVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527
D 468 PLVKAHTLQSGTVVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527
QY 475 PLTKSTNLGSGTSVYKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534
D 475 PLTKSTNLGSGTSVYKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534
QY 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587
D 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587
QY 535 LQFHTSIDGRPINQGNFSAITSSGSLQSGFTVGTFTPFNFSGSVFTLSAHVFNSSG 594
D 535 LQFHTSIDGRPINQGNFSAITSSGSLQSGFTVGTFTPFNFSGSVFTLSAHVFNSSG 594
QY 588 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647
D 588 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647
QY 595 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654
D 595 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654
QY 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707
D 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707
QY 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714
D 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714
QY 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767
D 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767
QY 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774
D 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774
QY 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 827
D 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 827
QY 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 808
D 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 808
QY 828 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 887
D 828 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 887
QY 809 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 868
D 809 GCTDNLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLE 868
QY 888 LETNIVYKEAKESVDALFVNSOYDQLOADNTIAMHAADKRVHRIEAYLPVLSVPGVN 947
D 888 LETNIVYKEAKESVDALFVNSOYDQLOADNTIAMHAADKRVHRIEAYLPVLSVPGVN 947
QY 869 WETNIVYKEAKESVDALFVNSOYDQLOADNTIAMHAADKRVHRIEAYLPVLSVPGVN 928
D 869 WETNIVYKEAKESVDALFVNSOYDQLOADNTIAMHAADKRVHRIEAYLPVLSVPGVN 928
QY 948 VDIPELAKGRIFTAFPLDYDARVNIKNGDFNGLSCWNVKGVHVDSEONNHRSLVVPWE 1007
D 948 VDIPELAKGRIFTAFPLDYDARVNIKNGDFNGLSCWNVKGVHVDSEONNHRSLVVPWE 1007
QY 929 AAIFEELEGRISTAFSLDYDARVNIKNGDFNGLSCWNVKGVHVDSEONNHRSLVVPWE 988
D 929 AAIFEELEGRISTAFSLDYDARVNIKNGDFNGLSCWNVKGVHVDSEONNHRSLVVPWE 988
QY 1008 AEVSQEVRCVGRGVLRYTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1067
D 1008 AEVSQEVRCVGRGVLRYTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1067
QY 989 AEVSQEVRCVGRGVLRYTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1048
D 989 AEVSQEVRCVGRGVLRYTAYKEGEGCVTIHEIENNTDELKFSNCVEEYVYNNVT 1048
QY 1068 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASVYBEKSYTDGRRDNPCCSNRGY 1127
D 1068 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASVYBEKSYTDGRRDNPCCSNRGY 1127
QY 1049 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASVYBEKSYTDGRRDNPCCSNRGY 1108
D 1049 CNDYTANOEYGGATSNRNGYDETYGSSNVPADYASVYBEKSYTDGRRDNPCCSNRGY 1108
QY 1128 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1174
D 1128 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1174
QY 1109 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1155
D 1109 GDTPLPAGYVTKELYEPETDKWIEGTGEGTGTIVDSVLELLMEE 1155

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RESULT 7

Q93T21

ID Q93T21

AC Q93T21

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Crystal protein CryIAb16

GN CRYIAB16

OS Bacillus thuringiensis (subsp. israelensis).

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillaceae; Bacillus.

OX NCBI_TaxID=1430;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=407;

RA Yu J., Tan L., Wu D., Pang Y.;

RT "Molecular characterization of a silent gene encoding a 130-kilodalton

crystal protein from *Bacillus thuringiensis* subsp. *israelensis*."

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF375608; AAK55546.1; -

DR InterPro; IPR001178; Endotoxin.

DR Pfam; PF00555; endotoxin; 1.

SQ SEQUENCE 1155 AA; 130747 MW; 7F0C98E0100C7698 CRC64;

Query Match

Best Local Similarity 67.0%; Score 4186.5; DB 2; Length 1155;

Mismatches 826; Conservative 85; Mismatches 231; Indels 45; Gaps 9;

QY 1 MENNIO--NOCVPYCNLNNEPEVEILNEER--STGRPLDLDLSLTRLFLLSFVPGVGAFL 58

D 1 MENNIO--NOCVPYCNLNNEPEVEILNEER--STGRPLDLDLSLTRLFLLSFVPGVGAFL 58

QY 59 FDLIMGFITPDSWLSFLQLIEQRIETLERNRAITTLRGLADSYEIVIALREWEAN 118

D 59 FDLIMGFITPDSWLSFLQLIEQRIETLERNRAITTLRGLADSYEIVIALREWEAN 118

QY 61 VDIIMGIFGSPQWDAFLVOIEQLINQRIEFAFNQAISRLGSLNLYQIYAFSFEWEAD 120

D 61 VDIIMGIFGSPQWDAFLVOIEQLINQRIEFAFNQAISRLGSLNLYQIYAFSFEWEAD 120

QY 119 PNNALREDVRIRFANTDDALTAINNLTSTFELPSSVVOAANLHLLRLDAYVFGQ 178

D 119 PNNALREDVRIRFANTDDALTAINNLTSTFELPSSVVOAANLHLLRLDAYVFGQ 178

QY 121 PTPNALREEMRIQFNDMSALTAIPFAVQNVYVPLLSVYVQAVNLHLSVLRDLVFGQ 180

D 121 PTPNALREEMRIQFNDMSALTAIPFAVQNVYVPLLSVYVQAVNLHLSVLRDLVFGQ 180

QY 179 GGLDITATVNNHYNLNLHRYTKHCLDLYNOGLNLTGNTROWARENQPRDLTLIV 238

D 179 GGLDITATVNNHYNLNLHRYTKHCLDLYNOGLNLTGNTROWARENQPRDLTLIV 238

QY 181 RGFDAATATNSYNDLTRIGNYTDHAWRYNTGLERVMGDPDSRDWIRYNQFRRLTLV 240

D 181 RGFDAATATNSYNDLTRIGNYTDHAWRYNTGLERVMGDPDSRDWIRYNQFRRLTLV 240

QY 239 LDVALFPNYDVRTPIQTSOLTRFYSSTVEDSPVSANIPNGFNRA---EFQVRPE 294

D 239 LDVALFPNYDVRTPIQTSOLTRFYSSTVEDSPVSANIPNGFNRA---EFQVRPE 294

QY 241 LDVLSLFPNYSRTPIRTVSQTLREIYNPVL-----NFDGFRGSAQIEGSI 294

D 241 LDVLSLFPNYSRTPIRTVSQTLREIYNPVL-----NFDGFRGSAQIEGSI 294

QY 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPFSGYVF--NPGGAIWADIAD 351

D 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPFSGYVF--NPGGAIWADIAD 351

QY 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407

D 352 PRPFYTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTTSDLSDEIP 407

QY 355 GCGVYTLSTLRYFPNFGINNOQLSLVDGTGFAYGTSNLPSSAVYRKSGTVDLSDEIP 414

D 355 GCGVYTLSTLRYFPNFGINNOQLSLVDGTGFAYGTSNLPSSAVYRKSGTVDLSDEIP 414

QY 408 PQNSGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467

D 408 PQNSGAPWNDYSHVNLNHYTVFVRWPGCEISGDSWRAPMSWTHRSATPTNTIDPERITQI 467

QY 415 PQNNVPPRQGFSLHSHVMSFSGSNSSVSIIRAPMSWTHRSATPTNTIDPERITQI 474

D 415 PQNNVPPRQGFSLHSHVMSFSGSNSSVSIIRAPMSWTHRSATPTNTIDPERITQI 474

QY 468 PLVKAHTLQSGTVVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527

D 468 PLVKAHTLQSGTVVVRGPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 527

QY 475 PLTKSTNLGSGTSVYKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534

D 475 PLTKSTNLGSGTSVYKPGFTGGDILRTSGGPFAYTIVNINGQLPQRYRARIYASTTN 534

QY 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587

D 528 LRIYVTVAGERIFAGQFNKTMGTGDLPTFQSPSYATINTAFTFPMSSQSTFVGADTFSSG 587

QY 535 LQFHTSIDGRPINQGNFSAITSSGSLQSGFTVGTFTPFNFSGSVFTLSAHVFNSSG 594

D 535 LQFHTSIDGRPINQGNFSAITSSGSLQSGFTVGTFTPFNFSGSVFTLSAHVFNSSG 594

QY 588 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647

D 588 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 647

QY 595 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654

D 595 NEVYIDRFELIPVTAFEAEDYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVC 654

QY 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707

D 648 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 707

QY 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714

D 655 LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQGGDV 714

QY 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767

D 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 767

QY 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774

D 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHET 774

QY 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 827

D 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 827

QY 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 808

D 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 808

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QY 828 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKWKDRKREKLE 887
Db 809 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKWKDRKREKLE 868
QY 888 LETNIVYKAKESVDALFVNSQYDQLOADNTAMIHAADKRVHRIEAYLPESLVPGVN 947
Db 869 WETNIVYKAKESVDVAVFVNSQYDQLOADNTAMIHAADKRVHRIEAYLPESLVPGVN 928
QY 948 VDFEELKGRIFTAFPLXDARNVKNKGDFNGLSCWNVKGVHDVEQNHRSLVLYVPEWE 1007
Db 929 AAFEELEGRIITAFSLYDARNVKNKGDFNGLSCWNVKGVHDVEQNHRSLVLYVPEWE 988
QY 1008 AEVSQVRVPCPGYILRVYATYKEGEGCVTHIENNTDELKFSNCVEEYIPNNVT 1067
Db 989 AEVSQVRVPCPGYILRVYATYKEEYEGCVTHIENNTDELKFSNCVEEYIPNNVT 1048
QY 1068 CNDYANQOEYGGATSRNRGDEYTGSSNSVPADYASVYEKSYTDGRDNPCEENRGY 1127
Db 1049 CNDYATQOEYEGTYSNRGDEYTGSSNSVPADYASVYEKSYTDGRDNPCEENRGY 1108
QY 1128 GDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLMEE 1174
Db 1109 GDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLMEE 1155

RESULT 8
Q9S514
ID Q9S514 PRELIMINARY; PRT: 1176 AA.
AC Q9S514;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE Insecticidal crystal protein.
GN CRY1
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C12;
RA Osman Y.A., Ibrahim M.A., Ashour S.A., Bulla L.A. Jr.;
RT "Nucleotide sequence and expression of a cry gene from Bacillus
RT thuringiensis strain C12.";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF081790; RAD46139.1;
DR HSP; P02965; IC1Y
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
SQ SEQUENCE 1176 AA; 133038 MW; 280654B3EDBF8C8 CRC64;

Query Match 67.0%; Score 4184; DB 2; Length 1176;
Best Local Similarity 69.6%; Pred. No. 1.8e-275;
Matches 829; Conservative 88; Mismatches 242; Indels 32; Gaps 12;

QY 1 MENNIQ-NOCVPYNCLNPEVEILNEER-STGRPLDIDLSLTFLLSEFPVGVGVAFLG 58
Db 1 MDNPNINCEIPNCLNSPEVEVLGERIETGYTPDIDLSLTFLLSEFPVGVGVAFLG 60
QY 59 FDLINGFIPDSWLSLLOLQIEORIETLERNRAITLRLGLADSYEYIEALREWEAN 118
Db 61 VDIWGIFGFSQMDAFVQTEQLNQRIEFAFNQAIKSLGSLNLYQIYAESFREWEAD 120
QY 119 PNAQLREDVRITFANTDALITAINNFTLSEIFLLSVYQAAHLHLRLDAYSFGQ 178
Db 121 PTPALREMRQFNDMSALTAIFLLAVQNVQVPLLSVYQAAHLHLRLDAYSFGQ 180
QY 179 GWGLDIATVNNHYNLNLINLHRYTKCLDTYNOGLENLKTNTROWARENDFRDLTLTV 238
Db 181 RWGFDATINSRNDLTRIGNYTDYAVRWNTGLSRVWGPDSRWRYNQFRRELTIV 240
QY 239 LDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVANIPNGF---NRAEFGVRPP 294

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Db 241 LDIVALFNSYDSRRYPIRTVSQLTREIYNPVL-----NEDGSFRGMAQRIETPEYRQP 294
QY 295 HLMDFNLSLVFAETVRSQTVWGHVLSRR--NTAGNRINFPSPSYGVNPGGAI--WIADE 350
Db 295 HLMDIILSIYTDVHURGFNYSHQITTSFVGSGFEFAFLFG--NAGNAAPPVLVSL 352
QY 351 DRRPFYRTSLSDPVEFV-----GGFGNPHVYVGLRGVAFQQTGNHRT-PRNSTGIDSLD 404
Db 353 TGLGIFRTLSPPYRKLIIILGSGPNNQELFVLDGTESFASLTNLNSTIYRQRTGVDLSD 412
QY 405 ETPPDQNSGAPWMDYGHVNLNHNVTFFVWPGEISGS-DSWRAPMFSWTHRSATPTNTIDPER 463
Db 413 VIPPDQNSVPPRAGFSHRLSHVPEML--SQAGAVVTLRASLFLRLDPSAEFNIIPSFT 469
QY 464 IQQIPLVKAHTLOSQTVVYRGPGFTGGDILRLRTSGGFFAYTVININGQLPQRVARIYA 523
Db 470 NYQIPTKSTNLGSGTSVYKPGFTGGDILRLRTSPGLISTLRVNIITAPLSQRYRARIYA 529
QY 524 STTNLIYVTVAGERIFAGQFNKMTDGTPLTFQSFSYATINTAFTFPMQSSFTVGADT 583
Db 530 STTNLFHTSIDGRPINQGNFYATMSSGSLQSGSFTVGFTFPFNSGSSVFTLSAHV 589
QY 584 FSSGNEVYIDREFELIPVTATFEAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSN 643
Db 590 FNSGNEVYIDRIEFVPAEYTFEAEYDLERAQNGVNOFLTSSNOIGLTKDGTDYHIDQVSN 649
QY 644 LVDCLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNPKGINRQLDGRWGRTDITIQ 703
Db 650 LVECLSDFCLEKRELSEKVKHAKRLSDERNLLQDPNPKGINRQLDGRWGRTDITIQ 709
QY 704 GDDVFKEVNTLPGTDECYPTLYOKIDESKLKPYTRYOLRGYIEDSODLEYLLRYNA 763
Db 710 GDDVFKEVNTLLGTDECYPTLYOKIDQSKLKATSTQLRGYIEDSODLEYLLRYNA 769
QY 764 KHETVNLGTSLWPLSVQSPIRKGEPNRCAPHLBNPDLDCSCRDGKCAHSHHFSL 823
Db 770 KQOTVNVPGTSLWPVSAKPIGKGEPNRCAPHLBNPDLDCSCRDGKCAHSHHFSL 829
QY 824 DIDVGTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKWKDRK 883
Db 830 DIDVGTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARKKWKDRK 889
QY 884 EKLEETNIVYKAKESVDALFVNSQYDQLOADNTAMIHAADKRVHRIEAYLPESLVI 943
Db 890 EKLEETNIVYKAKESVDALFVNSQYDQLOADNTAMIHAADKRVHRIEAYLPESLVI 949
QY 944 PGVNVDFEELKGRIFTAFPLXDARNVKNKGDFNGLSCWNVKGVHDVEQNHRSLV 1003
Db 950 PGVNAAFEELEGRIITAFSLYDARNVKNKGDFNGLSCWNVKGVHDVEQNHRSLV 1009
QY 1004 PEKEAEVSQVRVPCPGYILRVYATYKEGEGCVTHIENNTDELKFSNCVEEYIPN 1063
Db 1010 PEKEAEVSQVRVPCPGYILRVYATYKEGEGCVTHIENNTDELKFSNCVEEYIPN 1069
QY 1064 NTVTCNDYATNQEYGGATYSNRGDEYTGSSNSVPADYASVYEKSYTDGRDNPCE 1123
Db 1070 NTVTCNDYATNQEYGGATYSNRGDEYTGSSNSVPADYASVYEKSYTDGRDNPCE 1125
QY 1124 NRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLMEE 1174
Db 1126 NRGYRDYTGIPVGYVTKLEYFPETDKVWIEIGETEGTFTIVDSVELLMEE 1176

RESULT 9
O06894
ID O06894 PRELIMINARY; PRT: 1171 AA.
AC O06894;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUL-1997 (TremBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE CRY1e4.
GN CRY1e4.

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Db	645	VECSDFECLDEKRELSEKVKHAKRLSDERNLQDPNFRGINQPDGRWGSGDITIQGG	704
Qy	705	DDVFKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGVIEDSQDLEIYLIRYNAK	764
Db	705	DDVFKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGVIEDSQDLEIYLIRYNAK	764
Qy	765	HETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD	824
Db	765	HETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD	824
Qy	825	IDVGCITDLNEDLDVWVTFKIKTODGHARLGNLFLEBEKPLVGGALARVKAERKKWRDKE	884
Db	825	IDVGCITDLNEDLDVWVTFKIKTODGHARLGNLFLEBEKPLVGGALARVKAERKKWRDKE	884
Qy	885	KLELFTNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHRIREAYLPELSVIP	944
Db	885	KLELFTNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHRIREAYLPELSVIP	944
Qy	945	GVNYDIEPEELKGRIFTAFYLDARNVKNKGFNGLSCWNVKGHDVBEQNHRHRSVLVVP	1000
Db	945	GVNAAIEEELGRIFFAFSLYDARNVKNKGFNGLSCWNVKGHDVBEQNHRHRSVLVVP	1000
Qy	1005	EWEAEVSQEVRCGRGYILRVYAYKEGYGEGCVTHETENNTDELKFSNCVEEYYPNN	1066
Db	1005	EWEAEVSQEVRCGRGYILRVYAYKEGYGEGCVTHETENNTDELKFSNCVEEYYPNN	1066
Qy	1065	TVTCNDYTANOQEVGGAYTSRNGYDITYGNSVSPADYASVYEEKSYTGDRDRNPESN	1122
Db	1065	TVTCNNYATQAEHEGYTSRNGYDEAYESNSV---HASVYEEKSYTDRRENPCSN	1122
Qy	1125	RGYDYLPLPAGVYKTELEVEPDTDKVWIEIGETGCTFIVDSVELLMEE	1174
Db	1122	RGYDYLPLPAGVYKTELEVEPDTDKVWIEIGETGCTFIVDSVELLMEE	1171
RESULT 10			
Q45735 PRELIMINARY; PRT; 1177 AA.			
ID	Q45735	PRELIMINARY;	PRT; 1177 AA.
AC	Q45735;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	Delta-endotoxin.		
OS	Bacillus thuringiensis.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;		
OC	Bacillaceae; Bacillus.		
OX	NCBI_TaxId=1428;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RA	MEDLINE=91197102; PubMed=2014985;		
RA	Von Tersch M.A., Robbins H.L., Jany C.S., Johnson T.B.;		
RT	"Insecticidal toxins from Bacillus thuringiensis subsp. keneae: Gene		
RT	cloning and characterization and comparison with B. thuringiensis		
RT	subsp. kurstaki CryIA(c) toxins."		
RL	Appl. Environ. Microbiol. 57:349-358(1991).		
RL	EMBL; M35524; AAA22338.1; -		
DR	HSSP; P02965; ICIV.		
DR	InterPro: IPR001178; Endotoxin.		
DR	Prfam; PF00555; endotoxin; 1.		
SQ	SEQUENCE 1177 AA; 133114 MW; C81F76D03F3BCCB5 CRC64;		
Query Match 66.5%; Score 4151.5; DB 2; Length 1177;			
Best Local Similarity 69.3%; Pred. No. 3e-273;			
Matches 834; Conservative 82; Mismatches 232; Indels 55; Gaps			

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QY 119 PNAQLREDVRIREFANTDADALITANNFTLSFEIPLLSVYVQANLHSLRLDRAVSFGQ 178
Db 121 PTPALREEMRIQNDMSALTTPALLAVQNYQVPLLSVYVQANLHSLRLDRAVSFGQ 180
QY 179 GWGLDIATVNNHYNRLINLHRYTKHCLDVTYNOGLENLGRNTQWARFNQFRRLDLTV 238
Db 181 RWGFDAAATINSRYNDLRLIGNYTDHAWRWYNTGLERWVGPDSDRWVYNGFRRLDLTV 240
QY 239 LDIVALPNVDVRYPTQTSQTLREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
Db 241 LDIVALPNVDVRYPTQTSQTLREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
QY 295 HLMDFMNSLFTVTAETVRSQTVMGCH--LVSSKNTAGNRINPSPVGVF-NPGGAIWIAD 351
Db 295 HLMDFMNSLFTVTAETVRSQTVMGCH--LVSSKNTAGNRINPSPVGVF-NPGGAIWIAD 351
QY 352 PRPYRTLSDPFVVGFGF---NPHYVLGRGVAFQO-TGTN-HTRFRNSGTIDSDEI 406
Db 355 GQGYRTLSS--TFYRRFPNIGINNQQQLSVLDGTEFAVGTSSNLPSAVYRKSGTVDLDEI 413
QY 407 PPQNSGAPWNDYSHVLNHTVFRWPGBEISGSDS----WRAPMFSWTHRSATPTNTDPE 462
Db 414 PPQNNVPPRQGFSHRLSHVSMFR-----SGSSSVSIIIRAPMFSWTHRSAEFNITASD 468
QY 463 RITQIPLVKAHTLOSQGTVVRGPGFTGGDILRRTSGGPFAYTIVNING-----QLP---- 513
Db 469 SITQIPAVKGNFLENG-SVISGPGFTGGDILRLSSGN-----NIQNGVIEFPIHPS 521
QY 514 --QRYRARIYASTNRLIYVTVAGERIFAGQFNKTMGTGDTPLTFQFSYATINTATFP 571
Db 522 TSRYRVRYASVTPPHLVNMGNSIFSNTVPATATSLDNLQSSDGEYFESANAF-- 579
QY 572 MSQSFVVGADTFSSGNEVYIDRELIPVATPEAYDRLERAQKAVNALFTSINOIGIKT 631
Db 580 --SSLGNIVGVNRFSGTGAIVIIDREFIPVATPEAYDRLERAQKAVNALFTSTNQLGLK 638
QY 632 DVTYHIDQVSNLVDCLSDPEFCDEKRELSKVHAKRLSDERNLLODPNFKGINRQLDR 691
Db 639 NVTYHIDQVSNLVTCLSDPEFCDEKRELSKVHAKRLSDERNLLODPNFKGINRQLDR 698
QY 692 GWRGSDTITQGGDVFKEKENVTLPGTFDECYPTLYOKIDESKLPKPYTRYQLRGYIEDS 751
Db 699 GWRGSDTITQGGDVFKEKENVTLPGTFDECYPTLYOKIDESKLPKPYTRYQLRGYIEDS 758
QY 752 ODLEIYLIRYNAKHETVNVLTGSLWPLSVQSPTRKCGEPNRCAPHLEWNPDLDCSRDG 811
Db 759 ODLEIYLIRYNAKHETVNVLTGSLWPLSAQSPIGKCGEPNRFAPHLEWNPDLDCSRDG 818
QY 812 EKCAHSHHFLSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLFLERKPLVGEALAR 871
Db 819 EKCAHSHHFLSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLFLERKPLVGEALAR 878
QY 872 VKRAEKWKROKREKLEETNIVYKEAKESVDALFVNSQYDQLOADTNITAMTHAADKRVHR 931
Db 879 VKRAEKWKROKREKLEETNIVYKEAKESVDALFVNSQYDQLOADTNITAMTHAADKRVHS 938
QY 932 IREAYLPELSIPGVNVDIPEELKGRIFTAPFLYDARNVKNQDNFNGLSCWNKGVHDV 991
Db 939 IREAYLPELSIPGVNAAIFEELEGRIPTAFSLYDARNVKNQDNFNGLSCWNKGVHDV 998
QY 992 EQQNHRSVLVPEWEAEVSEVRCVPCGRGILRVATYKEGYGCGCVTHIEIENNTDLK 1051
Db 999 EQQNHRSVLVPEWEAEVSEVRCVPCGRGILRVATYKEGYGCGCVTHIEIENNTDLK 1058
QY 1052 FSNCEVEEVPNNVTNCNDXTANOEYGGAYTSRNRGYDETYGSSNVPADYASVYEKS 1111
Db 1059 FSNCEVEEVPNNVTNCNDXTANOEYGGAYTSRNRGYNEA---PSVPADYASVYEKS 1114
QY 1112 YDGRGNPCBSNRYGQDYPPLPAGYVTKLEYEPTDKWIEIGETGTFIVDSVELLL 1171
Db 1115 YDGRGNPCBSNRYGQDYPPLPAGYVTKLEYEPTDKWIEIGETGTFIVDSVELLL 1174
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QY 1172 MEE 1174
Db 1175 MEE 1177
PRELIMINARY; PRT; 1177 AA.
ID Q03743
AC Q03743; 1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 135 kDa CRYSTAL protein (Delta endotoxin) (CRYSTALINE ENTOMOCIDAL
DE protoxin).
GN CRYIA(C)3.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Feitelson J.S.;
RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART OF
CC THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-
CC TERMINUS.
DR EMBL; M73248; AAA22339.1; -.
DR HSP; P02965; ICIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1177 AA; 133156 MW; FDB2E6C1BB909DAF CRC64;
Query Match 66.4%; Score 4145.5; DB 2; Length 1177;
Best Local Similarity 69.2%; Pred. No. 7.5e-273;
Matches 83; Conservative 83; Mismatches 232; Indels 55; Gaps 18;
```


Db 944 YLPESLVIPGVNAAIFEELEGRIETAFSLYDARNVIKNGDFNGLSCWNKGHVDEBQN 1003
 Qy 996 NHRSLVVPWEAEVQSVRVCPCRGYILRVYAYKEGEGCVTHIEINNTDELKFSNC 1055
 Db 1004 NQSRSLVVPWEAEVQSVRVCPCRGYILRVYAYKEGEGCVTHIEINNTDELKFSNC 1063
 Qy 1056 VEEVYIPNTVTCNDYTNQEEYGGAYTSRRNGYDETYGNSVSPADYASVYEKSYTDG 1115
 Db 1064 VEEVYIPNTVTCNDYTNQEEYGGAYTSRRNGYNEA---PSVPADYASVYEKSYTDG 1119
 Qy 1116 RDNPCSNRGYDTPPLPAGYVTKELSYFFETDKWIEIGETEGTFIVDSVELLMEE 1174
 Db 1120 RENPCSNRGYDTPPLPAGYVTKELSYFFETDKWIEIGETEGTFIVDSVELLMEE 1178

RESULT 13
 Q45768 PRELIMINARY: PRT: 1178 AA.
 AC Q45768;
 DT 01-NOV-1996 (TremBLrel. 01, Created)
 DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
 DE Gene, complete cds.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PS85A1;
 RA Feltelson J.S.;
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M73249; AAA73077.1; -
 DR HSPF; P02965; ICYI.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 SQ SEQUENCE 1178 AA; 133296 MW; 1336524F410E8863 CRC64;

Query Match 66.3%; Score 4142; DB 2; Length 1178;
 Best Local Similarity 69.0%; Pred. No. 1.3e-272;
 Matches 827; Conservative 85; Mismatches 242; Indels 44; Gaps 14;

Qy 1 MENNIQ-NOCYPYCNLPNPEVEILNEER-STGRKLPDLSLSTRLLSEFPVGVGVAFLG 58
 Db 1 MDNPNINECPYCNLPNPEVEILNEER-STGRKLPDLSLSTRLLSEFPVGVGVAFLG 60
 Qy 59 FDLWGFTPSDWSFLQIEOLISQRIETLERNRAITTLRGLADSYEYIIPALREWEAN 118
 Db 61 VDIWGFSPQSDWFLQIEOLISQRIETLERNRAITTLRGLADSYEYIIPALREWEAN 120
 Qy 119 PNAOLREDVRIRANTDALTATNNFTLTSFEIPLLSVYVOAANLHLSLRDAVSFGQ 178
 Db 121 PTNPALEMRIRQFNDMSALTATPLAVQNYQVPLSVYVOAANLHLSLRDAVSFGQ 180
 Qy 179 GWGLDIATVNNHYNRLINLHRYTHKCLDITYNOGLENLGTNTROWARNQFRDLITLV 238
 Db 181 RWGFDAAINSYNDLTRIGNYTDYAVRWYNTGLRWGPDSDRWYRNOFRRLTLTV 240
 Qy 239 LDIVALFNYDVRTPIQTSOLTRTEITSSVIEDSPSANTPNFGNRA----EFGVRPP 294
 Db 241 LDIVALFNYDVRTPIQTSOLTRTEITSSVIEDSPSANTPNFGNRA----EFGVRPP 294
 Qy 295 HLMDFPNSILFVTAETVRSOTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWADED 351
 Db 295 HLMDFPNSILFVTAETVRSOTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWADED 354
 Qy 352 PRPFYRTLSDPVEFVRG---GFGNPHY-VLGLRGVAFQOTGTNHTFRNSGTIDSLDETP 407
 Db 355 GGVYRTLSLTLYRPPNFINGINQQLSVLDGTEFYAGTSSNLPASVYKSGVDSLDEIP 414
 Qy 408 PODNSGAPWNDYSHLVNHVTFVRWPEIGSGSDSRAPMFSWTHRSATPTNTIDPRITQI 467
 Db 415 PGNVVPVPRQGSFRLSHVSMFRSGFSNSVSIIRAPMFSWTHRSATPTNTIDPRITQI 474

Qy 468 PLVKAHTLQSGTVTVRPGCFGTGGDILRRTSGGFFAYTIVNING----QLP-----QRY 516
 Db 475 PAVKGNFLPENG-SVISGPGFTGGDLVRLNSSN-----NIONRGYIEVPFIHPPSTSY 527
 Qy 517 RARIRYASTTNLRITYTVAGERIFAGQFNKMTMDGPTLTFQSFYSYATINTAFTFPMQS 576
 Db 528 RVRVRYASVTPIHLNVMNGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT---SSLG 584
 Qy 577 FTVGADTFSSGNEVYIDREFELIPVTATPEAEYDLERAKAVNALFTSINQIGIKTDVTDY 636
 Db 585 NIVGVNFSGTAVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGKTNVTDY 644
 Qy 637 HLDQVSNLVDCLSDREFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGNRLDRGWRGS 696
 Db 645 HLDQVSNLVTLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRPEKRWGGS 704
 Qy 697 TDITIQRGDDVFEKENYVTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSDLEI 756
 Db 705 TGITIQGGDDVFEKENYVTLSGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSDLEI 764
 Qy 757 YLIRYNAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDDLDCSRDGEKCAH 816
 Db 765 YLIRYNAKHETVNVLTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDDLDCSRDGEKCAH 824
 Qy 817 HSHHFSLDIDVCGTDLNEDLVWVIFKIKTQDGHARLGNLEFLSEKPLVGEALARKRAE 876
 Db 825 HSHHFSLDIDVCGTDLNEDLVWVIFKIKTQDGHARLGNLEFLSEKPLVGEALARKRAE 884
 Qy 877 KWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHIREAY 936
 Db 885 KWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHIREAY 944
 Qy 937 LPESLVIPGVNVDIFEELKGRIFTAFPLYDARNVIKNGDFNGLSCWNKGHVDEEQQN 996
 Db 945 LPESLVIPGVNAAIFEELEGRIETAFSLYDARNVIKNGDFNGLSCWNKGHVDEEQQN 1004
 Qy 997 HRSVLVPEWEAEVQSVRVCPCRGYILRVYAYKEGEGCVTHIEINNTDELKFSNCV 1056
 Db 1005 QRSVLVPEWEAEVQSVRVCPCRGYILRVYAYKEGEGCVTHIEINNTDELKFSNCV 1064
 Qy 1057 EBEVYIPNTVTCNDYTNQEEYGGAYTSRRNGYDETYGNSVSPADYASVYEKSYTDGR 1116
 Db 1065 EBEVYIPNTVTCNDYTNQEEYGGAYTSRRNGYNEA---PSVPADYASVYEKSYTDGR 1120
 Qy 1117 RDNPCSNRGYDTPPLPAGYVTKELSYFFETDKWIEIGETEGTFIVDSVELLMEE 1174
 Db 1121 RENPCSNRGYDTPPLPAGYVTKELSYFFETDKWIEIGETEGTFIVDSVELLMEE 1178

RESULT 14
 Q93TF9 PRELIMINARY: PRT: 1160 AA.
 AC Q93TF9;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
 DE Insecticidal crystal protein.
 GN CRYIDB.
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B-Pr-88;
 RA Li C., Zhang J., Huang D., Li G.;
 RL "A crystal endotoxin from Bt strain B-Pr-88."
 DR Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF358862; AAK48937.1; -
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 SQ SEQUENCE 1160 AA; 130952 MW; B18B04193D87695E CRC64;

Query Match		66.2%; Score 4136; DB 2; Length 1160;
Best Local Similarity		69.1%; Pred. No. 3.3e-272;
Matches	816; Conservative 98; Mismatches 239; Indels 28; Gaps 15;	
Qy	1	MENNIOQCVNCLNNPEVEILNEER-STGRPLDLSLTLFLSEFVPGVAGFLP 59
Db	1	MDINHQCIPYCNLSPAILDAERLETGNVADISLGLINFLYSNFPVGGFTVGLL 60
Qy	60	DLWGFTPPSDWSIFLLOLEQLEORLETLERNRAITLRLGLADSYEIIYIARWEANP 119
Db	61	ELWGFVGPSCWEFLQACIQQLSQRLEEFARNQALSRLEGLSNFYIITETFRWKEPD 120
Qy	120	NNAQLREDVRIRFANTDDALITAINFTLTSFEIPLLSVYVQAANLHLSLLRDVAFSGG 179
Db	121	SNPALREEMTQFNVMNSALITAIPLLRVNVYVALLSVYVQAANLHLSVLRDVSYGOR 180
Qy	180	WGLDIATVNNHYNELNLIHRYTKHCLDTYNOGLENLGCTNTQWARFNOFRDLTLTVL 239
Db	181	WGFDPATVNNRYSDLTRLIHYTDHCVIYDGLKNLEGRSLSDWVYVNRFRRLTISVL 240
Qy	240	DIVALEPNYDVRTPYQTSQLETRITSVIEDSPVS--ANIPNGFNRAEFG-VRPPLH 296
Db	241	DIIAFPNPDIEAYPIQTASQLETRITSVIEDSPVS--ANIPNGFNRAEFG-VRPPLH 299
Qy	297	MDPNSLFTVAETVRSQTVWGGHLYSS--RNTAGNRINPFSYG-VFNPGCAIWIADDEPR 353
Db	300	VDLNFTIYDTSALAYWGGHLYSS--RNTAGNRINPFSYG-VFNPGCAIWIADDEPR 359
Qy	354	PFYRTSDPVEFGFNGFNHYVGLGRVAFQOQGTNHTFTFRNSGTIDSLDEPPQDNGS 413
Db	360	PIPRTLS--YFT--GLNNPNVAGIEGVEQNTISR--SIYRSGPIDSFSELPQDVS 413
Qy	414	APNDYSHVNLHVTVRWKPEIGSGSWRAPMFSWTHRSATPTNTIDPRTIQLPVKAH 473
Db	414	SPAIGYSHRCHATTFLF--RISG-PRIAGTVFSWTHRSASPIVNEVSPSRITQIPWKAH 469
Qy	474	TLOGGTVWRGPGFTGGDILRRYSGGFAYTIVNINQGLPQRYAKIRIYASTNLRIYVT 533
Db	470	TLASGASVKGPGFTGGDILTRNSMGDLGALRVFTGRLPQSYIIFRYASVANRSGTFR 529
Qy	534	VAGERIFAGQNKMDPGLTFTQSTSYATINTAFTPMQSSFTVAGADFTSSGNEVYID 593
Db	530	YSQPSYGIQPKTMDAGEALTSFAHTTLFTPTFSRAQEEDL---YIQSG--VYID 584
Qy	594	RFELIPVATFEARYDLERAKAVNALETSINOIGIKTDYDHIQVSNLVDCLSDDEC 653
Db	585	RIFELIPVATFESEINLERAKAVNALETSINOIGIKTDYDHIQVSNLVDCLSDDEC 644
Qy	654	LDEKRELSEKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDITIQGDDVFKENYV 713
Db	645	LDEKRELSEKVKHAKRLSDERNLLQDPNFKINRQPDGRGWRGSTDITIQGDDVFKENYV 704
Qy	714	TLPGTDECTPYLYQKIDESKLKPYTRYQYRGYIEDSQLEIYLIRYNAKHETVNLGT 773
Db	705	TLPGTDECTPYLYQKIDESKLKPYTRYQYRGYIEDSQLEIYLIRYNAKHETVNLGT 764
Qy	774	GSLWPLSVQSPGIRKCGEPNRCAPLHWNPDLCSCRCGECAHSHHFDLDIDWGCTDLN 833
Db	765	GSLWPLSVQSPGIRKCGEPNRCAPLHWNPDLCSCRCGECAHSHHFDLDIDWGCTDLN 824
Qy	834	BDLVWVIFKTKTDQGHARGLNLEFLEKPLVGBALARVRAEKWKDKREKLELEFNIV 893
Db	825	BDLVWVIFKTKTDQGHARGLNLEFLEKPLVGBALARVRAEKWKDKREKLELEFNIV 884
Qy	894	YKEAKESVDALFVNSQDQLOADNMIAMIAADRVIRIERYALPELSPVGVNDFEE 953
Db	885	YKEAKESVDALFVNSQDQLOADNMIAMIAADRVIRIERYALPELSPVGVNDFEE 944
Qy	954	LKGRIFTAFYLDARNYIKNGDFNNGLSWNVKGHVDVEQNNHRSVLVVPWEAEVSQE 1013
Db	945	LEGRIFTAFYLDARNYIKNGDFNNGLSWNVKGHVDVEQNNHRSVLVVPWEAEVSQE 1004
Qy	1014	VRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVBEVYPNNTVTCNDYTA 1073
Db	1005	VRVCPGRGYILRVTAAYKEGYGEGCVTTHEVNDNTDELKFSNCEQVYPGNTVACNDY-- 1062
Qy	1074	NOEYGGAYTSRNGYDETYGSSNVPADVASVVEEKSYTDGDRDPCESNRGVDYVPL 1133
Db	1063	KNHGANACSRNGYDEYESNSSIPADYVVEEAYTDGQGNPSEFNRG---HTPL 1119
Qy	1134	PAGYVTKLEYFPETDKWIEIGETEGFIVDSVELLIMEE 1174
Db	1120	PAGYVTALEYFPETDVWIEIGETEGFIVDSVELLIMEE 1160
RESULT 15		
Q9AM83		
ID	Q9AM83	PRELIMINARY; PRT; 1118 AA.
AC	Q9AM83;	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	Insecticidal crystal protein BTRX24.	
OS	Bacillus thuringiensis serovar kuntharX24.	
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;	
OC	Bacillaceae; Bacillus.	
OX	NCBI_TaxID=147284;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Nagarathnam P., Xavier R., Jayaraman K., Murugan V.;	
RT	"Characterization and full-length sequencing of insecticidal crystal	
RT	protein (cry) of novel Bacillus thuringiensis subsp. kuntharX24 and	
RT	its specific toxicity towards three economically important pests:	
RT	Spodoptera litura, Helicoverpa armigera and Plutella xylostella."	
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF27924; AAK14336.1; --	
DR	HSP; P02965; ICIY.	
DR	InterPro; IPR001178; Endotoxin.	
DR	Pfam; PF00555; endotoxin; 1.	
SQ	SEQUENCE 1118 AA; 126817 MW; 33DA5B8C2CDF059D CRC64;	
Query Match		58.0%; Score 3624.5; DB 2; Length 1118;
Best Local Similarity	66.7%; Pred. No. 1.9e-227;	
Matches	721; Conservative 88; Mismatches 227; Indels 45; Gaps 9;	
Qy	1	MENNIOQCVNCLNNPEVEILNEER-STGRPLDLSLTLFLSEFVPGVAGFLP 58
Db	1	MDNNINCEPIYCNLSNPEVEVLGERIETGYTIDISLSTOFLSEFVPGAGVGL 60
Qy	59	FDLWGTTPSDWSIFLLOLEQLEORLETLERNRAITLRLGLADSYEIIYIARWEAN 118
Db	61	VDIHWGIFGSPQWDAFLVQIEQLINQRIEFAFNQALSRLEGLSNLYQIYAESPREWAD 120
Qy	119	PNAQLREDVRIRFANTDDALITAINFTLTSFEIPLLSVYVQAANLHLSLLRDVAFSGQ 178
Db	121	PTNPALREEMRLOFNDAANSALTALPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVG 180
Qy	179	WGGLDIATVNNHYNELNLIHRYTKHCLDTYNOGLENLGCTNTQWARFNOFRDLITV 238
Db	181	RWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERWGPDSRWIRYNQFRRLTLTV 240
Qy	239	LDIVALEPNYDVRTPYQTSQLETRITSVIEDSPVSANIPNGFNA---EGVRPP 294
Db	241	LDIVALEPNYDVRTPYQTSQLETRITSVIEDSPVSANIPNGFNA---EGVRPP 294
Qy	295	HLMDPNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINPFSYGVE-NPAGCAIWIAD 351
Db	295	HLMDIINLSITITDARGEIYWSHQINASPVGSGPFTFLYGTMGNAAPQRIVAQL 354
Qy	352	PRPFVNTLSDPVVRG---GFONPHY-VLGRGVAFQOTGTNHTFTFRNSGTIDSLDEIP 407
Db	355	GGQVYRTLSSTLYRRFPNIGINNQOLSVDLGTGTFAYGTSSNLPASVYRKSGTVDLDEIP 414
Qy	408	PDNSCAPNDYSHVNLHVTVRWKPEIGSGSWRAPMFSWTHRSATPTNTIDPRTIQL 467

Db 415 PQNNVPPROGSHRLSHVSMFSGFSNSVSIIIRAPMFSNIHRSAEFNNIIPSSQITOI 474
QY 468 PLVKAHTLOSQTWVRGPGFTGGDILRRTSGPPFAYTIVNINGOLPORRYRIRYASTTN 527
Db 475 PLTKSNLNGSGTSVVKGPFTGGDILRRTSGQISIRVNIITAPLSQRYRIRYASTTN 534
QY 528 LRIYVTVAGRIIFAGOFNKMTDGLPTFQSFYAITNTAFTFPMSSQSFYVADTFSSG 587
Db 535 LQHTSIDGRPIINQGNFSATMSGSLQSAFMTVGTTPFNFSNGSSVFTLSAHVNSG 594
QY 588 NEVYIDREFELIPYATFAEYDIERAKAYNALFTSINOIGIKITDVTYHIDQVSNLVC 647
Db 595 NEVYIDREFELIPYATFAEYDIERAKAYNALFTSINOIGIKITDVTYHIDQVSNLVC 654
QY 648 LSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQGGDV 707
Db 655 LSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSDITIQGGDV 714
QY 708 FKENYVTLPGTFDECYPTIYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIIRYNAKHET 767
Db 715 FKENYVTLPGTFDECYPTIYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIIRYNAKHET 774
QY 768 VNYLGTSLWPLSVQSPDKRCGPNRCAPHLEWNPDLDCSCROGEKCAHSHHFSLDIDV 827
Db 775 VNYLGTSLWPLSVQSPDKRCGPNRCAPHLEWNPDLDCSCROGEKCAHSHHFSLDIDV 808
QY 828 GCTDLNEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLE 887
Db 809 GCTDLNEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLE 868
QY 888 LETNIVYKEAKESVDALFVNSQYDQLOADTNIAHAAKRVHRIREAYLPELSVPVGN 947
Db 869 WETNIVYKEAKESVDALFVNSQYDQLOADTNIAHAAKRVHRIREAYLPELSVPVGN 928
QY 948 VDIFFELKGRIFTAFTLYDARNVKNKGNLSCWNVKGVHDVVEQNNHRSVLVPEWE 1007
Db 929 AALFEELKGRIFTAFTLYDARNVKNKGNLSCWNVKGVHDVVEQNNHRSVLVPEWE 988
QY 1008 AEVSQEVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYPPNNTVT 1067
Db 989 AEVSQEVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYPPNNTVT 1048
QY 1068 C 1068
Db 1049 C 1049

Search completed: November 27, 2002, 20:24:22
Job time : 98 secs

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OM protein - protein search, using sw model

Run on: November 27, 2002, 17:21:14 ; Search time 37 seconds
(without alignments)
1316.033 Million cell updates/sec

Title: US-09-837-961-8
Perfect score: 6244
Sequence: 1 MENNIONQCPYNCLNPEV.....IGETGTFIVDSVELLMEE 1174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6244	100.0	1174	1	C1FA_BACTA
2	5399.5	86.5	1169	1	C1FB_BACTM
3	4424.5	70.9	1181	1	C1AE_BACTL
4	4329	69.3	1176	1	C1AA_BACTK
5	4320	69.2	1179	1	C1AD_BACTA
6	4303	68.9	1166	1	C1GA_BACTU
7	4282.5	68.6	1185	1	C1DA_BACTA
8	4230.5	67.8	1172	1	C1HA_BACTU
9	4224.5	67.7	1169	1	C1GB_BACTZ
10	4223.5	67.6	1189	1	C1CA_BACTE
11	4211.5	67.4	1155	1	C1AB_BACTK
12	4173	66.8	1171	1	C1EA_BACTX
13	4148	66.4	1178	1	C1AC_BACTK
14	4146	66.4	1160	1	C1DB_BACTU
15	4134	66.2	1176	1	C1CB_BACTG
16	4127.5	66.1	1155	1	C1HB_BACTM
17	4098	65.6	1176	1	C1AG_BACTU
18	4025.5	64.5	1167	1	C1JA_BACTU
19	3874	62.0	1174	1	C1EB_BACTA
20	3788	60.7	1170	1	C1JB_BACTU
21	3690	59.1	1215	1	C1KA_BACTM
22	3552.5	56.9	1229	1	C1BB_BACTU
23	3465	55.5	1228	1	C1BA_BACTK
24	3437.5	55.1	1233	1	C1BC_BACTM
25	3411	54.6	1231	1	C1BD_BACTZ
26	3376	54.1	1227	1	C1BE_BACTU
27	2633	42.2	911	1	C1AF_BACTU
28	2138.5	34.2	1138	1	C7AB_BACUK
29	2129.5	34.1	1138	1	C7AA_BACTU
30	2126.5	34.1	1138	1	C7AB_BACUA
31	2006.5	32.1	1157	1	C8AA_BACUK
32	1947.5	31.2	1157	1	C9CA_BACTO
33	1922.5	30.8	1169	1	C8BA_BACUK

34	1838	29.4	1150	1	C9EA_BACTA	Q92nl9	Bacillus th
35	1825.5	29.2	1169	1	C9DA_BACTP	O06014	Bacillus th
36	1713.5	27.4	1163	1	CQAA_BACTF	Q9x597	Bacillus th
37	1685.5	27.0	1160	1	C8CA_BACTG	Q45706	Bacillus th
38	1630.5	26.1	1156	1	C9AA_BACTG	Q99031	Bacillus th
39	1597.5	25.6	1109	1	CSAA_BACTF	Q9x682	Bacillus th
40	1519	24.3	1136	1	C4AA_BACTI	P05519	Bacillus th
41	1495.5	24.0	1180	1	C4BA_BACTI	P16480	Bacillus th
42	1367	21.9	719	1	CLIB_BACTE	Q45709	Bacillus th
43	1360	21.8	719	1	CLIA_BACTK	Q45752	Bacillus th
44	1328.5	21.3	719	1	CLID_BACTU	Q9xdl1	Bacillus th
45	1302	20.9	719	1	CLIC_BACTU	O87404	Bacillus th

ALIGNMENTS

RESULT 1

ID	C1FA_BACTA	STANDARD;	PRT;	1174 AA.
AC	Q03746;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pesticidal crystal protein cryIaPa (Insecticidal delta-endotoxin			
DE	CRYIF(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein).			
GN	CRY1FA OR CRY1F(A) OR CRYIF.			
OS	Bacillus thuringiensis (subsp. aizawai).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1433;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-E66346;			
RX	MEDLINE=91286178; PubMed=2061280;			
RA	Chambers J.A., Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,			
RA	Gawron-Burke C.;			
RT	"Isolation and characterization of a novel insecticidal crystal			
RT	protein gene from Bacillus thuringiensis subsp. aizawai.";			
RL	J. Bacteriol. 173:3966-3976(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NRRL B-18484 / PS811;			
RT	Payne J.M., Sick A.J.;			
RT	"Bacillus thuringiensis isolate active against lepidopteran pests, and			
RT	genes encoding novel lepidopteran-active toxins.";			
RL	Patent number US5188960, 23-FEB-1993.			
CC	-1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT			
CC	EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.			
CC	-1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING			
CC	SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART			
CC	OF THE SPORE COAT.			
CC	-1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE			
CC	N-TERMINUS.			
CC	-1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M63897; AAA22348.1; -			
DR	EMBL; M73254; AAA22347.1; -			
DR	HSSP; P02965; IC1Y.			
DR	InterPro; IPR001178; Endotoxin.			
DR	Pfam; PF00555; endotoxin; 1.			
KW	Toxin; Sporulation.			
SQ	SEQUENCE 1174 AA; 133621 MW; B51E9751D7F91C61 CRC64;			
	Query Match 100.0%; Score 6244; DB 1; Length 1174;			
	Best Local Similarity 100.0%; Pred. No. 0;			

Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNNIQOCVPYCNLNNPEVEILNEERS*GRPLDLSLSTRFLLSSEFVPGVGVAFLGD 60
 Db 1 MNNNIQOCVPYCNLNNPEVEILNEERS*GRPLDLSLSTRFLLSSEFVPGVGVAFLGD 60
 QY 61 LIWGFTTSDWSLFLQLIQLEQLTETLERNRAITTLRGLADSYEIIYEALREWEANPN 120
 Db 61 LIWGFTTSDWSLFLQLIQLEQLTETLERNRAITTLRGLADSYEIIYEALREWEANPN 120
 QY 121 NQALREDVIRANTDDALITAINFTLTSFEIPLSVYVQAANLHLSLLRDVAFSGQW 180
 Db 121 NQALREDVIRANTDDALITAINFTLTSFEIPLSVYVQAANLHLSLLRDVAFSGQW 180
 QY 181 GDIIATVNNHYNRLNLHRYTHKCLDVTYNOGLENLRTNTQWARFNQFRDLTLTVID 240
 Db 181 GDIIATVNNHYNRLNLHRYTHKCLDVTYNOGLENLRTNTQWARFNQFRDLTLTVID 240
 QY 241 IVALPPNDVTRYPITQTSQTLREIYTSVIEDSPVSANIPNGENKRAEGVRRPHLMDFM 300
 Db 241 IVALPPNDVTRYPITQTSQTLREIYTSVIEDSPVSANIPNGENKRAEGVRRPHLMDFM 300
 QY 301 NSLFTVTAETVRSQTVWGHLYSSRNAGNINFPISYGVNPGGAIWIADDPFRFYRTLS 360
 Db 301 NSLFTVTAETVRSQTVWGHLYSSRNAGNINFPISYGVNPGGAIWIADDPFRFYRTLS 360
 QY 361 DPVVRGFGFNPHYVGLRGVAFQOTGTHHTFRNSGTIDSLDRIPODNGSAPWNDYS 420
 Db 361 DPVVRGFGFNPHYVGLRGVAFQOTGTHHTFRNSGTIDSLDRIPODNGSAPWNDYS 420
 QY 421 HVLNHTVTRVWPGEISGSDSRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
 Db 421 HVLNHTVTRVWPGEISGSDSRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
 QY 481 VVRGPGFTGGILLRTSGGPAYITVINGQLPQYRARIYASTNLRIVYVAGERIF 540
 Db 481 VVRGPGFTGGILLRTSGGPAYITVINGQLPQYRARIYASTNLRIVYVAGERIF 540
 QY 541 AGQNKMTDGTDLTFQSFVATINTATFPMQSOSFVAGADTFSSGNEVYIDREFLIPV 600
 Db 541 AGQNKMTDGTDLTFQSFVATINTATFPMQSOSFVAGADTFSSGNEVYIDREFLIPV 600
 QY 601 TATFAEYDLERAQKAVNALETINSIQIGIKTDVTDHYDQVSNLVDCLSDFCDEKREL 660
 Db 601 TATFAEYDLERAQKAVNALETINSIQIGIKTDVTDHYDQVSNLVDCLSDFCDEKREL 660
 QY 661 SEKYKAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDVFKENVYTLPGTFD 720
 Db 661 SEKYKAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDVFKENVYTLPGTFD 720
 QY 721 ECPYTYLYQKIDESKLPYTRYQLRGYTEDSODLEIYLIRYNAKHETVNVLTGSLWPLS 780
 Db 721 ECPYTYLYQKIDESKLPYTRYQLRGYTEDSODLEIYLIRYNAKHETVNVLTGSLWPLS 780
 QY 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHFLSDIDVGCITDINEDLDVWV 840
 Db 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHFLSDIDVGCITDINEDLDVWV 840
 QY 841 IFKTKTODGHARLGNLEFELEKPLVGEALARKVRAEKWRDKREKLETVNIVYKEAKES 900
 Db 841 IFKTKTODGHARLGNLEFELEKPLVGEALARKVRAEKWRDKREKLETVNIVYKEAKES 900
 QY 901 VDALFVNSQYDQLOADNMIAMHAADKRVHRIREAYLPESLVGVNVYDIEELKGRIFT 960
 Db 901 VDALFVNSQYDQLOADNMIAMHAADKRVHRIREAYLPESLVGVNVYDIEELKGRIFT 960
 QY 961 AFFLYDARNVTKNGDFNNGLSQWNVKGVHDVVEQNNHRSVLVWPWEAEVSOEVRVCPGR 1020
 Db 961 AFFLYDARNVTKNGDFNNGLSQWNVKGVHDVVEQNNHRSVLVWPWEAEVSOEVRVCPGR 1020
 QY 1021 GYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVEEYVNNVTVCNDYTANQEEYGG 1080
 Db 1021 GYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVEEYVNNVTVCNDYTANQEEYGG 1080

QY 1081 ATTSNRNGYDETYGNSNSVPADYASVYIEKSYTDGRRDNPCESNRGYGYTLPAGYVTK 1140
 Db 1081 ATTSNRNGYDETYGNSNSVPADYASVYIEKSYTDGRRDNPCESNRGYGYTLPAGYVTK 1140
 QY 1141 ELEYFETDKVWIEGETEGTETGTFIVDSVELLMEE 1174
 Db 1141 ELEYFETDKVWIEGETEGTETGTFIVDSVELLMEE 1174

RESULT 2

CIFB_BACTM
 ID C1FB_BACTM STANDARD; PRT; 1169 AA.
 AC 066377; Q9RC19;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIb (Insecticidal delta-endotoxin
 DE CryIb(b)) (Crystalline entomocidal protoxin) (132 kDa crystal protein).
 GN CRIFB OR CRIF(b) OR CRYINA67-1.
 OS Bacillus thuringiensis (subsp. morrisoni).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_taxID=1441;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song F., Zhang J., Ding Z., Chen Z., Li G., Huang D.;
 RT "A novel cryIb gene from Bacillus thuringiensis subsp. morrisoni";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INA67;
 RA Masuda K., Asano S.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 DR EMBL; AF062350; AAF21767.1; -;
 DR EMBL; AB012288; BAA25298.1; -;
 DR HSP; P02965; LC1Y.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 DR Toxin; Sporulation.
 KW CONFLICT 338 338 V -> I (IN REF. 2).
 FT CONFLICT 382 382 G -> A (IN REF. 2).
 FT CONFLICT 1002 1002 V -> I (IN REF. 2).
 FT CONFLICT 1012 1012 E -> K (IN REF. 2).
 FT CONFLICT 1053 1053 MISSING (IN REF. 2).
 FT CONFLICT 1085 1085 G -> R (IN REF. 2).
 SQ SEQUENCE 1169 AA; 132284 MW; EFCAAF6F6EE7BC1E CRC64;

Query Match 86.5%; Score 5399.5; DB 1; Length 1169;
 Best Local Similarity 86.6%; Pred. No. 0;
 Matches 1018; Conservative 59; Mismatches 91; Indels 7; Gaps 4;

QY 1 MNNNIQOCVPYCNLNNPEVEILNEERS*GRPLDLSLSTRFLLSSEFVPGVGVAFLGD 60
 Db 1 MNNNIQOCVPYCNLNNPEVEILNEERS*GRPLDLSLSTRFLLSSEFVPGVGVAFLGD 60
 QY 61 LIWGFTTSDWSLFLQLIQLEQLTETLERNRAITTLRGLADSYEIIYEALREWEANPN 120

Db 61 LTWGFITPSEWFLQIQEQIETLERNRAITTLRGLADSYEVYLEALREWEENP 120
QY 121 NAQLREDVIRFANTDDALITAINNFTLTSFPIPLSVVQAAHLSLRLDRAVSFGQSW 180
Db 121 NAQLREDVIRFANTDDALITAINNFTLTSFPIPLSVVQAAHLSLRLDRAVSFGQSW 180
QY 181 GLDIATVNNHYNRLNLHRYTKHCLDVTYNOGLENLRTGNTQWAFNPFRRDLTLTVD 240
Db 181 GLDIATVNNHYNRLNLHRYTKHCLDVTYNOGLENLRTGNTQWAFNPFRRDLTLTVD 240
QY 241 IVALEPNDVIRPTOTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 300
Db 241 IVALEPNDVIRPTOTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 300
QY 301 NSLFTVTAETVRSQTVGGHLSVSSNTAGNINFPSPVGVNPGGAIWAIEDPRPFYRTLS 360
Db 301 NSLFTVTAETVRSQTVGGHLSVSSNTAGNINFPSPVGVNPGGAIWAIEDPRPFYRTLS 360
QY 361 DPVYRGGFGNPHYVLGRVAFQQTGNTHTFRNSGTIDSLDETPQDNSGAPNDYS 420
Db 361 DPVYRGGFGNPHYVLGRVAFQQTGNTHTFRNSGTIDSLDETPQDNSGAPNDYS 420
QY 421 HVLNHTVFWPVGEGISGDSWRAPFWSWTHRSATPNTTIDPERITQIPLVKAHTLQSGTT 480
Db 421 HVLNHTVFWPVGEGISGDSWRAPFWSWTHRSATPNTTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VYRGGFTGGDILRTSGGPEATVIVNINGOLPQRYRARIYASTNLRIVYVAGERIF 540
Db 481 VYRGGFTGGDILRTSGGPEATVIVNINGOLPQRYRARIYASTNLRIVYVAGERIF 540
QY 541 AGQFNKMTDGTDLPLFQSFYSATINTAFTPMSSQSFVTGADTFSSGNEVYIDRFELIPV 600
Db 541 OGNFORTWNRGNLSEGNFRTAGFSPFSNAQSFPLTGLTQAFSN-QEVIYDRIEFVFA 599
QY 601 TATFAEVDLERAQKAVNALFTSINQIGIKTDVTHIDQVNLVDCLSDEFCLDKREL 660
Db 601 TATFAEVDLERAQKAVNALFTSINQIGIKTDVTHIDQVNLVDCLSDEFCLDKREL 660
QY 661 SEKVHAKRLSPERNLQDPNFKGNQRLDRGRWGSTDITIGRDDVPKENVYLPGLTFD 720
Db 661 SEKVHAKRLSPERNLQDPNFKGNQRLDRGRWGSTDITIGRDDVPKENVYLPGLTFD 720
QY 721 ECPYLYXKIDESKLKPYTRYQLRGYIEDSODLEYLIRYNAKHETVNVGLTGSWLPLS 780
Db 721 ECPYLYXKIDESKLKPYTRYQLRGYIEDSODLEYLIRYNAKHETVNVGLTGSWLPLS 780
QY 781 VQSPIKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHFSLDIDVGCITDLNEDLDVWV 840
Db 781 VQSPIKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHFSLDIDVGCITDLNEDLDVWV 840
QY 841 IPKIXTQDGHARLGNLEFLEEXPLVGEALARKVRAKKKWRDKREKLELETNIVYKEAKES 900
Db 841 IPKIXTQDGHARLGNLEFLEEXPLVGEALARKVRAKKKWRDKREKLELETNIVYKEAKES 900
QY 901 VDALLFVNSQYDQADNTAMIAADKRVHRIEAYLPESLVIPGVNVDIFEELKGRIFT 960
Db 901 VDALLFVNSQYDQADNTAMIAADKRVHRIEAYLPESLVIPGVNVDIFEELKGRIFT 960
QY 961 AFELLDARVINKGNFENGLSCWNVKGVHVDVEQNHRSVLVVYVPEWAEVSQEVRCVPCR 1020
Db 961 AFELLDARVINKGNFENGLSCWNVKGVHVDVEQNHRSVLVVYVPEWAEVSQEVRCVPCR 1020
QY 1021 GYLIRVTAKEGEGCVTHIEIENNTDELK-F-SNCEVEEYVNNVTCTDNTANOEYEG 1079
Db 1021 GYLIRVTAKEGEGCVTHIEIENNTDELK-F-SNCEVEEYVNNVTCTDNTANOEYEG 1079
QY 1080 GAYTSNRGIDETYGSSNPADYASVYSEKSYTDGRDRONPCESNRGYDTPPLPAGYVT 1139
Db 1080 GAYTSNRGIDETYGSSNPADYASVYSEKSYTDGRDRONPCESNRGYDTPPLPAGYVT 1139
QY 1140 KELEYFPETDQWIEIGETEGTFIVDSVLELLMEE 1174
Db 1140 KELEYFPETDQWIEIGETEGTFIVDSVLELLMEE 1174

Db 1135 ABLEYFPETDQWIEIGETEGTFIVDSVLELLMEE 1169
RESULT 3
CIAE_BACTL STANDARD; PRT: 1181 AA.
AC Q03748;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cryIae (Insecticidal delta-endotoxin
DE CRYIAE(e) (Crystalline entomocidal protoxin) (134 kDa crystal protein).
GN CRYIAE OR CRYIA(E) OR ENDI.
OS Bacillus thuringiensis (subsp. alesti).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1440;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92011442; PubMed=1655719;
RA Lee C.S., Aronson A.I.;
RT "Cloning and analysis of delta-endotoxin genes from Bacillus
RT thuringiensis subsp. alesti".
RL J. Bacteriol. 173:6635-6638(1991).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOKULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC
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CC EMBL; M65252; AA22410.1; -
CC HSSP; P02965; ICIY.
CC InterPro; IPR001178; Endotoxin.
CC Pfam; PF00555; endotoxin; 1.
CC Toxin; Sporulation.
CC SEQUENCE 1181 AA; 133737 MW; FE86D2138C37D0FD CRC64;
Query Match 70.9%; Score 4424.5; DB 1; Length 1181;
Best Local Similarity 72.1%; Pred. No. 6.le-278;
Matches 857; Conservative 93; Mismatches 216; Indels 23; Gaps 9;
QY 1 MENNIO-NOCVPVCLNNPEVEITNEER-STGRPLDIDSLSTRFLISEFVPGVGVAFGL 58
Db 1 MDNPNKINCEIPYCNLSNPEVEVLGGERIETGYTPDIDSLSTQFLISEFVPGVGVAFGL 60
QY 59 FDLWGFITPDSWFLQIQEQIETLERNRAITTLRGLADSYEVYLEALREWEAN 118
Db 61 IDLWGFVGVQWDAFLVQIQEQIETLERNRAITTLRGLADSYEVYLEALREWEAN 120
QY 119 PNAQLREDVIRFANTDDALITAINNFTLTSFPIPLSVVQAAHLSLRLDRAVSFGQ 178
Db 121 PTPALREEMRIQFNDMSALTAIFLFTVQNVQVPLSVVQAAHLSLRLDRAVSFGQ 180
QY 179 GWGLDIATVNNHYNRLNLHRYTKHCLDVTYNOGLENLRTGNTQWAFNPFRRDLTLTVD 238
Db 181 RWGLDVAITNSYNDLTRLIGTYTDFAVRWYNTGLERVWGPDSRDWRVYNQFRELITLV 240
QY 239 LDIALFPNDVIRPTOTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 298
Db 241 LDIVSLFPPNDVIRPTOTSQTLREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 298
QY 299 FMSLFTVTAETVRSQTVGGH--LVSSRTNAGNINFPSPVGVNPGGAIWAIEDPRPF 355
Db 299 FMSLFTVTAETVRSQTVGGH--LVSSRTNAGNINFPSPVGVNPGGAIWAIEDPRPF 355

Db 299 ILNSITTYDAHGYYWYSGHQIMASPVGSGPFTTFLYXTMGNAPOQRIVQAQLGGGV 358
 QY 356 YRTLSDFEVRGGFGNGHYVLGLRG-----VAFQQTGNGHTTFSNGTIDSLDE 405
 Db 359 YRTLSL--TFYR---NP-FIIGNQBLSLVDGTFAYGSSNLPASVYRKSGTVDSLDE 412
 QY 406 IPPQDNGAPWNDYSHVLNHYTFVRNFGELSGSDSWRAPMFSWTHRSATNTIDPERIT 465
 Db 413 IPPQDNNVPPRQGFSLHSHVSMRPSGSSSVSIIRAPMFSWTHRSAEFNIIIPSSQIT 472
 QY 466 QIPLVKATHTLOSCTVVRGPGFTGGDILRTSGGPFATYVINGQIPQYRARIYAST 525
 Db 473 QIPLTSTNLGSGTVYKPGFTGGDILRTSPQGISLRLNITAPLSQRYRIRYAST 532
 QY 526 TNLRIYTVACERIFAGQFNKMTDGPLOFQSFYSYATINTAFFPMSQSFVVGADTFS 585
 Db 533 TNLQFHSIDGRPIINQGNFSATMSGGSLQSGSPRTGFTTFFNSGSSVFTLSAHVFN 592
 QY 586 SGNEVYIDRFLIPVATFAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLV 645
 Db 593 SGNEVYIDRIEFVPAVTFEAYDLERAQKAVNALFTSPNQIGLTKTDVTDYHIDQVSNLV 652
 QY 646 DCLDFCLDKRLSKVHAKLSBERNLLQDPNFKGNRLDRGWRGSTDITIOGRD 705
 Db 653 ECLDFCLDKRLSKVHAKLSBERNLLQDPNFKGNRLDRGWRGSTDITIOGRD 712
 QY 706 DVFKENYVTLPGTDECPYLYOKIDESKLPYTRYOLRGYIEDSQDLEIYLIRYNAKH 765
 Db 713 DVFKENYVTLPGTDECPYLYOKIDESKLPYTRYOLRGYIEDSQDLEIYLIRYNAKH 772
 QY 766 ETAVNLGTGSLWPLSVOSPIRKCQEPNRCAPHLWNPDLQSCDRGKCAHSHSHFSLDI 825
 Db 773 ETAVNLGTGSLWPLSVFESSIGCKEPCNRCAPHLWNPDLQSCDRGKCAHSHSHFSLDI 832
 QY 826 DVGCTDLNEDLVVWIFKIKTQDGHARLGNLEFLKPLVGEALARYKRAKKWRDKREK 885
 Db 833 DVGCTDLNEDLVVWIFKIKTQDGHARLGNLEFLKPLVGEALARYKRAKKWRDKREK 892
 QY 886 LELEFNIVYKAKESVDALFVNSYDQLOADNTAMTHADKRVHREAYLPELSVIPG 945
 Db 893 LOLEFNIVYKAKESVDALFVNSYDQLOADNTAMTHADKRVHREAYLPELSVIPG 952
 QY 946 VNVDFEELKGRIFTAFELYDARNVIKNGDFNGLSCWNVKGVHGVDEQNNHRSVLVVPPE 1005
 Db 953 VNAGIFEELGRIPTAYSLYDARNVIKNGDFNGLSCWNVKGVHGVDEQNNHRSVLVVPPE 1012
 QY 1006 WEAEVSQEVRCVPGRGYILRYTAKYEGYEGCVTHIEIENNTDELKTSNCVVEEYVNNPT 1065
 Db 1013 WEAEVSQEVRCVPGRGYILRYTAKYEGYEGCVTHIEIENNTDELKTSNCVVEEYVNNPT 1072
 QY 1066 VTCNDYTANQBEYGGAYTSRNRGYDETYGSSNVPADYASVYEKSYTDGRDNPCCSNR 1125
 Db 1073 VTCNDYTANQBEYGGAYTSRNRGYDETYGSSNVPADYASVYEKSYTDGRDNPCCSNR 1132
 QY 1126 GYGDYTPLPAGYVTKELYFPETDKVWIEIGETGTFIVDSVELLMEE 1174
 Db 1133 GYGDYTPLPAGYVTKELYFPETDKVWIEIGETGTFIVDSVELLMEE 1181

RESULT 4

C1AA_BACTK STANDARD; PRT; 1176 AA.
 ID C1AA_BACTK STANDARD; PRT; 1176 AA.
 AC P02965; P16478; P09664; Q0965; P09665;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
 DE CryIIa(a)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
 GN CRYIIA OR CRYIA(A) OR CRYIA(A) OR CRY-1-1 OR CRYA OR ICP OR CRYBNS3-1.
 OS Bacillus thuringiensis (subsp. kurstaki),
 OS Bacillus thuringiensis (subsp. aizawai),
 OS Bacillus thuringiensis (subsp. entomocidus), and
 OS Bacillus thuringiensis (subsp. sotto).

 OG Plasmid 68 Kb.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBL_TaxID=29339, 1433, 1436, 29340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.kurstaki; STRAIN=HD-1-Dippel;
 RX MEDLINE=85207613; PubMed=2581950;
 RA Schnef H.E., Wong H.C., Whiteley H.R.;
 RT "The amino acid sequence of a crystal protein from Bacillus
 RT thuringiensis deduced from the DNA base sequence.";
 RL J. Biol. Chem. 260:6264-6272(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.kurstaki; STRAIN=BNS3;
 RA Tounsi S., J'Mal A., Zouari N., Jaoua S.;
 RT "Cloning and nucleotide sequence of a novel cryIIa-type gene from
 RT Bacillus thuringiensis subsp.kurstaki.";
 RL Biotechnol. Lett. 21:771-775(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.kurstaki; STRAIN=IPL7;
 RA Simizu M., Oshie K., Nakamura K., Takada Y., Oeda K.;
 RT "Cloning and expression in Escherichia coli of the 135-kDa
 RT insecticidal protein gene from Bacillus thuringiensis subsp. aizawai
 RT IPL7.";
 RL Agric. Biol. Chem. 52:1565-1573(1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.entomocidus;
 RX MEDLINE=89098405; PubMed=2911478;
 RA Masson L., Marcotte P., Prefontaine G., Brousseau R.;
 RT "Nucleotide sequence of a gene cloned from Bacillus thuringiensis
 RT subspecies entomocidus coding for an insecticidal protein toxic for
 RT Bombyx mori.";
 RL Nucleic Acids Res. 17:446-446(1989).
 RN [5]
 RP SEQUENCE OF 1-934 FROM N.A.
 RC SPECIES=B.t.sotto;
 RX MEDLINE=85323070; PubMed=2989108;
 RA Shibano Y., Yamagata A., Nakamura N., Iizuka T., Sugisaki H.,
 RA Takanami M.;
 RT "Nucleotide sequence coding for the insecticidal fragment of the
 RT Bacillus thuringiensis crystal protein.";
 RL Gene 34:243-251(1985).
 RN [6]
 RP SEQUENCE OF 1-333 FROM N.A.
 RC SPECIES=B.t.kurstaki; STRAIN=HD-1-Dippel;
 RX MEDLINE=83109004; PubMed=6296116;
 RA Wong H.C., Schnef H.E., Whiteley H.R.;
 RT "Transcriptional and translational start sites for the Bacillus
 RT thuringiensis crystal protein gene.";
 RL J. Biol. Chem. 258:1960-1967(1983).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 33-609.
 RC SPECIES=B.t.kurstaki; STRAIN=HD-1-Dippel;
 RX MEDLINE=96059803; PubMed=7490762;
 RA Grochulski P., Masson L., Borisova S., Pusztai-Carey M.,
 RA Schwartz J.L., Brousseau R., Cygler M.;
 RT "Bacillus thuringiensis CryIIa(a) insecticidal toxin: crystal
 RT structure and channel formation.";
 RL J. Mol. Biol. 254:447-464(1995).
 CC -1- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
 CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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EMBL; J01554; ; NOT_ANNOTATED_CDS.
 DR EMBL; Y09863; CAA70856.1; -
 DR EMBL; M11250; AAA22353.1; -
 DR EMBL; D00348; BAA00257.1; -
 DR EMBL; M10917; AAA22552.1; -
 DR EMBL; X13435; CAA31886.1; -
 DR PIR; A23962; USBSXH.
 DR PIR; A22617; A22617.
 DR PIR; J02241; J02241.
 DR PIR; S02215; S02215.
 DR PIR; A22798; A22798.
 DR PDB; 1C1Y; 27-JAN-97.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 KW Toxin; Sporulation; Plasmid; 3D-structure.
 FT VARIANT 77 77 P -> L (IN STRAINS BNS3, IPL7 AND SOTTO).
 FT VARIANT 148 148 L -> F (IN STRAINS IPL7 AND SOTTO).
 FT VARIANT 302 302 S -> R (IN STRAIN SOTTO).
 FT VARIANT 918 918 Q -> R (IN STRAIN SOTTO).
 FT CONFLICT 1009 1009 V -> L (IN REF. 1).
 SQ SEQUENCE 1176 AA; 133119 MW; E2E15AF12E5DD85 CRC64;
 Query Match 69.3%; Score 4329; DB 1: Length 1176;
 Best Local Similarity 71.4%; Pred. No. 9e-272;
 Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;
 QY 1 MENNIO-NOCVNPNCLNPEVEILNEER-STGRPLDLSLSLTFLLSEFPVCGVAFGL 58
 DB 1 MDNPNINEICPNCLNPEVEILNEER-STGRPLDLSLSLTFLLSEFPVCGVAFGL 60
 QY 59 FOLLGFTPDSWELLQIEIQRITLERNRAITLRLGLADSYETIIEALREWEAN 118
 DB 61 VDIWGIFGSDWAPVQIEOLINORIEEFARNAQISRLGSLNLYQIYAESFREWEAD 120
 QY 119 PNAOLREDVRIRFANTDALLTAINNFTLSPEILSLSVYQAAHLHLLRDVAFSG 178
 DB 121 PNPALREEMRIFOEDMNSALTTAIPLLAVQNVQVLLSVYQAAHLHLLRDVAFSG 180
 QY 179 GMLGDTATNNHYNRLINLIHRYTKHCLDTYNGLENLRTNROWARENQFRDLTLV 238
 DB 181 RMGFEAATINSRYNDLRIGNYDYAVRYNTGLERVGPDSRDWRVYNQFRDLTLV 240
 QY 239 LDIVLFPNYDRTPIQTSSQLTRIEYTSVIEDSPVGSANIPNGF----NRAEFQVRPP 294
 DB 241 LDIVLFSNYDSRRYPRTVSQTLREIYNPVL-----NFDGSRGMAQRIEQNIQRP 294
 QY 295 HLMDFMNSLFVRAETVRSQTVGGHVLSSR--NTAGNRINEPSYGVFNPGGAI--WIADE 350
 DB 295 HLMDFMNSLFVRAETVRSQTVGGHVLSSR--NTAGNRINEPSYGVFNPGGAI--WIADE 350
 QY 351 DRRPYRTLSDFEVR-----GGFGNPHVVLGRVAFQQTGTNTHRT--FRNSGTIDSLD 404
 DB 353 TGLGIFRTLSPLRYRIILGSPNNQELFVLDGTETESFASLTNLTSTIYRQGTVDSLD 412
 QY 405 EIPPDQNSGAPNDYSHVNHVTVFVWQPEIGSG--DSWRAPMFSWTHRSATPTNTIDPR 463
 DB 413 VTPPDQNSVPPRAGFGRHLSHTMTL---SQAAGAVYTLRAPTFSWQHRSAEFNIIIPSSQ 469
 QY 464 ITQIPLVKAHTLQSGTVYVGGFTGGDILRLRTSGGPFATYIVNINQGLPQRYRARIYA 523
 DB 470 ITQIPLTKSTNLGSGVSVKGGFTGGDILRLRTSPQISTLRVNTAPLSQRYRARIYA 529
 QY 524 STTNLIYTVAGERIFAGQNKMTDGTPLTFQSPSYATINTAFTPPKSSQSFVAGDT 583
 DB 530 STTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRTVGTFTPPFNSGSSVFTLSAHV 589
 QY 584 FSGNGEVYIDRPELIPVATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSN 643
 DB 584 FSGNGEVYIDRPELIPVATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSN 643

DB 590 FNSGNEVYIDRPELIPVATFAEYDLERAQKAVNALFTSSNOIGIKTDVTDYHIDQVSN 649
 QY 644 LYDCLSDPECLDEKRELSKVKHAKRLSDERNLQDPNFKGINROLDRGWRGSTDITIQ 703
 DB 650 LYDCLSDPECLDEKRELSKVKHAKRLSDERNLQDPNFKGINROLDRGWRGSTDITIQ 709
 QY 704 GDDVFKENYVTLPGTFDECYPTLYQKIDESKLPKPYTRYQLRGYIEDSQDLEILYRYNA 763
 DB 710 GDDVFKENYVTLPGTFDECYPTLYQKIDESKLPKPYTRYQLRGYIEDSQDLEILYRYNA 769
 QY 764 KHTVNVLTGSLWPLSVQSPKRCGEPNRCAPHLWNPDLDCSCRDGKCAHSHHPSL 823
 DB 770 KHTVNVLTGSLWPLSVQSPKRCGEPNRCAPHLWNPDLDCSCRDGKCAHSHHPSL 829
 QY 824 DIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEPKEKPLVGEALARKVRAEKKWRDKR 883
 DB 830 DIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEPKEKPLVGEALARKVRAEKKWRDKR 889
 QY 884 EKLEETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHRIEAYLPESLVI 943
 DB 890 EKLEETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHRIEAYLPESLVI 949
 QY 944 PGVNDIFPEELKGRIFTAFPLDARNVKNGLSCWNVKGVHVDVEEQNNHRSVLV 1003
 DB 950 PGVNAIIFEELEGRIPTAFSLYDARNVKNGLSCWNVKGVHVDVEEQNNHRSVLV 1009
 QY 1004 PEWEAEVSOEVRVCGPGRVILRVAYKEGYGEGCVTHIENNTDELKPSNCVEEVPYN 1063
 DB 1010 PEWEAEVSOEVRVCGPGRVILRVAYKEGYGEGCVTHIENNTDELKPSNCVEEVPYN 1069
 QY 1064 NTVTCNDYATANOEEYGGAYTSRRNGYDEYSGNSSVPADYASVYEEKSYTDGRRDNPCES 1123
 DB 1070 NTVTCNDYATANOEEYGGAYTSRRNGYDEYSGNSSVPADYASVYEEKSYTDGRRDNPCES 1125
 QY 1124 NRGYGYDTPLPAGYVTKLEYPPETDKVWIEIGETEGTFIVDSVELLMEE 1174
 DB 1126 NRGYGYDTPLPAGYVTKLEYPPETDKVWIEIGETEGTFIVDSVELLMEE 1176
 RESULT 5
 ID CIAD_BACTA STANDARD; PRT; 1179 AA.
 AC Q03744;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cryIAD (insecticidal delta-endotoxin
 DE CryIA(d)) (crystalline entomocidal protoxin) (133 kDa crystal protein).
 GN CRYIAD OR CRYIA(D).
 OS Bacillus thuringiensis (subsp. aizawai).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1433;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-18484 / PS811;
 RA Payne J.M., Sick A.J.;
 RT "Bacillus thuringiensis isolate active against lepidopteran pests, and
 RT genes encoding novel lepidopteran-active toxins.";
 RL Patent number US5246852, 21-SEP-1993.
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC
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CC EMBL; M73250; AAA22340.1; -
DR HSSP; P02965; ICIT.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1179 AA; 133376 MW; 8BB639FCDF862FAD CRC64;

Query Match 69.28; Score 4320; DB 1; Length 1179;
Best Local Similarity 70.7%; Pred. No. 3.5e-271;
Matches 838; Conservative 101; Mismatches 222; Indels 24; Gaps 9;

QY 4 NIQOCVPYCNINPEVILNEER-STGRPLDLSLSLRELLSEFVPGVGFGLFDLI 62
DB 5 NNQOCVPYCNINPEVILNEER-STGRPLDLSLSLRELLSEFVPGVGFGLFDLI 64
QY 63 WGFITPDSWLSFLQIOLIQRIETLERNRAITLRLGLADSYEIIYALREWEANPNA 122
DB 65 WGFVPSQWDAFLVQIOLINQRIETLERNRAITLRLGLADSYEIIYALREWEADPTNP 124
QY 123 QLREVRIRFANTDALTAINNITLTSFEIPLSVVVOAANLHLSLLRDVAVSFGQWGL 182
DB 125 ALTEEMRIQFNDMSALTAIPLTVQNYQVPLSVVVOAANLHLSLVROVSFQWGF 184
QY 183 DIATVNNHYNLINLHRYTKHCLDITYNOGLENGTNRQWAFNRFRDLTLTVLDIV 242
DB 185 DVATINSYNDLRLIGTYDYAVRWYNTGLRWGDPDRWYNOFRRLTLTVLDIV 244
QY 243 ALFPNDYRTPIOTSSOLTREITSSVIEDSPVSANIPNGF---NRAEGRVPPHLM 298
DB 245 SLFPNDYRTPIOTSSOLTREITSSVIEDSPVSANIPNGF---NRAEGRVPPHLM 298
QY 299 FMNSLFTVATVRSQVYWGHLVSR--NTAGNRINPFSYVFNPGGAIWAEDPPFY 356
DB 299 LLNSTIYDVRGFRNYSGHQITASVPGFAGPEFTPRYGTMGNAAPPVLISITGLGIF 358
QY 357 RFLSDPVPVR--GGFGNPHVVLGRVAF--OQTGNTNHTRTFRNSGTDLSLDEIPQD 410
DB 359 RFLSDPVPVR--GGFGNPHVVLGRVAF--OQTGNTNHTRTFRNSGTDLSLDEIPQD 418
QY 411 NSGAPWNDYSHLVHTVVRVMPGEISGS--DSWRAPMFSTWRSHTPTNTIDPRTITQPL 469
DB 419 NSVPARAGFSLHSHVTL---SQAAGAVYTLRAFTSWRSRSEFSLNIPSSQITQPL 475
QY 470 VKAHTLQSGTVVRPGTGGDILRTSGGPFATYVNNINGQLPQVRYRYASTNLR 529
DB 476 TKSINLGSSTSVKGGTGGDILRTSGGPFATYVNNINGQLPQVRYRYASTNLR 535
QY 530 LYVTVAGRIIFAGQNKMTDGLPTFOSFSYVAINTAFTPMQSQSTYVCAQTFSSGNE 589
DB 536 FHTSDGRPIQNGFATMSGGNLQSGSFTAGFTTFNFSNGSSITFUSAHVFNSGNE 595
QY 590 VYIDFELPVTATPAEYDLERAKAYNALFTSINIGITDVTYDHYDQVSNLVDCLS 649
DB 596 VYIERIEVPAEYDLERAKAYNALFTSINIGITDVTYDHYDQVSNLVDCLS 655
QY 650 DEFCLDERKRELSEKVKHAKRLSDERNLLODQNFNGINQRLDGRWGSTDITIQGDDVFK 709
DB 656 GEFCLDERKRELSEKVKHAKRLSDERNLLODQNFNGINQRLDGRWGSTDITIQGDDVFK 715
QY 710 ENYVTLPGTFDDBCYTYLYQYIDSKLKPTRYQLRGVIEDSODLEYILRYNAKHETVN 769
DB 716 ENYVTLPGTFDDBCYTYLYQYIDSKLKPTRYQLRGVIEDSODLEYILRYNAKHETVN 775
QY 770 VLGTGSLMPLSVQSPIRKCGEPNRCAPHLNPNLDSCDRDGERCAHSHHFSLDIDVGC 829
DB 776 VPGTGSMLPVSVENPIGKGEENRCAPOLEWNPDLDCSDRGERCAHSHHFSLDIDVGC 835
QY 830 TDLNEDLDWVIFKIKTQGHARLGNLBELEKPLVGLARVRAEKWKDRKREKLELE 889
DB 836 TDLNENLGVWIFKIKTQGHARLGNLBELEKPLVGLARVRAEKWKDRKREKLOVE 895

QY 890 TNIVYKEAXESVDALFVNQYDQLOADTNIAHAAKRVHIREAYLPESLVIPGVNVD 949
DB 896 TNIVYKEAXESVDALFVNQYDQLOADTNIAHAAKRVHIREAYLPESLVIPGVNAG 955
QY 950 IFEELKGRIFTAFFLYDARNVKNGDFNGLSCWNVKGVHDVVEQNNHRSVLVPEWEAE 1009
DB 956 IFEELKGRIFTAYSLYDARNVKNGDFNGLSCWNVKGVHDVVEQNNHRSVLVPEWEAE 1015
QY 1010 VSOEVRVCPGRGYILRVATYKEGYGCGCVTHIEIENNTDELKFSNCEVEEVPNNVTVCN 1069
DB 1016 VSOEVRVCPGRGYILRVATYKEGYGCGCVTHIEIENNTDELKFSNCEVEEVPNNVTVCN 1075
QY 1070 DYTANEEYGGAYTSNRNGYDETYGSSNVPADYASYVEEYKSYTDGRDNPCESNRGYD 1129
DB 1076 DYTANEEYGGAYTSNRNGYDETYGSSNVPADYASYVEEYKSYTDGRDNPCESNRGYD 1134
QY 1130 YTPLPAGYVTKLEYPPETDKYWIETEGTEGTFIVDSVELLMEE 1174
DB 1135 YTPLPAGYVTKLEYPPETDKYWIETEGTEGTFIVDSVELLMEE 1179

RESULT 6

ID C1GA_BACTU STANDARD; PRT; 1166 AA.
AC Q45746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein crylGa (insecticidal delta-endotoxin
DE CrylGa(a)) (CrylGa(a)) (insecticidal delta-endotoxin)
DE CrylGa(a)) (CrylGa(a)) (insecticidal delta-endotoxin)
GN CRYG(A) OR CRYG(A).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BTS00349A;
RA Lambert B.;
RL Submitted (Apr-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPIGUT CELL OF INSECTS.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; Z22510; CA880233.1; -
DR HSSP; P02965; ICIT.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1166 AA; 132003 MW; 3A98B2D2CA086DCC CRC64;

Query Match 68.9%; Score 4303; DB 1; Length 1166;
Best Local Similarity 71.1%; Pred. No. 4.3e-270;
Matches 851; Conservative 78; Mismatches 214; Indels 54; Gaps 12;

QY 1 MENNIONCVPYCNINPEVILNEER-STGRPLDLSLSLRELLSEFVPGVGFGLFD 60
DB 1 MEISDQNPYVYCNINPEVILNEER-STGRPLDLSLSLRELLSEFVPGVGFGLFD 60
QY 61 LIWGTQPSDWSLFLQIOLIQRIETLERNRAITLRLGLADSYEIIYALREWEANPN 120

Db	61	IIWAGLGVQWNSLFLRQIEQLRQIEITELERNRATAILLGLSSYNYLYEAREWENDEN	120
Qy	121	NAOZLRVIRFANTDDALITAINNF ¹ LTISFEIPLSVYVQAA ¹ NHL ¹ SLLRDAVSGQW	180
Db	121	NPASQERVTRERLTDDAIVTGLPTLAINRLEVNL ¹ SVITQAA ¹ NHL ¹ SLLRDAVYFGERW	180
Qy	191	GLDIATVNNHYNRLINLHRYTHKCLD ¹ TYNOGL ¹ ENRG ¹ TNTOWARF ¹ NRD ¹ LT ¹ VLVD	240
Db	181	GLTQANIEDL ¹ TRETS ¹ NIQ ¹ ESDHCARW ¹ NOGL ¹ NEIGGIS ¹ ---RRYLD ¹ Q ¹ RD ¹ L ¹ AT ¹ SVLD	236
Qy	241	IVALFPNVDRV ¹ TYPIOT ¹ SSOL ¹ TREI ¹ YSSV ¹ IEDSP ¹ YSAN ¹ IPNGF ¹ NR ¹ AE ¹ GV ¹ PPH ¹ MD ¹ PM	300
Db	237	IVALFPNI ¹ DIIR ¹ TYPIQ ¹ SOL ¹ TREI ¹ YSP ¹ ----VAG ¹ INFGL ¹ SIAN ¹ -LRAPH ¹ LM ¹ DFI	290
Qy	301	NSL ¹ FV ¹ AT ¹ RSQ ¹ VTW ¹ GGHL ¹ VSSRNTA ¹ --GNR ¹ INF ¹ PSY ¹ GVFN ¹ PGAI ¹ WIAD ¹ ED ¹ PR ¹ PF ¹ R	357
Db	291	DRIVI ¹ YNSVR ¹ STPY ¹ MAGHE ¹ VSRR ¹ TQ ¹ GGOG ¹ NEIR ¹ PLGV ¹ -----AANA ¹ EP ¹ -----	337
Qy	358	TLSDP ¹ VFVR ¹ -GGGNPH ¹ ---YVL ¹ LGK ¹ VA ¹ FOQT ¹ GNHT ¹ -----RTFRN ¹ --S	397
Db	338	---PVTIR ¹ TG ¹ FTDEQR ¹ QWRAR ¹ SRV ¹ SPSSQ ¹ DFSL ¹ VDAG ¹ FLT ¹ IFS ¹ AVSI ¹ YRNG	393
Qy	398	GTIDSLDEI ¹ PQD ¹ NSGAP ¹ W ¹ NDY ¹ SHVL ¹ NHY ¹ TFV ¹ KW ¹ PGEI ¹ SGDS ¹ WRAP ¹ MT ¹ SW ¹ THRSAT ¹ PN	457
Db	394	FNTD ¹ IDEI ¹ PIEG ¹ D--PFTGY ¹ SHR ¹ CH ¹ VGF ¹ CLASS ¹ PF ¹ --SGYAR ¹ API ¹ FSW ¹ THRSAT ¹ LN	449
Qy	458	TIDPER ¹ TIQ ¹ PLV ¹ KAHT ¹ LSQGT ¹ VWRGP ¹ FTGG ¹ DI ¹ LRR ¹ TSGG ¹ PF ¹ Y ¹ TVIN ¹ QOL ¹ PO ¹ RV ¹ R	517
Db	450	TIAPD ¹ VI ¹ TIQ ¹ PLV ¹ KAF ¹ NLH ¹ SGAI ¹ VKGP ¹ FTGG ¹ DI ¹ LRR ¹ TVN ¹ VSFG ¹ DM ¹ RVN ¹ ITAP ¹ USQ ¹ RV ¹ R	509
Qy	518	ARIRYAST ¹ NLRI ¹ VTV ¹ VAGER ¹ IFAG ¹ OFN ¹ KMT ¹ GD ¹ PL ¹ TQ ¹ FSY ¹ AT ¹ INT ¹ AF ¹ TFPM ¹ QS ¹ SF	577
Db	510	VRIRYAST ¹ DLQ ¹ FY ¹ TNING ¹ T ¹ INIG ¹ FN ¹ SS ¹ MD ¹ SGD ¹ LO ¹ YGR ¹ ERV ¹ AG ¹ TF ¹ PT ¹ TFSD ¹ AN ¹ TF	569
Qy	578	TVGAD ¹ TSSG ¹ NEW ¹ YID ¹ R ¹ FELI ¹ PTA ¹ FE ¹ BY ¹ DLER ¹ AK ¹ AV ¹ NAL ¹ FTS ¹ INOIG ¹ IK ¹ T ¹ OV ¹ TYH	637
Db	570	TIGAFGSP ¹ NNE ¹ VID ¹ RIE ¹ VP ¹ PAE ¹ V ¹ FE ¹ BY ¹ DLER ¹ AK ¹ AV ¹ NAL ¹ FTS ¹ INOIG ¹ IK ¹ T ¹ OV ¹ TYH	629
Qy	638	IDQY ¹ SNL ¹ VDCL ¹ SDE ¹ FLDK ¹ REL ¹ SEK ¹ VIA ¹ KRL ¹ SD ¹ ERN ¹ LQD ¹ PN ¹ EK ¹ IN ¹ Q ¹ LDR ¹ GW ¹ RST	697
Db	630	IDK ¹ VSNL ¹ VECL ¹ SDE ¹ FLDK ¹ REL ¹ SEK ¹ VIA ¹ KRL ¹ SD ¹ ERN ¹ LQD ¹ PN ¹ ER ¹ GIN ¹ Q ¹ RD ¹ GW ¹ RST	689
Qy	698	DI ¹ TIQ ¹ GD ¹ VD ¹ FK ¹ BNY ¹ VL ¹ PG ¹ T ¹ DEC ¹ Y ¹ TY ¹ LQ ¹ ID ¹ ESK ¹ LK ¹ PT ¹ RY ¹ LQ ¹ RGY ¹ IED ¹ SOD ¹ LEI ¹ Y	757
Db	690	DI ¹ TIQ ¹ GD ¹ VD ¹ FK ¹ BNY ¹ VL ¹ PG ¹ T ¹ DEC ¹ Y ¹ TY ¹ LQ ¹ ID ¹ ESK ¹ LK ¹ VT ¹ RY ¹ LQ ¹ RGY ¹ IED ¹ SOD ¹ LEI ¹ Y	749
Qy	758	LIRYNAKHET ¹ VN ¹ VL ¹ GTSL ¹ WPL ¹ SVQ ¹ SP ¹ IRK ¹ CGEP ¹ NP ¹ CAP ¹ HL ¹ EW ¹ NFD ¹ LCS ¹ RD ¹ GK ¹ CAH ¹ H	817
Db	750	LIRYNAKHET ¹ VN ¹ VG ¹ GSU ¹ WPL ¹ SAQ ¹ SP ¹ IRK ¹ CGEP ¹ NP ¹ CAP ¹ HL ¹ EW ¹ NFD ¹ LCS ¹ RD ¹ GK ¹ CAH ¹ H	809
Qy	818	SHH ¹ FLSD ¹ IDV ¹ CG ¹ TD ¹ LNE ¹ D ¹ VW ¹ IF ¹ K ¹ IQ ¹ DGH ¹ ARL ¹ GN ¹ LE ¹ EEK ¹ PLV ¹ GEAL ¹ ARV ¹ KRAE ¹ K	877
Db	810		

[illegible]

Db 241 DIVAFPPNIDINTYPIQTATQTLREVYLDLFFINENLSPAASYPT--FSAESAIIIRSPHL 299
 Qy 297 MDENSLFVTAETVRSQTVGSHLVSS--RNTAGRNINFPDYG-VFNPGGNIMIADEDPR 353
 Db 300 VDFLNSFTIYDLSARAYWGSHLVNFRPTGTTNLRSPDYGREGTERPVTITASPSV 359
 Qy 354 PFYRTLSDFVFRGGFGNPHYVLGRVAFQQTGTNHTRTFRNSGTIDSLDEIPQDMSG 413
 Db 360 PIFRFLS--YIT-GLDLSNFPVAGIEGVFQNTISR--SIYKSGSPDSFSELPPQDASV 413
 Qy 414 APWNDYSHVLNHFVFRVPGGSLGSDSHRAPMFWTHRSAPTNTIDPERITQIPLVKAH 473
 Db 414 SPAIGYSHRLCHATELE---RISG--PRIAGTVFVSWTHRSASPTNEVSPSRITQIPWKAH 469
 Qy 474 TIQSGTIVVRGPGFGDILARTSGGPFAYTIVNINGLPQRYARIRIYASTTNLRIYVT 533
 Db 470 TLASGASVKGFGFGDILRNSNGELGLRVFTGRLPOSYYIRFAYASVANRSQTER 529
 Qy 534 VAGERIFAGQFNKMTDGTPLTFQSFVATINTAFTPFMSOSSFTVGADTFSSNEVIID 593
 Db 530 YSQPPSYGISPKTKMDAGEPLTISRFAHTTLFTPTTFSSRAQEEFDL---YIQSG--YVID 584
 Qy 594 RELPLVATPAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDEFC 653
 Db 585 RLFTPTVATPAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVACLSDEFC 644
 Qy 654 LDEKRELSEKVKHAKRLSDERNLLODPNFKGINROLDRGWRGSDTITQRGDDVFKENYV 713
 Db 645 LDEKRELSEKVKHAKRLSDERNLLODPNFKGINROLDRGWRGSDTITQGGDDVFKENYV 704
 Qy 714 TLPGGFDECPYLYOKIDESKLPYTRYQLRGYTEDSDQLEIYLIRYNKAKHTVNVLTG 773
 Db 705 TLPGGFDECPYLYOKIDESKLPYTRYQLRGYTEDSDQLEIYLIRYNKAKHTVNVLTG 764
 Qy 774 GSWLPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLIDVGCCTDLN 833
 Db 765 GSWLPLSVENQIGCGEPNRCAPHLEWNPDLHCSRDGKCAHSHHPSLIDVGCCTDLN 824
 Qy 834 EDLDVWVIFKIKTOGHARGLNLEFKPLVGEALARKVRAEKWKDKREKLENTIV 893
 Db 825 EDLGVWVIFKIKTOGHARGLNLEFKPLVGEALARKVRAEKWKDKREKLENTIV 884
 Qy 894 YKEAKESVDALFVNSOYDQLOADTNIAHAAKRVHRIREAYLPESLVPGVNVNIDIFE 953
 Db 885 YKEAKESVDALFVNSOYDQLOADTNIAHAAKRVHRIREAYLPESLVPGVNAIFEE 944
 Qy 954 LKGRIFTAFPLDARVINKGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSQE 1013
 Db 945 LEERIFTAFSLDARNIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSQE 1004
 Qy 1014 VRVCPGRGVIILRTAYKEGYGGCVTIHEIENNTDELAFNSCVEEVEYVNNFTVCNDYTA 1073
 Db 1005 VRVCPGRGVIILRTAYKEGYGGCVTIHEIENNTDELAFNSCVEEVEYVNNFTVCINTA 1064
 Qy 1074 NOBEYGGATSNRNGVDETYGNSVYPADYASVYEKSYTDGRRONPCESNRGYGDTPL 1133
 Db 1065 TOBEYEGTYSNRNGVDEYAGNPNPYPADYASVYEKSYTDGRRONPCESNRGYGDTPL 1124
 Qy 1134 PAGYVTKLEYEPETDKVWIEIGETEGTIVDSVLELLMEE 1174
 Db 1125 PAGYVTKLEYEPETDKVWIEIGETEGTIVDSVLELLMEE 1165

RESULT 8

ID C1HA_BACTU STANDARD; PRT: 1172 AA.
 AC Q45748;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIIa (insecticidal delta-endotoxin
 DE CRYII(a)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
 GN CRYIIA OR CRYIIA(A).

OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ETS02069AA;
 RA Lambert B.;
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF INSECTS.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 CC EMBL; Z22513; CAA80236.1; .
 DR HSP; P02965; LCIX.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1172 AA; 132980 MW; 9BEC1B1071C71270 CRC64;

 Query Match 67.8%; Score 4230.5; DB 1; Length 1172;
 Best Local Similarity 69.9%; Pred. No. 2.1e-265;
 Matches 834; Conservative 92; Mismatches 220; Indels 47; Gaps 11;

 Qy 4 NIQNCQVPYNCLNPNVEILNEERSTGR---LPLDLSLSITRELFSEFVPGVGAFLGF 60
 Db 5 NNQNVYPYNCLSNPENEILDESLSRSEQVAEISLGLTRELLSLLPGASFGFALFD 64
 Qy 61 LINGFTPPDSNLFLOIEQRIETLERNAITRLGLADSYEIIYEALREWEANPN 120
 Db 65 IIVGVIGDPDQNLFLAQIEOLIDQRIEAVHVRNOAISLEGLGSDSYEVIETSEWEASPN 124
 Qy 121 NAQLREVDVIRFANTDALLITANNFTLTSFEPLLSVYVQAAANLHLSLLRDVAVSGQW 180
 Db 125 NEALQDVNRNFSNTDALLITAFILREQGFELPLLSVYVQAAANLHLSLLRDVAVSQW 184
 Qy 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNOGLENRAGNTROWARNQFRDLITVLID 240
 Db 185 GLDPTVTVNNHYNRLINLINTYSDHCAQWNRGLDNFGVS---ARYLDFQREVITSLVD 240
 Qy 241 IVALFPNDVTRVPIQTSOLTRIEYTSVIE--DSPVSANIPNGFNRAEFGVRRPHLMDP 299
 Db 241 IVALFPNDVTRVPIQTSOLTRIEYTSVIE--DSPVSANIPNGFNRAEFGVRRPHLMDP 293
 Qy 300 MNSLFTVAETVRSTQVGGHLSVRNTA--GNRINFPSTGVFNPGGAIWIADEDPRPF-- 355
 Db 294 LTRLVITGVQSGIYHWAGHEISSRTTGNLSNITQPPFYCT-----AASADRAFNM 344
 Qy 356 -----YRTLSDPVVRGFGFNPHVVLGRVAFQQTGTNHT--FRNSGIDSL 403
 Db 345 NIHSETIYRTLSAPIYSVSGGISPNRTRVVEGVRLIARDNNLDLPFLYRKRGDLDF 404
 Qy 404 DEIPQDMSGAPNDYSHVLNHNVTFFVRWQCEISGDSWRAPMFSWTHRSAPTNTIDPR 463
 Db 405 TELPDESTPPYIGYSHRCHAFARSPVILPSPNFARLPVFSWTHRSASPTNEVSPSR 464
 Qy 464 ITQIPLVKAHTLQSGTIVVRGPGTGGDILRRT--SGGPFAYTIVNINGLPQRYARIR 521
 Db 465 ITQIPWVKAHTLASGASVKGPGTGGDITRNINNLGDLGLTRVTVTGRLPQSYIRLR 524
 Qy 522 YASTTNRIYTVVAGERIFAGQFNKMTDGTDLTFQSFVATINTAFTPFMSOSSFTVGA 581

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525 YASVANSNGVFRHLPOPSYSGTSPRTMGTDPLTSRSFALTTLFTPTLTRAQEFNL-- 582
582 DTSSGNEVVIDREFELIPVATAEAYDLERAQKAVNALTSINQIGIKTDYDHYHDQV 641
583 -TIPRG--VYIDREFYFVDPATFAGYDLERAQKAVNALFTSTNQRGLKTDITDYHDQV 639
642 SNLVDCLSDFCDLDEKRELSEKVKHAKRLSDERNLQDPNFKGNRCLDRGWSGTDITI 701
640 SNLVECLSDFCDEKRELSEKVKHAKRLSDGRNLLQDRNFISINGLDRGWSGTDITI 699
702 QRGDDVFKENYVTLPGTFDECYPTLYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRY 761
700 QGSDDVFKENYVTLPGTFDECYPTLYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRY 759
762 NAKHETVNLVGTSLWPLSVQSPTRKCGENRCAPHLEWNPDLDCSCRDGEKCAHSHHF 821
760 NAKHEIVNVPGTSLWPLSVQSPTRKCGENRCAPHLEWNPDLDCSCRDGEKCAHSHHF 819
822 SLDDVGCCTDLNEDLDVWVIFKIKTQDGHARLGNLEBEKPLVGEALARKRAKKWRD 881
820 SLDDVGCCTDLNEDLDVWVIFKIKTQDGHARLGNLEBEKPLVGEALARKRAKKWRD 879
882 KREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNMIHAADKRVHRIEAYLPELS 941
880 KREKLEETNIVYKEAKESVDALFVNSQYDQLQADTNMIHAADKRVHRIEAYLPELS 939
942 VIPGVNVDIFEEELKGRIFTAFYLDARNVKNKGNFNGLSWNVKGVHDVVEEQNNHRSVL 1001
940 VIPGVNVDIFEEELKGRIFTAFYLDARNVKNKGNFNGLSWNVKGVHDVVEEQNNHRSVL 999
1002 VPEWEAEVSQEVRCVPGRCYILRVATYKEGYGEGCVTIEIENNTDELKFSNCVEEYV 1061
1000 VPEWEAEVSQEVRCVPGRCYILRVATYKEGYGEGCVTIEIENNTDELKFSNCVEEYV 1059
1062 PNNVTVCNDYANQOEYGGATYGRNRYDETYGNSNVSPADYASVYEEKSYTDGRRDNC 1121
1060 PSNTVTCNDYANQOEYEGTYTSRNGYDEAYESNSVPANYASVYEEKAYTDGRRNSC 1119
1122 ESNRGYGDYTPAGYVTRKLEYFPEPTDKWVIEIGETEGTFIVDSVELLMEE 1174
1120 EFNRGYRDYTPAGYVTRKLEYFPEPTDKWVIEIGETEGTFIVDSVELLMEE 1172

RESULT 9
C1GB_BACTZ
ID C1GB_BACTZ STANDARD; PRT: 1169 AA.
AC Q9ZAZ6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pesticidial crystal protein cryIgb (Insecticidal delta-endotoxin
DE CryIgb(b)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
GN CRYIGB OR CRYIGB(B) OR CRYH2.
OS Bacillus thuringiensis (subsp. wuhanensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=52024;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-525;
RX MEDLINE=20153386; PubMed=10688690;
RA Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
RT "Cloning of two new cry genes from Bacillus thuringiensis subsp.
RT wuhanensis strain";
RL Curr. Microbiol. 40:227-232(2000).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PIERIS RAPAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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CC -----
DR EMBL; U70725; AAD10291.1; -.
DR HSSP; P02965; ICIY.
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1169 AA; 132904 MW; D1EFCL508A8B10BD CRC64;

Query Match 67.7%; Score 4224.5; DB 1; Length 1169;
Best Local Similarity 70.1%; Pred. No. 5.1e-265;
Matches 834; Conservative 78; Mismatches 241; Indels 37; Gaps 10;

QY 1 MENNQNOCVPYNCNLPNVEILLNEERSTGRPLDLSLSTRFLLSEFPVGVGAFGLFD 60
DB 1 MEINNQOCVPYNCNLPNVEILLNEERSTGRPLDLSLSTRFLLSEFPVGVGAFGLFD 60
QY 61 LIWGFITPDSWLSFLQIEOLIEQRIETLERNRAITTLGLADSYEYIEALREWEANPN 120
DB 61 LIWGFITPDSWLSFLQIEOLIEQRIETLERNRAITTLGLADSYEYIEALREWEANPN 120
QY 121 NAOLREDVRIRFANTDDALITANNFTLTSFEIPLSVVQAAANLHLRLDADVSFGQW 180
DB 121 NAOLREDVRIRFANTDDALITANNFTLTSFEIPLSVVQAAANLHLRLDADVSFGQW 180
QY 121 NPASKERVTRFRTDDALLTGYPLMAIPGFEALATLSVYAQSANLHALLRDAVFFGERW 180
DB 121 NPASKERVTRFRTDDALLTGYPLMAIPGFEALATLSVYAQSANLHALLRDAVFFGERW 180
QY 181 GLDIATVNNHYNLNLHRYTKHCLDLYNOGLENLGNTNROWARNQFRDLTLVLD 240
DB 181 GLDIATVNNHYNLNLHRYTKHCLDLYNOGLENLGNTNROWARNQFRDLTLVLD 240
QY 181 GLAQTNIDLYSLKNSIRDYTNHCVFYNIGLNLNVR---PEYRQRELTISVLD 236
DB 181 GLAQTNIDLYSLKNSIRDYTNHCVFYNIGLNLNVR---PEYRQRELTISVLD 236
QY 241 IVALFNVDYRTYPIOTSSOLTRFETISSVIESPYVSANPNFNGFNRAEFVGRPHLMDFM 300
DB 241 IVALFNVDYRTYPIOTSSOLTRFETISSVIESPYVSANPNFNGFNRAEFVGRPHLMDFM 300
QY 237 LVALFPNIDIRTYPIPTKSOLTRFETIDPII-----SPGAQAGYTLQDV-LRPHLMDFL 290
DB 237 LVALFPNIDIRTYPIPTKSOLTRFETIDPII-----SPGAQAGYTLQDV-LRPHLMDFL 290
QY 301 NSLFTVAETVRSQTVWGGHLV-SSRTAGNKRINFPSPYGVFNPGGAIWADDEP----- 352
DB 301 NSLFTVAETVRSQTVWGGHLV-SSRTAGNKRINFPSPYGVFNPGGAIWADDEP----- 352
QY 291 NLLIYTGVEGRHWRHAGHEVESRGTGMNIRFLYGT-----AATAETRFRTIPS 342
DB 291 NLLIYTGVEGRHWRHAGHEVESRGTGMNIRFLYGT-----AATAETRFRTIPS 342
QY 353 -----RPFYTLSDPVPVVRGFGN--PHYVLGL-RGVAFQQTGTNHTRTFRNSGTIDSLD 404
DB 353 -----RPFYTLSDPVPVVRGFGN--PHYVLGL-RGVAFQQTGTNHTRTFRNSGTIDSLD 404
QY 343 TFPGLNLFYTLTSLAPIFRDEPGANIIIRYRTSLVEGVGTQP--NNGQLYRVRGTLSDSLD 401
DB 343 TFPGLNLFYTLTSLAPIFRDEPGANIIIRYRTSLVEGVGTQP--NNGQLYRVRGTLSDSLD 401
QY 405 EIPPONSGAPNDYSHVLNHYTVFVRWPGELSGSDSWRAPMFWSTHESATPTWIDPERI 464
DB 405 EIPPONSGAPNDYSHVLNHYTVFVRWPGELSGSDSWRAPMFWSTHESATPTWIDPERI 464
QY 402 QLPLEGESSL--TEYSHRICHVRFAQSLRNAEPLDVARVPMFVSWTHRSATPTWIDPDI 459
DB 402 QLPLEGESSL--TEYSHRICHVRFAQSLRNAEPLDVARVPMFVSWTHRSATPTWIDPDI 459
QY 465 TQIPLVKAHTLOSQTVVRGPGTGGDILRRTSGGPFAYTVININGQLPQRYRARIYAS 524
DB 465 TQIPLVKAHTLOSQTVVRGPGTGGDILRRTSGGPFAYTVININGQLPQRYRARIYAS 524
QY 460 TQIPLVKAENLHSSATVVRGPGTGGDILRRTNAGNEDMRVNTITAPLSQRYRVRIYAS 519
DB 460 TQIPLVKAENLHSSATVVRGPGTGGDILRRTNAGNEDMRVNTITAPLSQRYRVRIYAS 519
QY 525 TTNRLYVTVVAGRIFAGQPKMTMDGDLTFQSFYSATINTAFTPMSSOSTVVGADTF 584
DB 525 TTNRLYVTVVAGRIFAGQPKMTMDGDLTFQSFYSATINTAFTPMSSOSTVVGADTF 584
QY 520 TANLQFHTSINGRAINQANFPATMNSGENLQSGSFVAGFTTPTFTSDALSTETIGAFSF 579
DB 520 TANLQFHTSINGRAINQANFPATMNSGENLQSGSFVAGFTTPTFTSDALSTETIGAFSF 579
QY 585 SSGNEVYIDREFELIPVATAEAYDLERAQKAVNALFTSINOIGIKTDYDHYHDQVSNL 644
DB 585 SSGNEVYIDREFELIPVATAEAYDLERAQKAVNALFTSINOIGIKTDYDHYHDQVSNL 644
QY 580 SSGNEVYIDREFELIPVATAEAYDLERAQKAVNALFTSINOIGIKTDYDHYHDQVSNL 639
DB 580 SSGNEVYIDREFELIPVATAEAYDLERAQKAVNALFTSINOIGIKTDYDHYHDQVSNL 639
QY 645 VDLCLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGNRCLDRGWSGTDITIQRG 704
DB 645 VDLCLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGNRCLDRGWSGTDITIQRG 704
QY 640 VECLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGNRCLDRGWSGTDITIQRG 699
DB 640 VECLSEDFCLDEKRELSEKVKHAKRLSDERNLQDPNFKGNRCLDRGWSGTDITIQRG 699
QY 705 DVDFKENYVTLPGTFDECYPTLYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRYNAK 764
DB 705 DVDFKENYVTLPGTFDECYPTLYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRYNAK 764
QY 700 DVDFKENYVTLPGTFDECYPTLYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRYNAK 759
DB 700 DVDFKENYVTLPGTFDECYPTLYLYQKIDESKLPYTRYQLRGYLEDSDQLEIYLIRYNAK 759
QY 765 HETVNVLTGSLWPLSVQSPTRKCGENRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD 824
DB 765 HETVNVLTGSLWPLSVQSPTRKCGENRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD 824

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760 HETVNPCTGSLWPLSAQSPIGKCGEPNRCATHLEWNPDLDCSCRDGKCAHSHHFSLD 819
 825 IDVGCTDLNEDLVWIFKIKTDGHLNLEFLKPLNGEALARKVRAEKWKDKRE 884
 820 IDVGCTDLNEDLVWIFKIKTDGHLNLEFLKPLNGEALARKVRAEKWKDKRE 879
 885 KLELETVIVYKEAKESVDALFVNSQYDQLOADTNIAHRAADKRVHRIEAYLPESVIP 944
 880 KLELETVIVYKEAKESVDALFVNSQYDQLOADTNIAHRAADKRVHRIEAYLPESVIP 939
 945 GVNVDIEELKGRFTFAFFLYDARNVJKNQDFNGLSCWNVKGVHVDVEQNNHRSVLVVP 1004
 940 GVNAAIEEELKGRFTFAFFLYDARNVJKNQDFNGLSCWNVKGVHVDVEQNNHRSVLVVP 999
 1005 EWEAEVSOEVRVCPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCEVEEYPNN 1064
 1000 EWEAEVSOEVRVCPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCEVEEYPNN 1059
 1065 TVTCNDYTAQOEYGGAYTSRNGYDYSNSVPADYASVYEKSYTDGRRDNPCESN 1124
 1060 TVTCNDYTAQOEYGGAYTSRNGYDYSNSVPADYASVYEKSYTDGRRDNPCESN 1119
 1125 RGYGDTPLPAGVYKLETFPDTKWIIEIGETEGTFIVDSVELLMEE 1174
 1120 RGYGDTPLPAGVYKLETFPDTKWIIEIGETEGTFIVDSVELLMEE 1169

RESULT 10

C1CA_BACTE STANDARD; PRT; 1189 AA.
 AC F05518; P10327; Q03742; Q45725;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 30-NOV-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cryIcA (Insecticidal delta-endotoxin
 DE CryIcA(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein).
 GN CRYICA OR CRYICA OR CRYIC.
 OS Bacillus thuringiensis (subsp. entomocidus), and
 OS Bacillus thuringiensis (subsp. aizawai).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1436, 1433;
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.entomocidus; STRAIN=60.5;
 RX MEDLINE=88289380; PubMed=3399402;
 RA Honee G., van der Salm T.P.M., Visser B.;
 RT "Nucleotide sequence of crystal protein gene isolated from B.
 RT thuringiensis subspecies entomocidus 60.5 coding for a toxin highly
 RT active against Spodoptera species";
 RL Nucleic Acids Res. 16:6240-6240(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.t.aizawai; STRAIN=NRRL B-18484 / P5811;
 RA Payne J.M., Sick A.J.;
 RT "Bacillus thuringiensis isolate active against lepidopteran pests, and
 RT genes encoding novel lepidopteran active toxins";
 RL Patent number US246852, 21-SEP-1993.
 RN [3]
 RP SEQUENCE OF 1-823 FROM N.A.
 RC SPECIES=B.t.aizawai; STRAIN=7-29;
 RX MEDLINE=89343627; PubMed=2548060;
 RA Sanchis V., Lerechus D., Menco M., Chauaux J., Guo S., Lecadet M.-M.;
 RT "Nucleotide sequence and analysis of the N-terminal coding region of
 RT the Spodoptera-active delta-endotoxin gene of Bacillus thuringiensis
 RT aizawai 7-29";
 RL Mol. Microbiol. 3:229-238(1989).
 RN [4]
 RP SEQUENCE OF 1-756 FROM N.A.
 RC SPECIES=B.t.aizawai; STRAIN=7-29 / K26-21;
 RA Strizhov N.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT

CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPOOPTERA
 CC SPECIES.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOROULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
 CC OF THE SPORE COAT.
 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; X07518; CAA30396.1; -
 CC EMBL; M73251; AAA22343.1; -
 CC EMBL; X13620; CAA31951.1; -
 CC EMBL; X96682; CAA65457.1; -
 CC PIR; S00944; S00944.
 CC PIR; S04181; S04181.
 CC HSP; P02965; ICIV.
 CC InterPro: IPR001178; Endotoxin.
 CC Pfam: PF00555; endotoxin; 1.
 CC Taxin; Sporulation.
 CC CONFLICT 124 124 A -> E (IN REF. 1).
 CC CONFLICT 294 294 A -> R (IN REF. 1).
 CC CONFLICT 366 366 N -> I (IN REF. 3).
 CC CONFLICT 376 380 WPAPP -> CORHH (IN REF. 3).
 CC CONFLICT 386 386 V -> G (IN REF. 3).
 CC CONFLICT 405 405 T -> Q (IN REF. 2).
 CC CONFLICT 453 453 H -> D (IN REF. 1).
 CC CONFLICT 775 775 R -> A (IN REF. 3).
 CC CONFLICT 853 853 V -> L (IN REF. 2).
 CC CONFLICT 864 864 G -> N (IN REF. 2).
 CC CONFLICT 931 931 D -> N (IN REF. 2).
 CC SEQUENCE 1189 AA; 134715 MW; 362768685916A0DF CRC64;
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 Best Local Similarity 68.9%; Pred. No. 6e-265;
 Matches 834; Conservative 95; Mismatches 224; Indels 57; Gaps 17;
 QY 1 MENNIONQCVNCLANPEVEILNEER-STGRPLDLSLTLFLLSEFPVGVGVARGLF 59
 DB 1 MENNIONQCVNCLANPEVEILNEER-STGRPLDLSLTLFLLSEFPVGVGVARGLF 59
 QY 60 DLWGFITFSDWSLFLQIQIEQLQIEQIETLERNRAITTLRLGLADSYEITAEALREWEANP 119
 DB 61 DFVWGVGPSOWDAFLVQIEQLINERIAEFARNAATANLEGLNNTFYVEAFKEWEEDP 120
 QY 120 NNAQLREDVRIREFANTDDALITAINFTLTSFIPILSVYVQAANLHLLRDVAFSGQG 179
 DB 121 NNPATRVIDRPRILDLERDIPSPRISGFEVPLSVYAQAANLHLLRDVAFSGQG 180
 QY 180 WGLDIATVNNHYNRLNLHRYTKHCLDTYNOGLENLGNTTQWARFQFRDLTLVL 239
 DB 181 WGLTTNNVNNYNRLNRHIDEYADHCAANTYNGNLNLPKSTYQDWTYKRLRDLTLVL 240
 QY 240 DIVALFPNDVTRTYPTQTSQTLREITYTSVIEDSP---VSANIPNGFNRAE-FGVRPPH 295
 DB 241 DIAAAPPNDNRRYPQVQGLTRVYTPDLINFNQLOLSVAQLPT-FNVMESSAIRNPH 299
 QY 296 LMDFMNSLFTVAB--TVRSQTVWGHVLSRNTAGNRINFPSPYGVENPGGAIWAIEDP- 352
 DB 300 LFDILNLNLTFTDWFVSGVRNFYWGGRHVTSLLIGGNITSPYGVENPGGAIWAIEDP- 351
 QY 353 -----RPFYRLSDPV--FVGGFNGNPHVL-GLRGVAFQQTGTNHTTFRNSGIDSL 403
 DB 352 RSFTENGPFVRLSNPTRLRLOQPWPAPPNLRGVGEVFE-STPTN-SFTYRGRGVDSL 409
 QY 404 DEIPPDNSGAPWNDYSHVLNHTVFRVWFGESGDSWRAP-----MFSWTHRSATPIN 457

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Db 410 TELPPEDNSVPPREGYSHRLCHATFVQSG-----TPFLTGGVTSWTHRSATLTN 460
QY 458 TIDPERITDIPVKAHTLOSITVVGPGFTGGDILIRTSGGPPATYVNINGQLPQRYR 517
Db 461 TIDPERINIPVKGPRVGGSVITGPGFTGGDILIRNTGDFVSLQVNWINSPIQRYR 520
QY 518 ARIRYASTNLRIVY-TVAGERIFAGQ-----FNKMTDGTDLPTQFSFYATINTAFWF 570
Db 521 LRFYASSRDARVILVTGAAGTGVGGQVSNMPLQKTMTEIGENLTSTRTYTFDFSPFSF 580
QY 571 PMSQSFY-----GADTFSSNEWIDREFELIPVTAFTFARYDYLERAKAVNALFTSI 624
Db 581 RANPDIGISEQPLFGAGSISSG-ELYIDKIELILADATFAESDLSLERAKAVNALFTSS 639
QY 625 NOIGIKITDVTYHIDOVSNLVDCLSEDFCLDEKRESEKVKHAKRLSDERNLLQDNFKG 684
Db 640 NQIGLKITDVTYHIDOVSNLVDCLSEDFCLDEKRESEKVKHAKRLSDERNLLQDNFKG 699
QY 685 INRQDRGRGSDTITIQRGDDVFKENYVTLPGTFDECYPTLYIQIDESKLPYTRYQL 744
Db 700 INRQDRGRGSDTITIQGDVDFKENVYVTLPGTVDECYPTLYIQIDESKLPYTRYEL 759
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Db 760 RGYIEDSQLEIYLIRYNKAKHETVNLGSLWPLSVQSPPIKCGEPNRCAPHLEWNPDL 819
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Db 820 DCSRCRGEKCAHSHFSLDIDVGCITDLNEDLDVWVIEFKITQDGHARLGNLEFLEKPL 879
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Db 880 LGEALARVRAEKKWRDKREKLENTIYVKEAKESVDALFVNSQYDQLQADTNIAHIA 939
QY 925 AKRVHRIEAYLPESLVPVGNVDIFELKGRIFTAFELYDARNVKNKGDFNNGLSOWN 984
Db 940 AKRVHRIEAYLPESLVPVGNVAAIFEELEGRIFTAFELYDARNVKNKGDFNNGLLCWN 999
QY 985 VKGHVDVEQNHRSLVVPWEAEYSQEVRCPCGRGYILRTVAYKEGYGEGCVTTHEIE 1044
Db 1000 VKGHVDVEQNHRSLVVPWEAEYSQEVRCPCGRGYILRTVAYKEGYGEGCVTTHEIE 1059
QY 1045 NNTDELKFSNCVEEYYPNNTVTCNDYTANQEEYGYAYTSRNGYDGYSGNSVSPADYA 1104
Db 1060 DNTDELKFSNCVEEYYPNNTVTCNNYTGQEEYEGYTSRNGYDGYSGNSVSPADYA 1119
QY 1105 SYVEEKSYTDGRDNPCESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1164
Db 1120 SYVEEKSYTDGRDNPCESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1179
QY 1165 DSVLELLMEE 1174
Db 1180 DSVLELLMEE 1189

RESULT 11
C1AB.BACTK
ID C1AB.BACTK STANDARD: PRT: 1155 AA.
AC P06578; P06577; P21257; P09666; P09667; P09667;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Pesticidal crystal protein cryIAB (Insecticidal delta-endotoxin
DE CRYIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal protein).
GN CRYIAB OR CRYIA(B) OR CRYIA(B) OR CRY-1-2 OR BT2 OR CRYICI.
OS Bacillus thuringiensis (subsp. kurstaki),
OS Bacillus thuringiensis (subsp. berliner), and
OS Bacillus thuringiensis (subsp. aizawai).
OG Plasmid.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29339, 1434, 1433;
RN [1]
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RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=87163505; PubMed=3557124;
RA Geiser M., Schweitzer S., Grimm C.;
RT "The hypervariable region in the genes coding for entomopathogenic
RT crystal proteins of Bacillus thuringiensis: nucleotide sequence of
RT the kurhd1 gene of subsp. kurstaki HD1.";
RL Gene 48:109-118(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RA Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
RT "Cloning and nucleotide sequencing of two insecticidal delta-
RT endotoxin genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
RL Agric. Biol. Chem. 51:455-463(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=NRD-12;
RA Hefford M.A., Brousseau R., Prefontaine G., Hanna Z., Condie J.A.,
RA Lau P.C.K.;
RT "Sequence of a lepidopteran toxin gene of Bacillus thuringiensis
RT subsp kurstaki NRD-12.";
RL J. Biotechnol. 6:307-322(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=HD-1;
RX MEDLINE=86223796; PubMed=3011746;
RA Thorne L., Garduno F., Thompson T., Decker D., Zounes M., Wild M.,
RA Walfield A.M., Pollock T.J.;
RT "Structural similarity between the lepidoptera- and diptera-specific
RT insecticidal endotoxin genes of Bacillus thuringiensis subsp.
RT 'kurstaki' and 'israelensis'.";
RL J. Bacteriol. 166:801-811(1986).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.kurstaki; STRAIN=S93;
RA Silva-Werneck J.O., De-Souza M.T., Dias J.M.C.S., Ribeiro B.M.;
RT "Characterization of Bacillus thuringiensis subsp. kurstaki strain S93
RT effective against the Fall armyworm, Spodoptera frugiperda and cloning
RT of a cryIAB gene.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.berliner; STRAIN=1715;
RX MEDLINE=86300092; PubMed=3743328;
RA Wabiko H., Raymond K.C., Bulla L.A. Jr.;
RT "Bacillus thuringiensis entomocidal protoxin gene sequence and gene
RT product analysis.";
RL DNA 5:305-314(1986).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.berliner; STRAIN=1715;
RX MEDLINE=87054026; PubMed=3023091;
RA Hoeft H., de Greve H., Seurinck J., Janssens S., Mahillon J.,
RA Ampe C., Vandekerckhove J., Vanderbruggen H., van Montagu M.,
RA Zabeau M., Vaeck M.;
RT "Structural and functional analysis of a cloned delta endotoxin of
RT Bacillus thuringiensis Berliner 1715.";
RL Eur. J. Biochem. 161:273-280(1986).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=HD-133;
RA Chak K.-F., Jen J.C.;
RT "Complete nucleotide sequence and identification of a putative
RT promoter region for the expression in Escherichia coli of the cryIA(b)
RT gene from Bacillus thuringiensis var. aizawai HD133.";
RL Proc. Natl. Sci. Coun. Repub. China 17B:7-14(1993).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.aizawai; STRAIN=IPL7;
RX MEDLINE=87248103; PubMed=3297927;
RA Oeda K., Oshie K., Shimizu M., Nakamura K., Yamamoto H., Nakayama I.,
RA Ohkawa H.;
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"Nucleotide sequence of the insecticidal protein gene of *Bacillus thuringiensis* strain aizawai IPL7 and its high-level expression in *Escherichia coli*.";
Gene 53:113-119(1987).
[10]
SEQUENCE FROM N.A.
SPECIES=B.t.aizawai; STRAIN=IC1;
MEDLINE=89083518; PubMed=3205732;
RA Haider M.Z., Ellar D.J.;
RT "Nucleotide sequence of a *Bacillus thuringiensis* aizawai IC1
entomocidal crystal protein gene.";
RT Nucleic Acids Res. 16:10927-10927(1988).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
CC -!- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in
insect-resistant maize by Monsanto, Northrup King and Ciba Geigy.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOPOXIN FAMILY.

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DR EMBL; M15271; AAA22561.1; -;
DR EMBL; M13898; AAA22330.1; -;
DR EMBL; M37263; AAA22420.1; -;
DR EMBL; M12661; AAA22613.1; -;
DR EMBL; AF059670; AAC64003.1; -;
DR EMBL; D80117; BAA00071.1; -;
DR EMBL; X04698; CAA28405.1; -;
DR EMBL; X54939; CAA38701.1; -;
DR EMBL; A09398; CAA00840.1; -;
DR EMBL; A03793; CAA00303.1; -;
DR EMBL; M16463; AAA22551.1; -;
DR EMBL; X13233; CAA31620.1; -;
DR PIR; JD0002; JD0002. -;
DR PIR; S11446; S11446. -;
DR PIR; S14555; S14555. -;
DR PIR; A26461; A26461. -;
DR PIR; A29838; A29838. -;
DR PIR; A26513; A26513. -;
DR PIR; S02134; S02134. -;
DR HSSP; P02965; IC1V. -;
DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation; Plasmid; Genetically modified food.
FT CONFLICT 207 207 GS -> R (IN REF. 4).
FT CONFLICT 282 283 GS -> AL (IN REF. 9).
FT CONFLICT 382 406 LKGGPPPYTEKAEP (IN REF. 4).
FT CONFLICT 410 410 L -> P (IN REF. 4).
FT CONFLICT 430 432 LSH -> CLAY (IN REF. 4).
FT CONFLICT 437 437 R -> Y (IN REF. 4).
FT CONFLICT 447 447 I -> V (IN REF. 4).
FT CONFLICT 450 450 A -> P (IN REF. 10).
FT CONFLICT 452 458 MFSWIHR -> NDSSWTYC (IN REF. 4).
FT CONFLICT 461 461 E -> N (IN REF. 3).
FT CONFLICT 463 465 NNI -> GDV (IN REF. 4).
FT CONFLICT 479 486 STNLGSGT -> LQSLWN (IN REF. 4).
FT CONFLICT 492 492 P -> L (IN REF. 4).
FT CONFLICT 501 505 RTTSP -> EELT (IN REF. 4).
FT CONFLICT 537 537 F -> L (IN REF. 10).
FT CONFLICT 542 542 D -> H (IN REF. 3).
FT CONFLICT 545 545 T -> I (IN REF. 10).
FT CONFLICT 568 568 P -> I (IN REF. 10).

FT CONFLICT 568 569 TV -> HL (IN REF. 3).
FT CONFLICT 665 665 K -> E (IN REF. 3).
FT CONFLICT 675 676 KR -> NG (IN REF. 3).
FT CONFLICT 703 703 S -> N (IN REF. 4).
FT CONFLICT 712 712 D -> H (IN REF. 4).
FT CONFLICT 731 731 P -> L (IN REF. 7 AND 10).
FT CONFLICT 785 785 P -> R (IN REF. 7 AND 10).
FT CONFLICT 836 836 N -> I (IN REF. 3).
FT CONFLICT 978 978 H -> Q (IN REF. 9).
FT CONFLICT 1016 1016 E -> T (IN REF. 3).
FT CONFLICT 1036 1036 C -> F (IN REF. 9).
FT CONFLICT 1060 1060 E -> G (IN REF. 3).
SQ SEQUENCE 1155 AA; 130623 MW; 43461A64C7AC7CAF CRC64;
Query Match 67.4%; Score 4211.5; DB 1; Length 1155;
Best Local Similarity 70.0%; Pred. No. 3.4e-264;
Matches 831; Conservative 83; Mismatches 228; Indels 45; Gaps 9;
QY 1 MENNIO-NOCVPYNCLNPEVEILNEER-STGLRPLDISLIRFLSEFVPGVGAVPGL 58
DB 1 MDNPNINECIPNCLSNPEVEVLGGERITGTTPDISLSLQTLSEFVPGAGFVGL 60
QY 59 FDIWGFITPDSLSFLQLEQLIEQRIETLERNRAITLRLGLADSYEYIEALREWEAN 118
DB 61 VDIWGFISQWDAFLVQLEQLINQRIEFARNAQLISLEGLSNLYQIYAESFREWEAD 120
QY 119 PNAQILREYVRIFANTDDALITAINNFTLTSEIPLLSVYQAAHLHLRLDRVAFSGQ 178
DB 121 PTPALREEMRIQFNDKNSALTAIPLFAVONTQVPLLSVYQAAHLHLRLDRVAFSGQ 180
QY 179 GWGLDIAIVNHNHNLINLHRYTKHCLDTYNOGLNLTNTROMARENOFRDLTLTV 238
DB 181 RWGFDATINSRYNDLTRIGNTDHVRWYNGLERWGPDSRWIRYKQFRELTLTV 240
QY 239 LDIVALFPNDYRTYPIQTSSTQTLREIYTSVIEDSPVSAINPFGNRA---EFGVRPP 294
DB 241 LDIVSLFPNDYRTYPIQTSSTQTLREIYTVNPLE-----NFDGSPRGSQAQIEGSRSP 294
QY 295 HLMDFMNSLPVTAETVRSQIVWGGH-LVSSRNTAGNRINFPYGVF-NFGGAIWADED 351
DB 295 HLMDFMNSLPVTAETVRSQIVWGGH-LVSSRNTAGNRINFPYGVF-NFGGAIWADED 351
QY 352 PRPFYRTLSDPVEVRG---GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTDLSLDEIP 407
DB 355 GQGVYRTLSLTYRPPNIGINNOQLSVLDGTEFAVGTSSNLFSAVYRKSGTVDLSDEIP 414
QY 408 PQDNGAPNDYSHVLNHNFTVFWPGEISGDSWRAPMFSWTHRSATPTNIDPERITQI 467
DB 415 PNNNVPPRQGFSHRLSHVSMFRSGFSNVSIIRAPMFSWIHRSABFNIIIPSSQITQI 474
QY 468 PLYKAHTLQSGTIVVRGPGGTGGDILRRTSGGPFAYTIVNINQLPQRYEARIRYASTTN 527
DB 475 PLYKSTNLGSGTIVVRGPGGTGGDILRRTSGGPFAYTIVNINQLPQRYEARIRYASTTN 534
QY 528 LRIYTVAGERIFAGFNKMTGDDPLTTFOSFYATINTAFTPPMQSSFTSGADTFSSG 587
DB 535 LQPTSIDGRPINQGNFSAFMSSGSLNCGSFRTVGTFTTFFNFSNGSSVFTLSAHVNSG 594
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DB 595 NEYVIDRFELIPVATFEAYDLERAKAVNALFTSINQIGIKTDYDHYDQVSNLVC 654
QY 648 LSDEFCLDEKRELSKVKHAKRLSDERNLLODPNFGINRQLDRGWRGSTDITIQGGDDV 707
DB 655 LSDEFCLDEKRELSKVKHAKRLSDERNLLODPNFGINRQLDRGWRGSTDITIQGGDDV 714
QY 708 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGVIEDSQLELYLYRYNAKHET 767
DB 715 FKENVYTLPGTFDECYPTLYQKIDESKLPYTRYQLRGVIEDSQLELYLYRYNAKHET 774
QY 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPOLDSCRDGKCAHSHHFLSDIDV 827
DB 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPOLDSCRDGKCAHSHHFLSDIDV 808

QY 828 GCTDLNEDLDVWVIEKIKTODGHARLGNLEFLEKPLVUGALARKVRAEKKWRDKREKLE 887
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 QY 888 LETNIVYKEAKESVDALFVNSQYDQLOQADTNIAIMIHAADRVRHRIREAYLPELSVPVGN 947
 Db 869 WETNIVYKEAKESVDALFVNSQYDQLOQADTNIAIMIHAADRVRHRIREAYLPELSVPVGN 928
 QY 948 VDFEELKGRIFAFPELYDARNVKNKDFNGLSCWNVKGHDVVEQNNHRSVLVVPWE 1007
 Db 929 AALFELEGSIPTAFSLYDARNVKNKDFNGLSCWNVKGHDVVEQNNHRSVLVVPWE 988
 QY 1008 AYSQVRCVPCRGYILRVAYKEGEGCVTTHIEFNNTDELKFSNCVBEVYPPNNTVT 1067
 Db 989 AYSQVRCVPCRGYILRVAYKEGEGCVTTHIEFNNTDELKFSNCVBEVYPPNNTVT 1048
 QY 1068 CNDYTANQEYGGAYTSRNGYDYSVSPADYASVYEEKSYTDGRRDNPCESNRGY 1127
 Db 1049 CNDYTANQEYGGAYTSRNGYDYSVSPADYASVYEEKSYTDGRRDNPCESNRGY 1108
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 Db 1109 GDTPLPAGVTVTELEYPPTDKWVIEIGTEGTFIVDSVELLMEE 1155

RESULT 12
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 ID C12A_BACTX
 AC Q57458; Q03741;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pesticidal crystal protein cryIEa (Insecticidal delta-endotoxin
 DE CryIE(a) (crystalline entomocidal protoxin) (133 kDa crystal protein).
 GN CRYIEA OR CRYIE(A) OR CRYIC(B) OR BTXI OR BTII.
 OS Bacillus thuringiensis (subsp. kenyaee).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=33930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91081338; PubMed=2259636;
 RA Bosse M., Masson L., Brousseau R.;
 RT "Nucleotide sequence of a novel crystal protein gene isolated from
 RT Bacillus thuringiensis subspecies kenyaee";
 RL Nucleic Acids Res. 18:7443-7443(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4F1;
 RX MEDLINE=91072224; PubMed=2254254;
 RA Visser B., Munsterman E., Stoker A., Dirkse W.G.;
 RT "A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-
 RT specific crystal protein.";
 RL J. Bacteriol. 172:6783-6788(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PS81F;
 RA Payne J.M., Sick A.J.;
 RT "Novel Bacillus thuringiensis isolate denoted B.t. PS81F, active
 RT against lepidopteran pests, and a gene encoding a lepidopteran-active
 RT toxin";
 RL Patent number US039523, 13-AUG-1991.
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE INCLUDING SPODOPTERA
 CC SPECIES.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
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 CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
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 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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 CC -----
 DR EMBL; X56144; CAA39609.1; -;
 DR EMBL; X53985; CAA37933.1; -;
 DR EMBL; M73252; AAA22345.1; -;
 DR HSSP; P02965; 1CIY.
 DR InterPro; IPR001178; Endotoxin.
 DR Pfam; PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 FT CONFLICT 862 N -> K (IN REF. 3).
 SQ SEQUENCE 1171 AA; 133252 MW; 5758FEBESABDB5ABE CRC64;
 Query Match 66.8%; Score 4173; DB 1; Length 1171;
 Best Local Similarity 69.1%; Pred. No. 1.le-261;
 Matches 822; Conservative 103; Mismatches 223; Indels 42; Gaps 13;
 QY 4 NIONQCVYPNCLNNPEVEILNEERSTGRPLDIDLSLSTRELLSEFVPGVAFGLFDLIW 63
 Db 5 NNONQCVYPNCLNNPENEIILDIERSNSTVATNIALEISR-LLASATPIGGILLGLFDIAW 63
 QY 64 GEITPDSWSLFLQIEOLIEORIEIERNRAITLRLGLADSYETIIEALREWEANPNNAQ 123
 Db 64 GSIGPSQWDLFLQIEILLIDOKIEEFARNQAIKLEGISLYGIYTAFAWEADPTNPA 123
 QY 124 LREDVRIRFANTDDALITANNFTLSFEIPLLSVYVQAANLHLSLRDAVDFQCGWGLD 183
 Db 124 LKEEMTQFNQDMSILVTAIPFSVQNVQVPLSVYVQAANLHLSLRDVSFQGWGFD 183
 QY 184 IAVNNHYNKLIINHRYTKHCLDITYNQLENL-RGNTROWARFNFRDLTLTVLDIV 242
 Db 184 IATINSRYNDLRLPIYTDYAVRWYNTGLDRLPRTGGLRNWARFNFRRELTSVLDII 243
 QY 243 ALFPNDVRYPIQTSSQLTREYTSVIE--DSPVSANIPNGENRAEFVGRPHLMDFM 300
 Db 244 SFRNVDLSRLYPIPTSQLTREYTVINITYRVGSPFENIENSA---IRSHLMDFL 300
 QY 301 NSLFVTAETVRSQTVMGHVLSSRNATAGNR-INFPSSGVFNPGGAIWIADEDPRP----- 354
 Db 301 NNLITDILLRGVYHAGHRTVSHFTGSSQVITPQYGI-----TAAEPRTIAPS 352
 QY 355 -----FYRTLSDPVEVRGFGNPHVVLGL---RGVAFQOTGNTNHTFRNNGSTIDSLD 404
 Db 353 TFPGLNLFYRTLSPNPFRRSENITP--TLGINVVGVGFIQP-NNAEVLVRSRGTVDSLN 409
 QY 405 EIPPDNSGAPWNDYSHVLNHTVFRKPGEISGDSWRAPMFSKTHRSATPTNTIDPERI 464
 Db 410 ELPIDGENSLV--GYSHRLSHVTLTR---SLYNTNITSLPTFVWTHHSATNTINPDI 464
 QY 465 TQPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGPPAYTIVNINGQLPQRIARIRYAS 524
 Db 465 TQPLVKGFRLLGGTSVKGFGTGGDILRNTIGEVSQVNSPITQRYLRFRYAS 524
 QY 525 TTNLRIVTVAGERIFAGQPNKMTDGTPLTFQSFVSATINTAFTPFMSOSSFTVGADTF 584
 Db 525 SRDARITVAIGGQIRVDMTLEKTEMEIGESLTSRTFSYTFNSNPFSPRANPDIIIRAEELP 584
 QY 585 SSGNEVYIDREFLIPYATATEAEVDLERAOKAVNALFTSINQIGIKTDVTDYHIDQVSNL 644
 Db 585 IRGELYIDKIEILADATFEEDYDLERAOKAVNALFTSNQLGLKTDVTDYHIDQVSNL 644
 QY 645 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDNPFGKINQOLDRGWGSTDITIQRG 704
 Db 645 VECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDNPFGKINQOLDRGWGSTDITIQGG 704
 QY 705 DDVFKENYVLPGTDECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEILYIRYNAK 764
 Db 705 DDVFKENYVLPGTDECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEILYIRYNAK 764

leafroller (Lepidoptera, Tortricidae).";
New Zealand J. Crop Hortic. Sci. 20:27-36(1992).
[5] SEQUENCE FROM N.A.
STRAIN=YBT-1520;
Sun M., Yu Z.;
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
OF THE SPORE COAT.
-!- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed i
insect-resistant cotton and tomato by Calgene (Monsanto) and in
maize by Dekalb Genetics.
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
N-TERMINUS.
-!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.

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[illegible]

Db 415 PQNNVPKQGFHSRLSHVMSFRSGFNSVSIIRAPMFSWIHRSAEFNIIASDSTIQI 474
 QY 468 PLVKAHTLQSGTTVVRPGTGGDILRRITSGGPPAYITVING-----QLP-----QRY 516
 Db 475 PAVKGNFLNG-SVIGSGTGGDLVRLNNGN-----NIONRGYIEVPIHFSTSTRY 527
 QY 517 RARIRYASTNLRIYVTVAGERIFAGQFNKIMTMDGPTLTFQSFYATINTAFTFPMQSS 576
 Db 528 RVRVYASVTPHILNVNMGSSIFSNVTPATATSLDNLQSSDPCYFESANAFT---SSLG 584
 QY 577 FTVGADTFSSGNEVYIDRFELIPVTAIFEAEDYLERAKAVNALFTSINQIGIKIDVTDY 636
 Db 585 NIVGRNFSGTAGVILDRFEIPVTALEAEYNLERAKAVNALFTSTNQLGKINTVTDY 644
 QY 637 HIDQVSNLVDCLSDFECDLDEKRELSEKVKHAKRLSDERNLLQDPNFKINQLDRGRGS 696
 Db 645 HIDQVSNLVTYLSDFCDLDEKRELSEKVKHAKRLSDERNLLQDPNFKINQLDRGRGS 704
 QY 697 TDTIQGDDVFKENYVTLPGTFDECYPTLYQKIDSKLKPTRYQLRGYIEDSQBLEI 756
 Db 705 TGITIQGDDVFKENYVTLPGTFDECYPTLYQKIDSKLKPTRYQLRGYIEDSQBLEI 764
 QY 757 YLIRYNAKHETVNVLGSLWPLSVQSPKCGPNRCAPHLENNPDLDCSCRDEKCAH 816
 Db 765 YLIRYNAKHETVNVLGSLWPLSVQSPKCGPNRCAPHLENNPDLDCSCRDEKCAH 824
 QY 817 HSHFSLDIDVCGTDLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVRAE 876
 Db 825 HSHFSLDIDVCGTDLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVRAE 884
 QY 877 KWRDRKRELEETNIVYKAKESVDALFVNSQYDQLOADTNIAHAAKRVHRIEAY 936
 Db 885 KWRDRKRELEETNIVYKAKESVDALFVNSQYDQLOADTNIAHAAKRVHRIEAY 944
 QY 937 LPESLVPVGNVDFEELKGRITAFPLXDARNVKNKDNGLSCNWKVGHVDVEQNN 996
 Db 945 LPESLVPVGNVDFEELKGRITAFPLXDARNVKNKDNGLSCNWKVGHVDVEQNN 1004
 QY 997 HRSVLVPEWEAEVQSVRVCPGRIYLTAYKEGYGEGCVTIHETENNTDELKFSNCV 1056
 Db 1005 QRSVLVPEWEAEVQSVRVCPGRIYLTAYKEGYGEGCVTIHETENNTDELKFSNCV 1064
 QY 1057 EEEVYNNVTCNDYANQOEYGAITSNRNGYDETYGSSNPADYASVYEKSYTDGR 1116
 Db 1065 EEEVYNNVTCNDYANQOEYGAITSNRNGYDETYGSSNPADYASVYEKSYTDGR 1120
 QY 1117 RNPCEENRGYDYPPLVPGVYVIRELFEETDKVWIEIGETGTFIVDSVELLMEE 1174
 Db 1121 RNPCEENRGYDYPPLVPGVYVIRELFEETDKVWIEIGETGTFIVDSVELLMEE 1178
 RESULT 14
 C1DB.BACTU STANDARD; PRT; 1160 AA.
 ID C1DB.BACTU
 AC Q45747;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pesticidal crystal protein cryIb (insecticidal delta-endotoxin
 DE CryIb(b) (crystalline entomocidal protoxin) (131 kDa crystal protein).
 GN CRYIb OR CRYIb(B).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RC STRAIN=BTS0349A;
 RA Lambert B.;
 RL Submitted (APR 1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
 CC EPIHELIAL CELLS OF INSECTS.
 CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 CC SPOREULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART

CC OF THE SPORE COAT.
 CC -!- MITOCHONDRIAL: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 CC N-TERMINUS.
 CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z22511; CAA80234.1; -
 DR HSP: P02965; ICIY.
 DR InterPro: IPR001178; Endotoxin.
 DR Pfam: PF00555; endotoxin; 1.
 KW Toxin; Sporulation.
 SQ SEQUENCE 1160 AA; 130968 MW; B18B18748B40695E CRC64;
 Query Match 66.4%; Score 4146; DB 1; Length 1160;
 Best Local Similarity 69.2%; Pred. No. 5.9e-260;
 Matches 817; Conservative 98; Mismatches 238; Indels 28; Gaps 15;
 QY 1 MENNIOQCVPYCNLNPVEVILNEER-STGRPLDLISLSTRELLSEFVPGVGVAFGLF 59
 Db 1 MDINHQCVPYCNLNPDAILLDAERLETGNTVADISGLINFLYFNFGGFIYGLL 60
 QY 60 DLWGTFTPSWSLFLQIEQLIEQRIETLERNRAITLRLGLADSYEYIEALREWNP 119
 Db 61 ELIWGFGVPSQWEIFLAIEQLISORTTEFARQCAISRLGSLNNYETITETFAWEKDP 120
 QY 120 NNAQLREDDVIRANTDDALITAINNETLSTFEPLISVYVQAAANLHLILRLDVSFGQ 179
 Db 121 SNPALREEMTQPNVMSALIAIPLLRVRYEVALLSVYVQAAANLHLVLRDVSFGQ 180
 QY 180 WGLDIAFVNNHYNRLINLHRYTKHCLDTYNOGLELRTNTROWAFNFRRLDTLTVL 239
 Db 181 WGPDPATVNSRYSDTLRIHYTDHCVTDYNDGLKNLEGSKLSDWVYVNRFRRLTISVL 240
 QY 240 DIVALFPNVDVRYPIOTSSQLTREIYTSVIEDSPVS--ANIPNGFNRAEFG-VRPFHL 296
 Db 241 DIIAFAFPNDIEAYPIQTASOLTREVYLDLPFVNETLSPASYPET-PSAAESAIRSPL 299
 QY 297 MDMNSLFTVAEVRVSTVWGHLVSS--RNTAGNRINFFSYG-VFNPGGAIWIADEDR 353
 Db 300 VDLNSETIITDLSAYWGWHLVNSFRGTNTNLRSLYREGTERFVTVISASPV 359
 QY 354 PFYRTLSDPVFVRGGFGNPHYVLGRVAFQQTGTNHTRTFRNSGTIDSLDETPQDQNSG 413
 Db 360 PIFRTLS--YFT--GLNPNPVAGIEGVFQNTISR--SIYKSGPIDSEFPQDVSV 413
 QY 414 APWDSYSHVNLNHTVFRWPCGEISGSWSRAPMFSWTHRSATPTNTIDPRTIOLPKAH 473
 Db 414 SPAIGYSHRLCHATFLE---RISG-PRIAGTVFSWTHRSASPINEVSPSRITQIPVVKAH 469
 QY 474 TLOGGTVVRGPGTGDILRRITSGGPPAYITVINGQLPQRYRARIYASTNLRIYVT 533
 Db 470 TLASGASVINGPGTGDILRRITSGGPPAYITVINGQLPQRYRARIYASTNLRIYVT 529
 QY 534 VAGERIFAGQFNKIMTMDGPTLTFQSFYATINTAFTFPMQSSFTVGDFFSGNEVYID 593
 Db 530 YSOPPSYGISFPKTMAGEALTSEFAHTLTFPIFSAQEEFDL---YIQSG--VYID 584
 QY 594 RFELIPVTAIFEAEDYLERAKAVNALFTSINQIGIKIDVTYHIDQVSNLVDCLSEFC 653
 Db 585 RIEFIPVDAFTESEINLERAKAVNALFTSTNQLGLKTDVTDYHIDQVSNLVDCLSEFC 644
 QY 654 LDEKRELSEKVKHAKRLSDERNLLQDPNFKINQLDRGRGSTDTIQGDDVFKENY 713
 Db 645 LDEKRELSEKVKHAKRLSDERNLLQDPNFKINQLDRGRGSTDTIQGDDVFKENY 704
 QY 714 TLPGTDECYPTLYQKIDSKLKPTRYQLRGYIEDSQBLEIYLRINAKHETVNLGT 773

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Db 705 TLTFDECYPTLYQKIDESKLAAYTYQLRGYIEDSQDLEIYLIRYNAKHEIVNPGT 764
QY 774 GSWLPLSVQSPILRGKGFENRCAPHLEWNPDLDCSCRDCEKCAHSHHPSFLDIDVGCIDL 833
Db 765 GSWLPLSVQSPILRGKGFENRCAPHLEWNPDLDCSCRDCEKCAHSHHPSFLDIDVGCIDL 824
QY 834 EDLDVWVIFKIKTDGCHARGNLNLEFLEKPLVGEALARKRAEKWRDKRKLKLETNIV 893
Db 825 EDLGVWVIFKIKTDGCHARGNLNLEFLEKPLVGEALARKRAEKWRDKRKLKLETNIV 884
QY 894 YKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEAYLPESLVIGVAVNDIFEE 953
Db 895 YKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEAYLPESLVIGVAVNDIFEE 944
QY 954 LKGRIFTAFLLDARNVKNKGNDFNGLSCWNVKGVHDVVEEQNNHRSVLVVPWEAEYSQE 1013
Db 945 LKGRIFTAFLLDARNVKNKGNDFNGLSCWNVKGVHDVVEEQNNHRSVLVVPWEAEYSQE 1004
QY 1014 VRVCGRGYILRVATYKESYGGCVTHIEIENNTDELKFSNCVEEVPNNVTTCNDYTA 1073
Db 1005 VRVCGRGYILRVATYKESYGGCVTHIEIENNTDELKFSNCVEEVPNNVTTCNDYTA 1062
QY 1074 NOEYGGAYTSNRGYDEFTYSSNVPADYASVYEEKSYTDGRRDNPCESTRGYDGYPL 1133
Db 1063 NKNHGANACSSNRGYDEFTYSSNVPADYASVYEEKSYTDGRRDNPCESTRGYDGYPL 1119
QY 1134 PAGYVTKLEYPPETDKVWIEGTEGTFIVDSVLELLMEE 1174
Db 1120 PAGYVTKLEYPPETDKVWIEGTEGTFIVDSVLELLMEE 1160

RESULT 15
C1CB_BACTG STANDARD: PRT: 1176 AA.
AC P56933;
AT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Pesticidal crystal protein cryIcb (insecticidal delta-endotoxin
DE CryIcb(b)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
GN CryIcb OR CryIcb(b).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=29338;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD-29;
RX MEDLINE=93236401; PubMed=8476286;
RA Kalman S.S.;
RT "Cloning a novel cryIc-type gene from a strain of Bacillus
RT thuringiensis galleriae.";
RL Appl. Environ. Microbiol. 59:1131-1137(1993).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS. TOXIC TO SPODOPTERA EXIGUA AND
CC TRICHPLOUSIA NI.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M97880; ; NOT_ANNOTATED_CDS.
CC HSP: P02965; 1C1Y.

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DR InterPro; IPR001178; Endotoxin.
DR Pfam; PF00555; endotoxin; 1.
KW Toxin; Sporulation.
SQ SEQUENCE 1176 AA; 132867 MW; 108233494C2AC018 CRC64;

Query Match 66.2%; Score 4134; DB 1; Length 1176;
Best Local Similarity 68.3%; Pred. No. 3.6e-259;
Matches 819; Conservative 98; Mismatches 234; Indels 48; Gaps 15;

QY 1 MENNIOQCVPYCLNPNVEILNEER-STGRPLRLDISLSLRFLESEFVPGVGVAFGLF 59
Db 1 MENNIOQCVPYCLNPNVEILNEER-STGRPLRLDISLSLRFLESEFVPGVGVAFGLF 60
QY 60 DLWTFIPSDWSLFLQIQEQIELELRNRAITTLRGLADSEIYIEALREWEANP 119
Db 61 DFVWGVGVPDFAFLVQIEQLINERIAAAYASAAISNLEGLNENFIYVEAFKEWADP 120
QY 120 NNAQLREDVRIRPANTDDALITAINNFTLTSPFIPLLSVVVOAANLHLSLLRDVAFSGG 179
Db 121 DNPVTRVVDREILDGLLERDIPSERTAGFEVPLLSVYAAANLHLSLLRDSSIFGAR 180
QY 180 WGLDIATVNNHYNRLINLHRYTKHCLDTYNOGLEMLRGNTTQWARFNOFRDLTLVL 239
Db 181 WGLTTINVENYNNRLIRHIDEYAHNCADTYNRLNNLPKSTYQDWITYNLRDLTLVL 240
QY 240 DIVALPENVDVRYPIQTSOLREIYTSVIEDSP---VSANIPNGENRABP-GVRPPH 295
Db 241 DIAAFPSIDNRKPIQSVGLREIYTDPLTFNFQOLASVAOLPT-FVWESNAIRTPH 299
QY 296 LMDFMNLSFTAE--TVRSQTVMGHLSNRNTPAGNRINFPSPSYGVPNGGAIWADEDP- 352
Db 300 LFDVLNLTFTDWSVGRNRYGWHGRVINSRIGGGNITSPIYG-----REANQEP 351
QY 353 -----RPFYRTLSDPVF--VRGFGNPHVL-GLRGVAFQQTGTHRTFRNSGIDSL 403
Db 352 RSFTENGFEVFTLSNPTFLPQOPWAPPENLRGVGEVEF-STPLN-SFTYRGRTVDLS 409
QY 404 DEIPPODSGAPWDXSHVLNHTFVRWPGCE---ISGSWSRAPMFESWTHRSATPTNTID 460
Db 410 TELPPEDNSVPPREGYSRHLCHATFVQSGTPELTIG-----PVFSWTHRSATDNIY 463
QY 461 PERITQIPLKVAHLOGSTVVRGPGFTGGDIILRRSGGPFATVIVNINGQLPQRTARI 520
Db 464 PDVINQIPLKAFNLTSQTSVVRGPGFTGGDIIRTVNGSVLSMSLNFSTMTLQRYRVY 523
QY 521 RYASTTNLRIVTVVAGERIFAGOFNKMDGDPDLPFQSPSYATINTAFTPPMSQSFTVG 580
Db 524 RYASQTMVMSVTVGGSTTGNGGFPSTMSANGALTQSFEFA-----EPVQISASGSQ 577
QY 581 ADTPSSGNEV-----YIDREFLPVATFAEYDLERAQKAVNALFTSINQIGKIDVTD 635
Db 578 GASISNNVGRQMFHLDRIEFLPVTSTFEEDYDLERAQAVNALFTSTNQLGLKIDVTD 637
QY 636 YHIDQVSNLVDCLSDPECLDEKRELSKVKHAKRLSDERNLLDOPNPKGNOLDGRWRG 695
Db 638 YHIDQVSNLVECLSDPECLDEKRELSKVKHAKRLSDERNLLDOPNPKGNOLDGRWRG 697
QY 696 STDTIQRGDDVKENYVTLFGTFDECYPYLYQKIDESKLAAYTYQLRGYIEDSQDLE 755
Db 698 STDTIQRGDDVKENYVTLFGTFDECYPYLYQKIDESKLAAYTYQLRGYIEDSQDLE 757
QY 756 IYLIRYNAKHEIVNPGTGLSWLPLSVQSPILRGKGFENRCAPHLEWNPDLDCSCRDCEKA 815
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QY 816 HSHHFSLDIDVGCIDLNEDLDVWVIFKIKTDGCHARGNLNLEFLEKPLVGEALARKRA 875
Db 818 HSHHFSLDIDVGCIDLNEDLDVWVIFKIKTDGCHARGNLNLEFLEKPLVGEALARKRA 877
QY 876 EKKWRDKREKLELETNIVTYKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEA 935
Db 878 EKKWRDKREKLEWETNIVTYKEAKESVDALFVNSOYDQADTNIAHHAADKRVHRIEA 937

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QY 936 YLPESVIPGVNVDIPEELKGRIFTAFFLYDARNVIKNGDFNNGLSQWNYKGHVDEEQN 995
||||| 938 YLPESVIPGVNAGIFEELGRIFTAYSLYDARNVIKNGDFNNGLLCWNLKGHVDEEQN 997
Db 938 YLPESVIPGVNAGIFEELGRIFTAYSLYDARNVIKNGDFNNGLLCWNLKGHVDEEQN 997
QY 996 NHRSLVVPWEAEVSVQEVRCVPCRGYILRVYAYKESYGEGCVTIHEIENNTDELKFSNC 1055
Db 998 NHRSLVVPWEAEVSVQEVRCVPCRGYILRVYAYKESYGEGCVTIHEIENNTDELKFSNC 1057
QY 1056 VEEVYPNNTVTCNDYTANQOEYGGAYTSNRGYDetyGNSSVPADYASVYEEKSYTDG 1115
Db 1058 VEEVYPNNTVTCNDYTATQOEYGGAYTSNRHGYGKSYESNSSVQADYASVYEEKADTDG 1117
QY 1116 RRDNPESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174
Db 1118 RRDNPESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1176
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Search completed: November 27, 2002, 20:22:34
Job time : 41 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 18:33:24 ; Search time 54 seconds
(without alignments)
2090.034 Million cell updates/sec

Title: US-09-837-961-8
Perfect score: 6244
Sequence: 1 MENNIOQCVPYNNCLNPEV.....IGETEGTIVDSVELLMEE 1174
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6244	100.0	1174	2 A42459	parasporal crystal
2	5406	86.6	1174	2 S32649	parasporal crystal
3	4424.5	70.9	1181	2 A41052	parasporal crystal
4	4342	69.5	1176	2 J0241	parasporal crystal
5	4329	69.3	1176	2 S02215	parasporal crystal
6	4328	69.3	1176	2 JC2219	parasporal crystal
7	4326	69.3	1176	2 A22617	parasporal crystal
8	4303	68.9	1166	2 S32645	parasporal crystal
9	4282.5	68.6	1165	2 S11446	parasporal crystal
10	4230.5	67.8	1172	2 S32689	parasporal crystal
11	4217.5	67.5	1189	2 S00944	parasporal crystal
12	4211.5	67.4	1155	2 JD0002	parasporal crystal
13	4194.5	67.2	1155	2 A39838	parasporal crystal
14	4191.5	67.1	1155	2 A26513	parasporal crystal
15	4189.5	67.1	1155	2 S02134	parasporal crystal
16	4186	67.0	1156	2 A29125	parasporal crystal
17	4173	66.8	1171	2 I40572	parasporal crystal
18	4151.5	66.5	1177	2 A49785	parasporal crystal
19	4148	66.4	1171	2 A37829	parasporal crystal
20	4148	66.4	1178	1 USBSXH	parasporal crystal
21	4146	66.4	1160	2 S32647	parasporal crystal
22	4134	66.2	1176	2 A48970	parasporal crystal
23	4037	64.7	1156	2 A29838	parasporal crystal
24	3465	55.5	1228	2 S00873	parasporal crystal
25	3120	50.0	934	2 A22798	parasporal crystal
26	2367.5	37.9	823	2 S04181	parasporal crystal
27	2129.5	34.1	1138	2 A48944	parasporal crystal
28	1947.5	31.2	1157	1 S49247	parasporal crystal
29	1850	29.6	1154	2 S39536	parasporal crystal

ALIGNMENTS

RESULT 1

A42459
parasporal crystal protein cryIFal - Bacillus thuringiensis (strain aizawai)
N:Alternate names: parasporal crystal protein cryIF
C:Species: Bacillus thuringiensis
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 01-Dec-2000
C:Accession: A42459
J:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, R. Bacteriol. 173, 3966-3976, 1991
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene
A:Reference number: A42459; MUID:91286178; PMID:2061280
A:Accession: A42459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <CHA>
A:Cross-references: GB:M63897; NID:gi42757; PIDN:AAA2348.1; PID:gi42758
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 100.0%; Score 6244; DB 2; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MENNIOQCVPYNNCLNPEVEILNEERSTGRPLDISLTRFLLSFEVPGVAFGLFD	60
DB	1	MENNIOQCVPYNNCLNPEVEILNEERSTGRPLDISLTRFLLSFEVPGVAFGLFD	60
QY	61	LWGFITPDSWLSFLQIEQLIQRITLERNRAITTLRLGLADSYEYIIEALREWEANPN	120
DB	61	LWGFITPDSWLSFLQIEQLIQRITLERNRAITTLRLGLADSYEYIIEALREWEANPN	120
QY	121	NAQLREDVIRFANTDDALITANNFTLTSTFEIPLLSVYVQAAANHLSLRDVAFSGQW	180
DB	121	NAQLREDVIRFANTDDALITANNFTLTSTFEIPLLSVYVQAAANHLSLRDVAFSGQW	180
QY	181	GLDIATVNNHYNKLINLHRYTHKCLDITYNOGLENLRGNTQWARPNQFRDLTLVLD	240
DB	181	GLDIATVNNHYNKLINLHRYTHKCLDITYNOGLENLRGNTQWARPNQFRDLTLVLD	240
QY	241	IVALFPNDVTRTPIOTSSOLTREITTSVIEDSPYSANIPNGFNRAEFGVRPPLMDFM	300
DB	241	IVALFPNDVTRTPIOTSSOLTREITTSVIEDSPYSANIPNGFNRAEFGVRPPLMDFM	300
QY	301	NSLFTVTAETVRSQTVGGHLYSSRNAGNINFPSSYGVFNPGGAIWIADEDDPPFYRTL	360
DB	301	NSLFTVTAETVRSQTVGGHLYSSRNAGNINFPSSYGVFNPGGAIWIADEDDPPFYRTL	360
QY	361	DPYFVRGGFGNPHYVGLRGVAFQQTGTNTRFRNSGTTDSLDEIPPDNSGAPNDYS	420
DB	361	DPYFVRGGFGNPHYVGLRGVAFQQTGTNTRFRNSGTTDSLDEIPPDNSGAPNDYS	420
QY	421	HVLNHTVFEWPGCEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKATLQSGTT	480

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Db 421 HVLNHWTFVRWPGEGISGDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
Qy 481 VVRGPGCTGDDTLRTSGGPFAYTIVNNGQLPQRYARIRYASTNLRIVTVAGERIF 540
Db 481 VVRGPGCTGDDTLRTSGGPFAYTIVNNGQLPQRYARIRYASTNLRIVTVAGERIF 540
Qy 541 AQCFNKMTDGTGDLTFQSFYSATINTAFTFPMSSQSFVAGDTFSSGNEVYIDRELLIPV 600
Db 541 AQCFNKMTDGTGDLTFQSFYSATINTAFTFPMSSQSFVAGDTFSSGNEVYIDRELLIPV 600
Qy 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCDEKREL 660
Db 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCDEKREL 660
Qy 661 SEKVHAKRLSDERNLLODPNFKGINROLDRGWRGSDITITQGGDDVFKENYVTLPGTFD 720
Db 661 SEKVHAKRLSDERNLLODPNFKGINROLDRGWRGSDITITQGGDDVFKENYVTLPGTFD 720
Qy 721 ECPYLYQKIDESKLKPYTRYQLRGYIDSDQLEIYIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYQKIDESKLKPYTRYQLRGYIDSDQLEIYIRYNAKHETVNVLTGSLWPLS 780
Qy 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSDRGDKCAHSHHFSLDIDVGCITDLNEDLDVWV 840
Db 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSDRGDKCAHSHHFSLDIDVGCITDLNEDLDVWV 840
Qy 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Qy 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPDLSVIPGVNVDIPEELKGRIFT 960
Db 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPDLSVIPGVNVDIPEELKGRIFT 960
Qy 961 AFFLYDARNVIKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVCPGR 1020
Db 961 AFFLYDARNVIKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVCPGR 1020
Qy 1021 GYLIRVTAYKEGEGCVTTHIEENNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEYGG 1080
Db 1021 GYLIRVTAYKEGEGCVTTHIEENNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEYGG 1080
Qy 1081 AYTSSNRGYDEYGSNSVPADYASVYEKSYTDGRRDNPCSNRGYGDYPLPAGYVTK 1140
Db 1081 AYTSSNRGYDEYGSNSVPADYASVYEKSYTDGRRDNPCSNRGYGDYPLPAGYVTK 1140
Qy 1141 ELEYPPETOKVWIEIGETEGTIFVDSVELLMEE 1174
Db 1141 ELEYPPETOKVWIEIGETEGTIFVDSVELLMEE 1174

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RESULT 2

S32649

Parasporal crystal protein cryIpa3 - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S32649

R:Lambert, B.

submitted to the EMBL Data Library, April 1993

A:Reference number: S32645

A:Accession: S32649

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1174 <LAW>

A:Cross-references: EMBL:222512; NID:g295865; PIDN:CAA80235.1; PID:g295866

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match

Best Local Similarity 86.6%; Score 5406; DB 2; Length 1174;

Matches 1017; Conservative 60; Mismatches 95; Indels 4; Gaps 3;

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Qy 1 MENNIOQCVPYNCLNHPVEIILNEERSTGRPLDLSLSLTRELLSEFVGVGVAGLEFD 60
Db 1 MKNKIQQCVPYNCLNHPVEIILNEERSTGRPLDLSLSLTRELLSEFVGVGVAGLEFD 60
Qy 61 LINGFITPSDWSFLQIQEQLIQRIETLERNRAITLRLGLADSYEIIYALREWZANPN 120
Db 61 LINGFITPSDWSFLQIQEQLIQRIETLERNRAITLRLGLADSYEIIYALREWZANPN 120
Qy 121 NAQLREDEVIRFANTDDALITANNFTLTSFEIPLLSVYVQAAHLSLRLDVAVSFGQW 180
Db 121 NAQLREDEVIRFANTDDALITANNFTLTSFEIPLLSVYVQAAHLSLRLDVAVSFGQW 180
Qy 181 GLDIATVNNHYNLNLHRYTKHCLDVTYNGLENLGNINTRQWARPNFRRLTTLTVLD 240
Db 181 GLDIATVNNHYNLNLHRYTKHCLDVTYNGLENLGNINTRQWARPNFRRLTTLTVLD 240
Qy 241 IVALFPNVDVRYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRAEGVRPPLMDFM 300
Db 241 IVALFPNVDVRYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRAEGVRPPLMDFM 300
Qy 301 NSLFVTAETVRSQTVMGHVLVSSRNTAGNRINFPSTYGVFNPGGAIWAIDEDPRPFYRTLS 360
Db 301 NSLFVTAETVRSQTVMGHVLVSSRNTAGNRINFPSTYGVFNPGGAIWAIDEDPRPFYRTLS 360
Qy 361 DPVVRGFGNPNHYVLGRGVAFOQTGNTNTRFRSGTIDSLDEIPQDNSCAPNDYS 420
Db 361 DPVVRGFGNPNHYVLGRGVAFOQTGNTNTRFRSGTIDSLDEIPQDNSCAPNDYS 420
Qy 421 HVLNHWTFVRWPGEGISGDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
Db 421 HVLNHWTFVRWPGEGISGDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
Qy 481 VVRGPGCTGDDTLRTSGGPFAYTIVNNGQLPQRYARIRYASTNLRIVTVAGERIF 540
Db 481 VVRGPGCTGDDTLRTSGGPFAYTIVNNGQLPQRYARIRYASTNLRIVTVAGERIF 540
Qy 541 AQCFNKMTDGTGDLTFQSFYSATINTAFTFPMSSQSFVAGDTFSSGNEVYIDRELLIPV 600
Db 541 AQCFNKMTDGTGDLTFQSFYSATINTAFTFPMSSQSFVAGDTFSSGNEVYIDRELLIPV 600
Qy 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCDEKREL 660
Db 601 TATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCDEKREL 660
Qy 661 SEKVHAKRLSDERNLLODPNFKGINROLDRGWRGSDITITQGGDDVFKENYVTLPGTFD 720
Db 661 SEKVHAKRLSDERNLLODPNFKGINROLDRGWRGSDITITQGGDDVFKENYVTLPGTFD 720
Qy 721 ECPYLYQKIDESKLKPYTRYQLRGYIDSDQLEIYIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYQKIDESKLKPYTRYQLRGYIDSDQLEIYIRYNAKHETVNVLTGSLWPLS 780
Qy 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSDRGDKCAHSHHFSLDIDVGCITDLNEDLDVWV 840
Db 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSDRGDKCAHSHHFSLDIDVGCITDLNEDLDVWV 840
Qy 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAKKWRDKREKLELETNIVYKEAKES 900
Qy 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPDLSVIPGVNVDIPEELKGRIFT 960
Db 901 VDALFVNSQYDQLOADNTAMIAHADKRVHRIREAYLPDLSVIPGVNVDIPEELKGRIFT 960
Qy 961 AFFLYDARNVIKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVCPGR 1020
Db 961 AFFLYDARNVIKNGDFNGLSCWNKGVHDVEEQNNHRSVLVVPWEAEVSEVRCVCPGR 1020
Qy 1021 GYLIRVTAYKEGEGCVTTHIEENNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEY 1078
Db 1021 GYLIRVTAYKEGEGCVTTHIEENNTDELKFSNCVBEVEYVNNVTCTNDYTANQEEY 1078
Qy 1079 GGAVTSNRGYDEYGSNSVPADYASVYEKSYTDGRRDNPCSNRGYGDYPLPAGYV 1138

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Db 1079 TDACNVNRGYEDAYGNPSTPHVHTPYEEETVTDERRNPCEANKGYNYTLPVGYV 1138
 Qy 1139 TKELEYPPETDKWIEIGETEGFIVDSVLELLMEE 1174
 Db 1139 TKELEYPPETDKWIEIGETEGFIVDSVLELLMEE 1174
 RESULT 3
 A41052
 parasporal crystal protein cryaEl - Bacillus thuringiensis (strain alesti)
 C:Species: Bacillus thuringiensis
 C:Date: 03-Apr-1992 #sequence-revision 03-Apr-1992 #text_change 01-Dec-2000
 C:Accession: A41052
 R:Lee, C.S.; Aronson, A.I.
 J. Bacteriol. 173, 6635-6638, 1991
 A:Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp
 A:Reference number: A41052; MUID:9201142; PMID:1855719
 A:Accession: A41052
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1181 <LEE>
 A:Cross-references: GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin
 Query Match 70.9%; Score 4424.5; DB 2: Length 1181;
 Best Local Similarity 72.1%; Pred. No. 7.4e-280;
 Matches 857; Conservative 93; Mismatches 216; Indels 23; Gaps 9;
 Qy 1 MENNIO-QCVPYNCLANPEVEILNEER-STGRULPLDISLIRFLSEFVPGVGAVGL 58
 Db 1 MDNNPKINEGIPNCLSENPEVVLGGRIETGYTPIDISLSTQFLSEFVPGAGFVGL 60
 Qy 59 FDLTWGITPSDSLFTLOLIEQRIETLERNRAITTLIRGLADSYEIIYIEALREAN 118
 Db 61 IDLWGVGSPGDAFLVQIEQLISQRIEFARQALSRLEGSLNYCIYAEAFREWD 120
 Qy 119 PNAQLREDYRIRFANDDALITAINFTLTSFPIPLSVYVQAAHLHLILLRDVAFSG 178
 Db 121 PTNPALREEMRIQFNDMSALTAIPFTVQNVQVPLSVYVQAVNHLSLVLRDVSFQG 180
 Qy 179 GWGLDIATVNNHYNRLINLIRYTHKCLDTYNOGLENLRTNQWARFNQFRDLTLV 238
 Db 181 RWGLDVATINSRYNDLRLICTYDYAVRYNTGLERVWGPDSRDWVRYNOFREELTLV 240
 Qy 239 LDIVALEPNVDVRYPIQTSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLM 298
 Db 241 LDIVLEPNVDSTRYPIRTVSQLTREIYTPVLEN--FDGSRGSAQRIEQSRPSLMD 298
 Qy 299 FMNSLFYTAETVRSQTVMGGH--LVSSRNTAGNRINPSPYGVF-NPGGAIWIADEDP 355
 Db 299 ILNSITTYDAHGGYVYWSGHQIMASPVGSGPEFTFLYGTWGNAAPOQRIVAQLCGV 358
 Qy 356 YRLSDPVFVRGFGNPHYVLGRG-----VAFQQTGNTHTFRNFGTIDSLDE 405
 Db 359 YRTLSS-TPYR---NP-FIIGINQRSLVDGTEFAYGSSNLPASVYRKSGTVDSLDE 412
 Qy 406 IPQDNSSGAPNDYSHVLNVHTFVRWPGELISGDSWRAPMFSWTHRSATPTNIDPERIT 465
 Db 413 IPQDNVPRQGFQSHLSHVSMFRSGFSNVSIVIRAPMFSWIHRSAEFNNTIPSSQIT 472
 Qy 466 QIPLVKAHTLQSGTIVYRGFGTGGDLIRTSQGPFFATTVININGQLPQRYRIRYAST 525
 Db 473 QIPLTKSTNLGSGTSVYKGFQGGDLIRTSQGISLVRNITAPLSQRYRIRYAST 532
 Qy 526 TNLRIYTVVAGERIFAGQFNKMTDGTGDLPTFQGSFYATINTAFTFPMSSQSFFVGDFTFS 585
 Db 533 TNLQFHTSIDGRPINQGNFSATWSSGGNQLSGSFRTYGVFTTFNFNSGSSVFTLSAHVN 592
 Qy 586 SGNEVYIDRELIPVATFAEYDLERAQXAVNALFTSINOIGIKTDTVTHIDQVSNLV 645
 Db 593 SGNEVYIDREFFVPAEYTFEAYDLERAQXAVNALFTSPNQIGLTKDTVTHIDQVSNLV 652

QY 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDITYNOGLENLRGNTROWARENQFRRLDITLV 238
 Db 181 RMGFDAATINSYNDLRLTGLNITDYAVRWYNTGLERWGPDSRWYRQFRRLDITLV 240
 QY 239 LDIVALFPMYDVRTYPIOTSSOLTREITSSVIEDSPVSANIPNGF----NRAEFGVRPP 294
 Db 241 LDIVALFPMYDVRTYPIOTSSOLTREITSSVIEDSPVSANIPNGF----NRAEFGVRPP 294
 QY 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPSPYGVENPGGAI--WIADE 350
 Db 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPSPYGVENPGGAI--WIADE 350
 QY 351 DRPPYRILSDPVFVR----GGFNGPHYVLGRVAFQQTGNHRT--FRNSGTIDSLD 404
 Db 353 TGLGIFERTLSPLRYRIILGSGPNNOELFVLDGTEFASLTNLPSTIYRQGVVDSLD 412
 QY 405 EIPPDNSGAPWNDYSHVLNHTVVRWPGETSGS--DSWRAPMFSWTHRSATPTNIDPER 463
 Db 413 VIPPDNSVPPRAGFSHRLSHVTML--SQAAGAVYTLRAPTFSWQHSRAEFNNIPSSQ 469
 QY 464 ITQIPLVKAHTILOSCTTVVRGPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 523
 Db 470 ITQIPLVKAHTILOSCTTVVRGPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 523
 QY 524 STTNLRIVTVAGERIFAGQNKMTMDGDLPTFQSFYSATINTAFTFPMSSOSFTVGADT 583
 Db 530 STTNLRIVTVAGERIFAGQNKMTMDGDLPTFQSFYSATINTAFTFPMSSOSFTVGADT 583
 QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAYNALFTSINQIGIKTDVTDYHIDQVSN 643
 Db 590 FNSGNEVYIDRFELIPVTATFEAYDLERAKAYNALFTSINQIGIKTDVTDYHIDQVSN 649
 QY 644 LVDCLSDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGNRLDGRWGSTDITIQ 703
 Db 650 LVECLSEDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGNRLDGRWGSTDITIQ 709
 QY 704 GDDVFEKNYVTLPGTDFECYPTLYQKIDESKLPKPYTRYOLRGVIEDSQLEIYLIRYNA 763
 Db 710 GDDVFEKNYVTLPGTDFECYPTLYQKIDESKLPKPYTRYOLRGVIEDSQLEIYLIRYNA 769
 QY 764 KHEVNVLTGSLWPLSAQSPIGKCGEPNRCAPHLENNPDLDCSCRGEKCAHSHHFSL 823
 Db 770 KHEVNVLTGSLWPLSAQSPIGKCGEPNRCAPHLENNPDLDCSCRGEKCAHSHHFSL 829
 QY 824 DIDVCGTDLNEDDLWVIFRIKTDGCHARLGNLEFLEEKPLVGBALARKVRAKKWRDKR 883
 Db 830 DIDVCGTDLNEDDLWVIFRIKTDGCHARLGNLEFLEEKPLVGBALARKVRAKKWRDKR 889
 QY 884 EKLEETNIVYKEAKESVDALFVNSQDQLOADNIAHAAKRVHRIREAYLPESVI 943
 Db 890 EKLEETNIVYKEAKESVDALFVNSQDQLOADNIAHAAKRVHRIREAYLPESVI 949
 QY 944 PGVNDVIFEELKGRIFTAFYLDARNYKNGDFNNGLSCHWNVKGVDEEONNHRSLV 1003
 Db 950 PGVNDVIFEELKGRIFTAFYLDARNYKNGDFNNGLSCHWNVKGVDEEONNHRSLV 1009
 QY 1004 PEWEAEVQSVRVCPGRGYILRVTAAYKEGEGCVTTHIENNTDELKFSNCVEEYV 1063
 Db 1010 PEWEAEVQSVRVCPGRGYILRVTAAYKEGEGCVTTHIENNTDELKFSNCVEEYV 1069
 QY 1064 NTVTCNDYTANOBEYGAYSRNGYDETYGNSSVFADYASVYEKSYTDGRDRNPCE 1123
 Db 1070 NTVTCNDYTANOBEYGAYSRNGYDETYGNSSVFADYASVYEKSYTDGRDRNPCE 1125
 QY 1124 NRGYGDYTPLPAGVYVTRKELVPEPTDKVWIEIGETGCTFIVDSVELLMEE 1174
 Db 1126 NRGYGDYTPLPAGVYVTRKELVPEPTDKVWIEIGETGCTFIVDSVELLMEE 1176

RESULT 5
 S02215

parasporal crystal protein cryA - *Bacillus thuringiensis* (strain entomocidus)
 C:Species: *Bacillus thuringiensis*

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-Dec-2000
 C:Accession: S02215
 C:Masson, L.; Marcotte, P.; Prefontaine, G.; Brousseau, R.
 Nucleic Acids Res. 17, 446, 1989
 A:Title: Nucleotide sequence of a gene cloned from *Bacillus thuringiensis* subspecies
 A:Reference number: S02215; MUID:89098405; PMID:2911478
 A:Accession: S02215
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1176 <NAS>
 A:Cross-references: EMBL:X13535; NID:g40266; PIDN:CAA31886.1; PID:g40267
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 69.3%; Score 4329; DB 2; Length 1176;
 Best Local Similarity 71.4%; Pred. No. 1.2e-273;

Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;

QY 1 MENNIIQ-NOCVPYNCLNNPEVEILNEER-STGRLLPDLISLTLRELLSEFPVGVGATGL 58
 Db 1 MNNPNINECIPNCLSNPEVEVLGGERIEGTPTIDISLTLQFLLEFVPGAGFVLGL 60
 QY 59 FDLIWFITTPSDWSLFLQIEQRIETLERNNRAITTLRGLADSYEITAEALREWEAN 118
 Db 61 VDIWIFGPGSQWDAPFVQIEQLINQRIETEFARQAISLECLSNLYQIYAESFREWAD 120
 QY 119 PNNQLREDVRIRANTDDALITANNFTLSFEIPLSVYVQAANLHLSLRDVSFGQ 178
 Db 121 PTNPALEEMRIQFNDMNSALTTPAILAVQNYQVPLLSVYVQAANLHLSLRDVSFGQ 180
 QY 179 GWGLDIATVNNHYNRLINLIHRYTKHCLDITYNOGLENLRGNTROWARENQFRRLDITLV 238
 Db 181 RMGFDAATINSYNDLRLTGLNITDYAVRWYNTGLERWGPDSRWYRQFRRLDITLV 240
 QY 239 LDIVALFPMYDVRTYPIOTSSOLTREITSSVIEDSPVSANIPNGF----NRAEFGVRPP 294
 Db 241 LDIVALFPMYDVRTYPIOTSSOLTREITSSVIEDSPVSANIPNGF----NRAEFGVRPP 294
 QY 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPSPYGVENPGGAI--WIADE 350
 Db 295 HLMDFMNSLFTVTAETVRSQTVWGGHLSVR--NTAGNRINPSPYGVENPGGAI--WIADE 350
 QY 351 DRPPYRILSDPVFVR----GGFNGPHYVLGRVAFQQTGNHRT--FRNSGTIDSLD 404
 Db 353 TGLGIFERTLSPLRYRIILGSGPNNOELFVLDGTEFASLTNLPSTIYRQGVVDSLD 412
 QY 405 EIPPDNSGAPWNDYSHVLNHTVVRWPGETSGS--DSWRAPMFSWTHRSATPTNIDPER 463
 Db 413 VIPPDNSVPPRAGFSHRLSHVTML--SQAAGAVYTLRAPTFSWQHSRAEFNNIPSSQ 469
 QY 464 ITQIPLVKAHTILOSCTTVVRGPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 523
 Db 470 ITQIPLVKAHTILOSCTTVVRGPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYA 529
 QY 524 STTNLRIVTVAGERIFAGQNKMTMDGDLPTFQSFYSATINTAFTFPMSSOSFTVGADT 583
 Db 530 STTNLRIVTVAGERIFAGQNKMTMDGDLPTFQSFYSATINTAFTFPMSSOSFTVGADT 589
 QY 584 FSSGNEVYIDRFELIPVTATFEAYDLERAKAYNALFTSINQIGIKTDVTDYHIDQVSN 643
 Db 590 FNSGNEVYIDRFELIPVTATFEAYDLERAKAYNALFTSINQIGIKTDVTDYHIDQVSN 649
 QY 644 LVDCLSDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGNRLDGRWGSTDITIQ 703
 Db 650 LVECLSEDEFCLDERKELSEKVKHAKRLSDERNLLQDPNFKGNRLDGRWGSTDITIQ 709
 QY 704 GDDVFEKNYVTLPGTDFECYPTLYQKIDESKLPKPYTRYOLRGVIEDSQLEIYLIRYNA 763
 Db 710 GDDVFEKNYVTLPGTDFECYPTLYQKIDESKLPKPYTRYOLRGVIEDSQLEIYLIRYNA 769
 QY 764 KHEVNVLTGSLWPLSAQSPIGKCGEPNRCAPHLENNPDLDCSCRGEKCAHSHHFSL 823
 Db 770 KHEVNVLTGSLWPLSAQSPIGKCGEPNRCAPHLENNPDLDCSCRGEKCAHSHHFSL 829

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QY 824 DIDVGCDDLNEEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 883
D 830 DIDVGCDDLNEEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 889
QY 884 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 943
D 890 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 949
QY 944 PGVNVDFEELKGRIFTAFGLYDARNVKNKNGDFNGLSCWNVKGVHVDVEEQNNHRSVLV 1003
D 950 PGVNAALFEELKGRIFTAFGLYDARNVKNKNGDFNGLSCWNVKGVHVDVEEQNNHRSVLV 1009
QY 1004 PEWEAEYSQEVRCVPCGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVFN 1063
D 1010 PEWEAEYSQEVRCVPCGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVFN 1069
QY 1064 NTVTCNDYTANQOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1123
D 1070 NTVTCNDYTANQOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1125
QY 1124 NRGYDTPPLPAGVYVTKLEYFPETDKWIEIGTEGTFIVDSVELLMEE 1174
D 1126 NRGYDTPPLPAGVYVTKLEYFPETDKWIEIGTEGTFIVDSVELLMEE 1176

RESULT 6
JC2219
parasporal crystal protein cryIAa - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 58, 830-835, 1994
A:Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an
A:Reference number: JC2219; MUID:94289859; PMID:7764972
A:Accession: JC2219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: DDBJ:D17518; NID:g506190; PIDN:BA04468.1; PID:g535781
C:Genetics:
A:Gene: cryIA(a)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 69.3%; Score 4328; DB 2: Length 1176;
Best Local Similarity 71.4%; Pred. No. 1.4e-273;
Matches 850; Conservative 86; Mismatches 223; Indels 32; Gaps 12;

QY 1 MENNIQ-NQCVPYNCLNPEVEILNEER-STGRPLDLSLTLRFLSEFVPGVGVAFGL 58
D 1 MDNPNINECIPYNCLNPEVEILNEER-STGRPLDLSLTLRFLSEFVPGVGVAFGL 60
QY 59 FDLTWGFTSDWSLFLQLQLEQRIETLERNAITTLRGLADSYETIETALREHNEAN 118
D 61 VDIWIGFGPSQMDAFVLQLEQINQIEEFARNAQISLRLEGLSNLYQIYAESFREWEAD 120
QY 119 PNNAQLREDVRIRFANTDDALITAINFTLSTPIPLSVYVQAANLHSLRLDVAESFGQ 178
D 121 PTPNALREEMRIQFNDMNSALITPAILLAVQNYQVPLSVYVQAANLHSLRLDVAESFGQ 180
QY 179 GWGLDIATVNNHRLNLIHRYTKHCLDNTYNOGLELGTNTQWAFRQFRDLTLTV 238
D 181 RWGFDAAATINSRYNDLRLIGNTYDAVRWNTGLRWGPDSDRWYRQFRDLTLTV 240
QY 239 LDIVALEPNDVRYPTQTSOLTRTYTSVIEDSPVSNANIPNGF----NRAEFGVRPP 294
D 241 LDIVALEPNDVRYPTQTSOLTRTYTSVIEDSPVSNANIPNGF----NRAEFGVRPP 294
QY 295 HLMDEMSLFTVTAFTVRSQVWGGHLYSSR--NTAGNRINFPSPGVNPNPGAI--WIADE 350
D 295 HLMDEMSLFTVTAFTVRSQVWGGHLYSSR--NTAGNRINFPSPGVNPNPGAI--WIADE 352
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QY 351 DPRPFYRTLSDPVFR-----GGFGNPHYVLGRVAFQQTGNTHTT-ERNSGTDSID 404
D 353 TGLGIFRTLSPLRYRILGSGPNQELFVDGTEFSASLTNTLPSTIYRQRTVDSID 412
QY 405 EIPQDNSGAFWNDYSVHLNHTFVRNPEIGS--DSWRAPMFMSWTHRSATPTNTIDPER 463
D 413 VIPQDNSVPRAGFSHLSHVITML---SQAAGAVYTLRAFTSQWHSRAEFNNIIPSSQ 469
QY 464 ITQPLVKAHTLQSGTTVVRGPGTGGDILRRTSGGPPAYTIVNINGQLPORYRARIYA 523
D 470 ITQPLTKSTNLGSGTSVYKPGTGGDILRRTSGGISTLRVNTITAPLSORYRARIYA 529
QY 524 STTNLRIVTVAGRIIRAGQENKMTDGTPLTFOSFSTATINTAFTFPMSSOSSFTVAGDT 583
D 530 STTNLRIVTVAGRIIRAGQENKMTDGTPLTFOSFSTATINTAFTFPMSSOSSFTVAGDT 589
QY 584 PSSNEVYIDFELIPVATFEAEYDLERAKAVNALTSINOIGIKTDVTDYHIDQVSN 643
D 590 FNSGNEVYIDFELIPVATFEAEYDLERAKAVNALTSINOIGIKTDVTDYHIDQVSN 649
QY 644 LVDCLSDFECLDEKRELSEKVKHAKRLSDERNLQDPPNFKGINBOLDRGWGSTDTITQR 703
D 650 LVDCLSDFECLDEKRELSEKVKHAKRLSDERNLQDPPNFKGINBOLDRGWGSTDTITQR 709
QY 704 GDDVFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYA 763
D 710 GDDVFKENYVTLPGTFDECYTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYA 769
QY 764 KHEVNVVLGTSGLWPLSVQSPDKGPNRCAPHLENNPDLDCSCRDGCEKCAHSHHFS 823
D 770 KHEVNVVLGTSGLWPLSVQSPDKGPNRCAPHLENNPDLDCSCRDGCEKCAHSHHFS 829
QY 824 DIDVGCDDLNEEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 883
D 830 DIDVGCDDLNEEDLVWVIFKIKTODGHARLGNLEFLEKPLVGEALARKVKAEEKWRDKR 889
QY 884 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 943
D 890 EKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHAAKRVHRIREAYLPELSVI 949
QY 944 PGVNVDFEELKGRIFTAFGLYDARNVKNKNGDFNGLSCWNVKGVHVDVEEQNNHRSVLV 1003
D 950 PGVNAALFEELKGRIFTAFGLYDARNVKNKNGDFNGLSCWNVKGVHVDVEEQNNHRSVLV 1009
QY 1004 PEWEAEYSQEVRCVPCGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVFN 1063
D 1010 PEWEAEYSQEVRCVPCGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVFN 1069
QY 1064 NTVTCNDYTANQOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1123
D 1070 NTVTCNDYTANQOEYGGAYTSRNGYDETYGNSVADYASVYEKSYTDGRDNPCES 1125
QY 1124 NRGYDTPPLPAGVYVTKLEYFPETDKWIEIGTEGTFIVDSVELLMEE 1174
D 1126 NRGYDTPPLPAGVYVTKLEYFPETDKWIEIGTEGTFIVDSVELLMEE 1176
```

RESULT 7

A22617

parasporal crystal protein cryIAa - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 01-Dec-2000

C:Accession: A22617

R:Schnepf, H.E.; Wong, H.C.; Whiteley, H.R.

J. Biol. Chem. 260, 6264-6272, 1985

A:Title: The amino acid sequence of a crystal

A:Reference number: A22617; MUID:85207613; PMID:2581950

A:Accession: A22617

A:Molecule type: DNA

A:Residues: 1-1176 <SCH>

A:Cross-references: GB:M11250; NID:g142764; PIDN:AAA22353.1; PID:g142765

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

```
Query Match      69.3%; Score 4326; DB 2; Length 1176;
Best Local Similarity 71.3%; Pred. No. 1.9e-273;
Matches 849; Conservative 87; Mismatches 223; Indels 32; Gaps 12;

QY 1 MENNIO-NQCVNCLNPEVEILNEER-STGRLLDLSLTRFLLSEFVGAVFGL 58
DB 1 MNNPNINICIPNCLNSPEVVLGERJETGTPTIDISLQTLSEFVPGAVLGL 60

QY 59 FDLWGFITPDSWLSFLQIEQIOLIBORIETLERNRAITLRLGADSYEYIIEALREWEAN 118
DB 61 VDIWINGIGPSOWDAFFVOIEQLINQRIEFAFARNOAISLEGLSNLYQIYAESFREWEAD 120

QY 119 PNAQLREDVRIRFANTDDALITAINNETLTSTFELPSVYVQAAANLHLSLLRDVAFSGQ 178
DB 121 PTPALREEMRIQFDMNSALTPTALLAVQNYQVPLLSVYVQAAANLHLSVLRDVSFGQ 180

QY 179 GNGLDIAVNNHYNRLINLIHRYTKHCLDTYNOGLENLGNTROWARFNQFRDLITV 238
DB 181 RWGFDAATINSRYNDLTRLIGNYTDYVRWYNTGLERVWGPDSRDWRVYNQFRRLITV 240

QY 239 LDIVALFNYDVRTPIOTSSQLTREIYTSVIEDSPVSANIPNGF----NPAEFGVRPP 294
DB 241 LDIVALFNSYDSRRPIKIVSOLTREIYTNPVLE-----NPDGFRGMAQRIEQNIQRP 294

QY 295 HLMDFMNSLFYTAETVRSQTVWGGHLVSSR--NTAGNRINPSPYGVFNPFGAI--WIADE 350
DB 295 HLMDILNSITIVDHRGFENYWSGHQITASPVGSGPEAFPLFG--NAGNAAPVLVSL 352

QY 351 DPREFYRLSDPVFR-----GGFONPHYVLGRVAFQQTGCTNHTRT--FRNSGTIDSID 404
DB 353 TGLGIFRFLSPLRYRIILIGSGPNQNELFLVDGTBFSPASLTTLNPLSIYRQRGVDSID 412

QY 405 BIPQDNGAPWNDYSHVLNHWTFVFWPGETSGS--DSWRAPMFSTHESAPTNTIDPER 463
DB 413 VIPQDNSVPRAGFSHLSHVTML---SQAAGAVYTRAFSTFWSHRSABFNLIIPSSQ 469

QY 464 ITQIPLVKAHTLQSTTVVRPGFTGGDILRRISGPPFAYTVININGQLPORIRARIYA 523
DB 470 ITQIPLKSTNLGSGTSVKGPGFTGGDILRRISGPPFAYTVININGQLPORIRARIYA 529

QY 524 STTNLRIVTVAGRIFAQGNKMTDQDPLTFQSFVATINTAFTFPMSSQSFVTGADT 583
DB 530 STTNLQHTSIDGRPINQNGNE SATMSGNSLQSGSFRTVGTTFPNSGSSVETLSAHV 589

QY 584 FSSGNEVVIDFELIPVYATFAEYDLERAKAVNALFTSINOGLKTDVTDYHDDQVSN 643
DB 590 FNSGNEVVIDRIEVPVPAEYFAEYDLERAKAVNELFTSSNQIGLKTVDYHDDQVSN 649

QY 644 LVCLSDFECLDKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITQR 703
DB 650 LVECLSDFECLDKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQ 709

QY 704 GDDVFKENYVTLPGTFDECPTYLYQIDESKLKPYTRYQLRGYIESQDLEIYLIRYNA 763
DB 710 GDDVFKENYVTLPGTFDECPTYLYQIDESKLKAYTRYQLRGYIESQDLEIYLIRYNA 769

QY 764 KHETVNLGSLWPLSQSPIRKCGPNRCAPHLENNPDLDCSCROGKCAHSHHFSL 823
DB 770 KHETVNPGLWPLSQSPIRKCGPNRCAPHLENNPDLDCSCROGKCAHSHHFSL 829

QY 824 DIDVGCTDLNEDLVWVIFKIKTDQDGHARLGNLEFLEKPLVGELARVKAERKKWDRK 883
DB 830 DIDVGCTDLNEDLVWVIFKIKTDQDGHARLGNLEFLEKPLVGELARVKAERKKWDRK 889

QY 884 EKLEETNIVYKEAKESVDALFVNSQDQLQADNTIAMIHAADKRVHIREAYLPESLVI 943
DB 890 EKLEWETNIVYKEAKESVDALFVNSQDQLQADNTIAMIHAADKRVHIREAYLPESLVI 949

QY 944 PGVNDVIFEEKLGRIFTAFSLYDARNVKNKGDFNNGLSCHNVKGVHDVYEQNNHRSVLV 1003
DB 950 PGVNAAFEELEGRIFTAFSLYDARNVKNKGDFNNGLSCHNVKGVHDVYEQNNHRSVLV 1009

Query Match      68.9%; Score 4303; DB 2; Length 1166;
Best Local Similarity 71.1%; Pred. No. 6e-272;
Matches 851; Conservative 78; Mismatches 214; Indels 54; Gaps 12;

QY 1 MENNIOQCVPYCNCLNPEVEILNEERSTGRLLDLSLTRFLLSEFVGAVFGLFD 60
DB 1 MEISDQNYIYPNCLNPESEIFNARNNSFGLVQSVSSGLTRFLEAAVPAEGALGFD 60

QY 61 LIWGFITPDSNLSFLQIEQIOLIBORIETLERNRAITLRLGADSYEYIIEALREWEAN 120
DB 61 IIWGALGVDSWLSFLRQIEQIOLIBORIETLERNRAITLRLGADSYEYIIEALREWEAN 120

QY 121 NAQLREDVRIRFANTDDALITAINNETLTSTFELPSVYVQAAANLHLSLLRDVAFSGQ 180
DB 121 NPASQERVTRFRDLDALITAVTGFLTLAINRVNLVNLVYVQAAANLHLSLLRDVAFSGQ 180

QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLGNTROWARFNQFRDLITLVID 240
DB 181 GLTQANTEDLYTRLSNIQEYSDHCARWYNOGLENGIS---RRYLDLFORDLITLVID 236

QY 241 IVALFPNVDVRYTPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRRPHLMDFM 300
DB 237 IVALFPNVDVRYTPIQTSQTLREIYTSV---VAGNINFGLSIANV-LRAPHLMDFI 290

QY 301 NSLFWTAETVRSQTVWGGHLVSSRNTA---GNRINPSPYGVFNPFGALWIADEPRFYR 357
DB 291 DRIVYVNSVRSTPYWAGHEVISRTQGGQNEIRFLYGV-----AANPE----- 337

QY 358 TLDSPDFVR--GGFONPH---VYVGLRGVAFQQTGCTNHT-----RFRN--S 397
DB 338 ---PVTRIRPTFDEQQRVRAFRSVVSPRSSQDLSLVDVAGFLIFSAVSYIRNGFG 393

QY 398 GTDLSDEIIPQNSGAPWNDYSHVLNHWTFVWRKPGIEISGSDSWRAPMFSTHESAPTIN 457
DB 394 FNTDTIDEIPIEGTD--PFTGYSHRLCHVGFLASSPFI--SQVARAPIFSMTWSRSLTN 449

QY 458 TIDPERTQIPLVKAHTLQSTTVVRPGFTGGDILRRISGPPFAYTVININGQLPORIR 517
DB 450 TIAPDVITQIPLVKAHTLQSTTVVRPGFTGGDILRRISGPPFAYTVININGQLPORIR 509

QY 518 ARIRYASTTNLRIVTVAGRIFAQGNKMTDQDPLTFQSFVATINTAFTFPMSSQSF 577
DB 510 VRIRYASTTDLQTYTNGTINIGNSSMTDSGDDLOYGFRVAVGFTTPTFFTSANSTF 569
```


RESULT 10

S32689
 parasporal crystal protein cry1Hal - Bacillus thuringiensis
 C:Species: Bacillus thuringiensis
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S32689
 R:Lambert, B.
 submitted to the EMBL Data Library, April 1993
 A:Reference number: S32645
 A:Accession: S32689
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1172 <LAN>
 A:Cross-references: EMBL:Z22513; NID:q296086; PIDN:CAA80236.1; PID:q296087
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 67.8%; Score 4230.5; DB 2; Length 1172;
 Best Local Similarity 69.9%; Pred. No. 3.2e-267;
 Matches 834; Conservative 92; Mismatches 220; Indels 47; Gaps 11;

Qy 4 NTQOCVYVNCNNEVEILNEERSTGR---LPDISLSLREFLSEFVGVGVAGFLPD 60
 Db 5 NNQNYVYVNCNNEVEILNEERSTGR---LPDISLSLREFLSEFVGVGVAGFLPD 64

Qy 61 LIWGFITPDSNLSFLLOIEQLTEQRIETLERNRAITTLRGLADSYEIXTEALREWEANPN 120
 Db 65 IIWGVIGPDWNLFLAQLEQLDQRIEAVRQAISRLLEGDSYEYIESUREWEASN 124

Qy 121 NQALREDVIRFANTDDALITAINFTLTFSFIPLLSVYVQAANLHLSLRDAVSFGQGW 180
 Db 125 NEALQDVNRNFSNTDNALITAIPIRQGGFPIPLLSVYVQAANLHLSLRDAVSFGQGW 184

Qy 181 GLDIATVNNHYNRLNLIHRYTKHCLDYNOGLENLRTGTQWAFNQRFRDLTLVLD 240
 Db 185 GLDTVTNNHYNRLNLIHRYTKHCLDYNOGLENLRTGTQWAFNQRFRDLTLVLD 240

Qy 241 IVALPPNDVRYPIQTSQTLREIYTSVIE-DSPVSANIPNGFNRAEFVGRPHLMD 299
 Db 241 IVALPPNDVRYPIQTSQTLREIYTSVIE-DSPVSANIPNGFNRAEFVGRPHLMD 293

Qy 300 MNSLVTATVRSQVWGGHLYSSRNTA--GNRINFPYGVNPGGAIWAIEDPRPF-- 355
 Db 294 LTRLYIVTGVSQGIYHWAGHESITRTGNLSNIQFPLYGT-----AASADRAFNM 344

Qy 356 -----YRLSDPVEVGGFGNHYVLGRGVAPOQTGTHHT-----FRNSTIDSL 403
 Db 345 NIHSSETYRLSAPYISVSGISPNRTVVGVRFLIARDNNLDSLPFLYRKEGTLD 404

Qy 404 DEIPQDNGSAPWNDYSHVLNHTVVRWPGELSGSDSWRAPFWSWTHRSATPTNIDPER 463
 Db 405 TELPPEDESTPPYIGYSHRLCHAREARSPVILEPNSFNARLPVFSWTHRSASTNEVSPSR 464

Qy 464 ITQIPLVKAHLQSTTVVRGPGTGGDLRT--SGGPFAYTVINQOLPQRYRARIR 521
 Db 465 ITQIPWKAHLTASGASIKGPGFTGGDITMRNNINLGLPLRTVTCRLPQSYIIRL 524

Qy 522 YASTNLRIYTVACERIFAGQFNKMTDGPDLTQSFSEYATINTAFTPKSSQSTVGA 581
 Db 525 YASVANSNGSVFHLPPQSYISFTPTGTGDELTGRSALTLFTPTITLTRAQEEFN-- 582

Qy 582 DTFSSNGEVIIDRFELIPVATFAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQV 641
 Db 583 -TIPRG--VIYDRIEFVVPDATFAEYDLERAQKAVNALFTSTNORGLKTDITDHIQV 639

Qy 642 SNLVCLDSFCLDKRELSEKVKHAKRLSDERNLLQDPNFKINGINRQLDRGWSGTDITI 701
 Db 640 SNLVCLDSFCLDKRELSEKVKHAKRLSDERNLLQDPNFKINGINRQLDRGWSGTDITI 699

Qy 702 ORGDDVFNKENVTLPGTDECYPTLYQKIDESKLKPYTRVOLRGYIEDSQDLEIYLR 761
 Db 700 QGSDVFNKENVTLPGTDECYPTLYQKIDESKLKPYTRVOLRGYIEDSQDLEIYLR 759

Qy 762 NAKHETVNVLTGSLWPLSYQSFIRKCGEPNRCAPHEWNPDLDCSCRDGKCAHSHHF 821
 Db 760 NAKHETVNVLTGSLWPLSYQSFIRKCGEPNRCAPHEWNPDLDCSCRDGKCAHSHHF 819

Qy 822 SLIDIVGCTDLNEDLVVIFIKITQDGHARGNLNLEFLEKPLVGALARVRAEKKWD 881
 Db 820 SLIDIVGCTDLNEDLVVIFIKITQDGHARGNLNLEFLEKPLVGALARVRAEKKWD 879

Qy 882 KREKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHIAADKRVHRIEAYLP 941
 Db 880 KREKLEETNIYVKEAKESVDALFVNSQDQLQADNTNIAHIAADKRVHRIEAYLP 939

Qy 942 VIPGVNVDIFEBELKGRIFTAFPLYDARNVKNKDFNNGSLSCWNVKGVHVDVEQNHR 1001
 Db 940 VIPGVNVDIFEBELKGRIFTAFPLYDARNVKNKDFNNGSLSCWNVKGVHVDVEQNHR 999

Qy 1002 VYPEWEAEVSQVRVPCGRGYILRVYATYKGEYGEQCVTIHETENNTDELKFCNVEEY 1061
 Db 1000 VYPEWEAEVSQVRVPCGRGYILRVYATYKGEYGEQCVTIHETENNTDELKFCNVEEY 1059

Qy 1062 PNNTVTCNDYTANQOEYGGAYTSRNRGYDETYGSSNVPADYASYEESYTDGRDNPC 1121
 Db 1060 PNNTVTCNDYTANQOEYEGTYTSRNOGYDEAYESNVPANYSYEEKAYTDGRRENSC 1119

Qy 1122 ESNRGYGYDTPLPAGYVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE 1174
 Db 1120 ESNRGYGYDTPLPAGYVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE 1172

RESULT 11

S00944
 parasporal crystal protein cry1cal - Bacillus thuringiensis (strain entomocidus 60.1)
 C:Species: Bacillus thuringiensis
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-Dec-2000
 C:Accession: S00944
 R:Honee, G.; van der Salm, T.; Visser, B.
 Nucleic Acids Res 16, 6240, 1988
 A:Title: Nucleotide sequence of crystal protein gene isolated from B. thuringiensis
 A:Reference number: S00944; MUID:8828980; PMID:3399402
 A:Accession: S00944
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1189 <HON>
 A:Cross-references: EMBL:X07518; NID:q40293; PIDN:CAA30396.1; PID:q40294
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 67.5%; Score 4217.5; DB 2; Length 1189;
 Best Local Similarity 68.8%; Pred. No. 2.3e-266;
 Matches 833; Conservative 96; Mismatches 224; Indels 57; Gaps 17;

Qy 1 MENNQOCVYVNCNNEVEILNEER-STGRPLDLSLSTRLSFLSEFVGVGVAGFL 59
 Db 1 MEENNQOCVYVNCNNEVEILNEER-STGRPLDLSLSTRLSFLSEFVGVGVAGFL 60

Qy 60 DLINGFITPDSNLSFLLOIEQLTEQRIETLERNRAITTLRGLADSYEIXTEALREWEANP 119
 Db 61 DLINGFITPDSNLSFLLOIEQLTEQRIETLERNRAITTLRGLADSYEIXTEALREWEANP 120

Qy 120 NNAQLREDVIRFANTDDALITAINFTLTFSFIPLLSVYVQAANLHLSLRDAVSFGQ 179
 Db 121 NNAQLREDVIRFANTDDALITAINFTLTFSFIPLLSVYVQAANLHLSLRDAVSFGQ 180

Qy 180 WGLDIATVNNHYNRLNLIHRYTKHCLDYNOGLENLRTGTQWAFNQRFRDLTLV 239
 Db 181 WGLDIATVNNHYNRLNLIHRYTKHCLDYNOGLENLRTGTQWAFNQRFRDLTLV 240

Qy 240 DIVALFPNDVRYPIQTSQTLREIYTSVIE-DSP--VSANIPNGFNRAEFVGRPH 295
 Db 241 DIVALFPNDVRYPIQTSQTLREIYTSVIE-DSP--VSANIPNGFNRAEFVGRPH 299

Qy 296 LMDFNLSLFTVAE--TVRSQTVWGGHLYSSRNTA--GNRINFPYGVNPGGAIWAIEDPR- 352
 Db 294 LMDFNLSLFTVAE--TVRSQTVWGGHLYSSRNTA--GNRINFPYGVNPGGAIWAIEDPR- 352

Db 300 LFDILNLLTFTDWFSGVRNFYWGHRVYSSILGGNITSPIYG-----REANQEP 351
QY 353 -----RPYRTLSDPV--FVRGFGNPHYVL-GLRGVAFOQTCTNHTFRNSGTIDSL 403
Db 352 RSTFNGPVRTUSNPRLRLQQPWAPPFNLRGVGEVF-STPTN-SFTYGRGTVDLSL 409
QY 404 DEIPPONSGAPWMDYSHVLNHNVTFFVRWPGEISGSDSWRAP-----MFSWTHRSAYPTN 457
Db 410 TELPPEDNSVPPREGYSHRLLCHAFVQVRSQ-----PPFLTGVVFSWDSAILTN 460
QY 458 TIDPERITQPLVKAHLQSGTTVVRRGPGFTGGDILRRTSGGPFAYTIVNINGOLPQRYR 517
Db 461 TIDPERINQPLVGRFVWGVTGVTITGFTGGDILRNTFGDFVSLQVNSIPTQRYR 520
QY 518 ARIYAATINRIYV-TVAGERIFAGO-----FNKMDTGDPDTTFOFSYATINTATFF 570
Db 521 LRFYASRDARVILVLCAGASTGVGGQVSNMPLQKMEIGENITSRTFRYDFSNPFSF 580
QY 571 PMOSSFTV-----GADTFSSGNEVYIDRPELIPVTATFEAYDLERAQKAVNALETSI 624
Db 581 RANPDIIIGISEQLPFGAGSISSG-ELYIDKIEIILADATPEAESDLERAQKAVNALETS 639
QY 625 NQIGIKTDVTDYHIDQVSNLVDCLSDPCLDEKRELSEKVKHAKRLSDERNLLQDPNFKG 684
Db 640 NQIGLKTVDVTDYHIDQVSNLVDCLSDPCLDEKRELSEKVKHAKRLSDERNLLQDPNFKG 699
QY 685 INRQDRGWRGSTDITQRGDDVFKENVTLPGTDFECYPTLYKQIDESKLKPYTRYQL 744
Db 700 INRQDRGWRGSTDITQGGDDVFKENVTLPGTDFECYPTLYKQIDESKLKAYTRYEL 759
QY 745 RGYTEDSQDLEIYLIRYNAKHETVNLGTSGLWPLSVQSPIRKCGEPNRCAPHLEWNPDL 804
Db 760 RGYTEDSQDLEIYLIRYNAKHETVNLGTSGLWPLSVQSPIRKCGEPNRCAPHLEWNPDL 819
QY 805 DCSRCDEKCAHSHHSLSLDVCGCTDLNEDLDVWVIFKIKTQGHARLGNLEFLEKPL 864
Db 820 DCSRCDEKCAHSHHSHTLDIDVGCTDLNEDLDVWVIFKIKTQGHARLGNLEFLEKPL 879
QY 865 VGEALARKAEKWRKREKLEETNIVYKEAKESVDALFVNSQYDLOQADTNIAHIA 924
Db 880 LGEALARKAEKWRKREKLEETNIVYKEAKESVDALFVNSQYDLOQADTNIAHIA 939
QY 925 ADKRVHRIEAYLPSELPVPGVNDVDFEELKGRIFTAFFLYDARNVKNKGNFNGLSOWN 984
Db 940 ADKRVHRIEAYLPSELPVPGVNAIFEEELGRIFTAYSLYDARNVKNKGNFNGLSOWN 999
QY 985 VKGHVDVEQNHRSLVLPWEAEVQEVRCVGRGYLKVATYKEGYGEGCVTHIEIE 1044
Db 1000 VKGHVDVEQNHRSLVLPWEAEVQEVRCVGRGYLKVATYKEGYGEGCVTHIEIE 1059
QY 1045 NNTDELAFSCVVEEVPNNVTTCNDXTANOEYGGATYSRNGYDETYGSSNSVPADYA 1104
Db 1060 NNTDELAFSCVVEEVPNNVTTCNDXTANOEYGGATYSRNGYDETYGSSNSVPADYA 1119
QY 1105 SVYEKSYTDGRRNPNCSNRGYYDYLPLPAGYVTKLEYPPETDKVWIEIGETEGFIV 1164
Db 1120 SVYEKSYTDGRRNPNCSNRGYYDYLPLPAGYVTKLEYPPETDKVWIEIGETEGFIV 1179
QY 1165 DSVELLMLLEE 1174
Db 1180 DSVELLMLLEE 1189

RESULT 12
JD00002
parasporal crystal protein cryIIAb3 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal pro
C:Species: Bacillus thuringiensis
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 01-Dec-2000
C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
R:Kondo, S.; Tamura, N.; Kunitake, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes fro

A:Reference number: A90025
A:Accession: A90025
A:Molecule type: mRNA
A:Residues: 1-1155 <KON>
R:Experimental source: subsp. kurstaki
R:Geiser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal pr
A:Reference number: A91560; MUID:87163505; PMID:3557124
A:Accession: A91560
A:Molecule type: DNA
A:Residues: 1-1155 <GEI>
A:Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A:Experimental source: subsp. kurstaki
R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product a
A:Reference number: A90955; MUID:86300092; PMID:3743328
A:Accession: A90955
A:Molecule type: DNA
A:Residues: 1-1155 <WAB>
A:Cross-references: GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:g142720
A:Experimental source: subsp. berliner
R:Chak, K.R.; Jen, J.C.
Submitted to the EMBL Data Library, October 1990
A:Description: Complete nucleotide sequence and expression in Escherichia coli of a c
A:Reference number: S14555
A:Accession: S14555
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1155 <CHA>
A:Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
R:Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandeke
Eur. J. Biochem. 161, 273-280, 1986
A:Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus t
A:Reference number: A26461; MUID:87054026; PMID:3023091
A:Accession: A26461
A:Molecule type: DNA
A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>
A:Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A:Experimental source: strain berliner 1715
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C:Genetics:
A:Gene: cry-1-2; bt2
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
F:82-586/Product: toxic peptide #status predicted <TXP>
F:82-300/Region: toxic #status predicted
F:300-586/Region: insecticidal #status predicted

Query Match 67.4%; Score 4211.5; DB 2; Length 1155;
Best Local Similarity 70.0%; Pred. No. 5.4e-266;
Matches 831; Conservative 83; Mismatches 228; Indels 45; Gaps 9;

QY 1 MENNIO-NOCVPYCNLNPVEIILNEER-STGRPLDISLSLTFLLSEFPYGVGVAFGL 58
Db 1 MDNPNNECIPYCNLSNPVEIILNEER-STGRPLDISLSLTFLLSEFPYGVGVAFGL 60
QY 59 FDLIWTGFTTSPDWSLFLQIDQLIEQRIETLERNAITTLRGLADSYEITAEALREWEAN 118
Db 61 VDIITGIFGPSQWDAFLVQIEQLINQRIEFAFNQATSRLEGLSNLQIYAESFWEAD 120
QY 119 PNAQLREDVRIRFANTDDALITAINNFTLTSFPIPLSVYVQANLHLSLLRDVAFSG 178
Db 121 PTPNALREEMRIQFNDMNSALTTPAFVQNYQVPLSVYVQANLHLSVLRDVSFVG 180
QY 179 GGLDITATVNNHNLNLHRYTHKCLDYNQGLENLGRNTNTQWAFNFRRLDILTV 238
Db 181 RWGDAATINRYNDLRLIGNYTHDVAWNTGLERVWGPDSRDWIRNGFRRLDILTV 240
QY 239 LDIVALEFPNDVRYTPIQTSQTLREYTSSTVEDSPYSANIPNGFNRA----BFGVRPP 294
Db 241 LDIVSLFPNDVSRYPITFTVSLTREYTNVPLE-----NFDGSRGSAOGIEGSRP 294

Qy 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINEPSYGVF--NPGGAIWIADRD 351
 Db 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINEPSYGVF--NPGGAIWIADRD 351
 Qy 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDELTP 407
 Db 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDELTP 407
 Qy 408 PODNSGAPNDYSHVNLNHTVFRWPGEGISGDSWRAPFMSWTHRSATPTNTIDPRTIQI 467
 Db 408 PODNSGAPNDYSHVNLNHTVFRWPGEGISGDSWRAPFMSWTHRSATPTNTIDPRTIQI 467
 Qy 415 PNNVPPRQGFQSHRSLSHVMSFRSFSNSVSIIRAPFMSWTHRSATPTNTIDPRTIQI 474
 Db 415 PNNVPPRQGFQSHRSLSHVMSFRSFSNSVSIIRAPFMSWTHRSATPTNTIDPRTIQI 474
 Qy 468 PLVKAHTLQSGTIVVRGPGFTGGDILRTSGGPFAYTIVNINQPLQRYRARIYASTIN 527
 Db 468 PLVKAHTLQSGTIVVRGPGFTGGDILRTSGGPFAYTIVNINQPLQRYRARIYASTIN 527
 Qy 475 PLTKSTNLGSGTVVKGFGTGGDILRTSGGPFAYTIVNINQPLQRYRARIYASTIN 534
 Db 475 PLTKSTNLGSGTVVKGFGTGGDILRTSGGPFAYTIVNINQPLQRYRARIYASTIN 534
 Qy 528 LRIYVTVAGERIFAGQFNKMTDGLTQFQSFYSATINTAFTFMSQSFTVGADTFSSG 587
 Db 528 LRIYVTVAGERIFAGQFNKMTDGLTQFQSFYSATINTAFTFMSQSFTVGADTFSSG 587
 Qy 535 LQFHTSIHGRPINQGNFSAATMSSGSLQSGSFRHLGFTTPNFNSGSSVFTLSAHVNSG 594
 Db 535 LQFHTSIHGRPINQGNFSAATMSSGSLQSGSFRHLGFTTPNFNSGSSVFTLSAHVNSG 594
 Qy 588 NEVYIDRELFIPVATFAEYDLERAQKAVNALFTSINOIGIKTKDVTYHIDQVSNLVD 647
 Db 588 NEVYIDRELFIPVATFAEYDLERAQKAVNALFTSINOIGIKTKDVTYHIDQVSNLVD 647
 Qy 595 NEVYIDRELFIPVATFAEYDLERAQKAVNELFTSSNOIGIKTKDVTYHIDQVSNLVD 654
 Db 595 NEVYIDRELFIPVATFAEYDLERAQKAVNELFTSSNOIGIKTKDVTYHIDQVSNLVD 654
 Qy 648 LSDFCLDEKRELSKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDTIQRGDDV 707
 Db 648 LSDFCLDEKRELSKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDTIQRGDDV 707
 Qy 655 LSDFCLDEKRELSKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDTIQRGDDV 714
 Db 655 LSDFCLDEKRELSKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDTIQRGDDV 714
 Qy 708 FKENVYTLPGTFDECPYLYOKIDESKLKPYTRYQLRGYIEDSDQLLEIYLRINAKHET 767
 Db 708 FKENVYTLPGTFDECPYLYOKIDESKLKPYTRYQLRGYIEDSDQLLEIYLRINAKHET 767
 Qy 715 FKENVYTLPGTFDECPYLYOKIDESKLKPYTRYQLRGYIEDSDQLLEIYLRINAKHET 774
 Db 715 FKENVYTLPGTFDECPYLYOKIDESKLKPYTRYQLRGYIEDSDQLLEIYLRINAKHET 774
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 Db 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 827
 Qy 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 808
 Db 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 808
 Qy 828 GCTDLNEDLVVWIFKIKTQDGHARLGNLEFLPEKPLVGEALARKKWRDKREKLE 887
 Db 828 GCTDLNEDLVVWIFKIKTQDGHARLGNLEFLPEKPLVGEALARKKWRDKREKLE 887
 Qy 809 GCTDLNEDLVVWIFKIKTQDGHARLGNLEFLPEKPLVGEALARKKWRDKREKLE 868
 Db 809 GCTDLNEDLVVWIFKIKTQDGHARLGNLEFLPEKPLVGEALARKKWRDKREKLE 868
 Qy 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTNIAHTRADKRVHRIEAYLPESVIGVN 947
 Db 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTNIAHTRADKRVHRIEAYLPESVIGVN 947
 Qy 948 VDIPELKGRIFTAFSLYDARNVKNKGNGLSCWNVKGVVDVEEQNHRSVLPVPEWE 1007
 Db 948 VDIPELKGRIFTAFSLYDARNVKNKGNGLSCWNVKGVVDVEEQNHRSVLPVPEWE 1007
 Qy 929 AAIFEELEGRIFTAFSLYDARNVKNKGNGLSCWNVKGVVDVEEQNHRSVLPVPEWE 988
 Db 929 AAIFEELEGRIFTAFSLYDARNVKNKGNGLSCWNVKGVVDVEEQNHRSVLPVPEWE 988
 Qy 1008 AEVSQEVRCVPGRGYILRVATYKEGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1067
 Db 1008 AEVSQEVRCVPGRGYILRVATYKEGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1067
 Qy 989 AEVSQEVRCVPGRGYILRVATYKEGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1048
 Db 989 AEVSQEVRCVPGRGYILRVATYKEGEGCVTIHEIENNTDELKFSNCVEEYVNNVT 1048
 Qy 1068 CNDYTANDEEYGGATSRNRYGDETYGSSNVPADYASVEKSTGDRRNPCESNRGY 1127
 Db 1068 CNDYTANDEEYGGATSRNRYGDETYGSSNVPADYASVEKSTGDRRNPCESNRGY 1127
 Qy 1049 CNDYTANDEEYGGATSRNRYGDETYGSSNVPADYASVEKSTGDRRNPCESNRGY 1108
 Db 1049 CNDYTANDEEYGGATSRNRYGDETYGSSNVPADYASVEKSTGDRRNPCESNRGY 1108
 Qy 1128 GDTPLPAGYVTKLEYPEDDKWIEITGEGTFIVDSVLELLMEE 1174
 Db 1128 GDTPLPAGYVTKLEYPEDDKWIEITGEGTFIVDSVLELLMEE 1174
 Qy 1109 GDTPLPAGYVTKLEYPEDDKWIEITGEGTFIVDSVLELLMEE 1155
 Db 1109 GDTPLPAGYVTKLEYPEDDKWIEITGEGTFIVDSVLELLMEE 1155

RESULT 13
 139838
 paraspore crystal protein - Bacillus thuringiensis
 C:Species: Bacillus thuringiensis
 C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000
 C:Accession: I39838
 R:Heford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
 J. Biotechnol. 6, 307-322, 1987
 A:Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki
 A:Reference number: 139838
 A:Accession: I39838

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1155 <RES>
 A:Cross-references: GB:M37263; NID:g142885; PID:AAA22420.1; PID:g142886
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 67.2%; Score 4194.5; DB 2; Length 1155;
 Best Local Similarity 69.8%; Pred. NO. 7e-265;
 Matches 828; Conservative 83; Mismatches 231; Indels 45; Gaps 9;

Qy 1 MENNIQ-NOCVPYCNLNPEVEILNEER-STGRPLDIDSLSTRFLLSPFVPGVAVFGL 58
 Db 1 MDNNEINCEPYNCLSPNEVEILGGERIETGYTIDISLQTLFLLSPFVPGVAVFGL 60
 Qy 59 FDLINGFTPPSDWSLFLQIEQLIQRITLERNRAITTLRGLADSYEYIEALREWEAN 118
 Db 61 VDIWIGIFGPSQWDAFLVQIEQLINORTEEPARNQAISREGLSNLYQIYAESFREWEAD 120
 Qy 119 PNAACOLREDVRIRFANTDDALITAINNTLTSFEPLISVYVQAAANLHSLRDVSGQ 178
 Db 121 PNPALREMRIOFQNDMSALTITPLFAVQNYQVELLSVYVQAAANLHSLRDVSGQ 180
 Qy 179 GWGLDIATVNNHYNLNLINLHRYTKHCLDTYNOGLENLRGNTROWARNQFRDLTLTV 238
 Db 181 RWGFDATINSRYNDLTRIGNYTDHAYWNTGLERVWGPDSRDWRINQFRDLTLTV 240
 Qy 239 LDIVALFNYDVRTPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRA----EFGVRPP 294
 Db 241 LDIVSLFNYDSRTPIRTVSQTLREIYTNPVLE-----NFDGSGFRGSAQOIGESIRSP 294
 Qy 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINEPSYGVF--NPGGAIWIADRD 351
 Db 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINEPSYGVF--NPGGAIWIADRD 351
 Qy 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDELTP 407
 Db 352 PRPFYRTLDSPVVRG--GFGNPHY-VLGLRGVAFQOTGTNHTRTFRNSGTDLSDELTP 407
 Qy 408 PODNSGAPNDYSHVNLNHTVFRWPGEGISGDSWRAPFMSWTHRSATPTNTIDPRTIQI 467
 Db 415 PNNVPPRQGFQSHRSLSHVMSFRSFSNSVSIIRAPFMSWTHRSATPTNTIDPRTIQI 474
 Qy 468 PLVKAHTLQSGTIVVRGPGFTGGDILRTSGGPFAYTIVNINQPLQRYRARIYASTIN 527
 Db 475 PLTKSTNLGSGTVVKGFGTGGDILRTSGGPFAYTIVNINQPLQRYRARIYASTIN 534
 Qy 528 LRIYVTVAGERIFAGQFNKMTDGLTQFQSFYSATINTAFTFMSQSFTVGADTFSSG 587
 Db 535 LQFHTSIHGRPINQGNFSAATMSSGSLQSGSFRHLGFTTPNFNSGSSVFTLSAHVNSG 594
 Qy 588 NEVYIDRELFIPVATFAEYDLERAQKAVNALFTSINOIGIKTKDVTYHIDQVSNLVD 647
 Db 595 NEVYIDRELFIPVATFAEYDLERAQKAVNELFTSSNOIGIKTKDVTYHIDQVSNLVD 654
 Qy 648 LSDFCLDEKRELSKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDTIQRGDDV 707
 Db 655 LSDFCLDEKRELSKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDTIQRGDDV 714
 Qy 708 FKENVYTLPGTFDECPYLYOKIDESKLKPYTRYQLRGYIEDSDQLLEIYLRINAKHET 767
 Db 715 FKENVYTLPGTFDECPYLYOKIDESKLKPYTRYQLRGYIEDSDQLLEIYLRINAKHET 774
 Qy 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 827
 Db 775 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDV 808
 Qy 828 GCTDLNEDLVVWIFKIKTQDGHARLGNLEFLPEKPLVGEALARKKWRDKREKLE 887
 Db 809 GCTDLNEDLVVWIFKIKTQDGHARLGNLEFLPEKPLVGEALARKKWRDKREKLE 868
 Qy 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTNIAHTRADKRVHRIEAYLPESVIGVN 947
 Db 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTNIAHTRADKRVHRIEAYLPESVIGVN 947

Db 869 WETNIVYKEAKESVDALFVNSQYDRLQADTNIAHIAADKRVHSIREAYLPELSVIPGVN 928
 QY 948 VDIFEEELKGRIFTAFYLDARNVIKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 1007
 Db 929 AAIFEEELKGRIFTAFSLYDAENVKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 988
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 Db 989 AEVSQEVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEVPNNVT 1048
 QY 1068 CNDYTAQEEYGGAYTSNRNGYDYGESNVPADYASVYEKSYTDGRRNPCEENRGY 1127
 Db 1049 CNDYTAQEEYGGAYTSNRNGYDYGESNVPADYASVYEKSYTDGRRNPCEENRGY 1108
 QY 1128 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1174
 Db 1109 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1155

RESULT 14
 A26513
 parasporal crystal protein - Bacillus thuringiensis (strain aizawai)
 C:Species: Bacillus thuringiensis
 C:Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 01-Dec-2000
 C:Accession: A26513
 R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, H.
 Gene 53, 113-119, 1987
 A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis
 A:Reference number: A26513; MUID:87248103; PMID:3297927
 A:Accession: A26513
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1155 <OE>
 A:Cross-references: GB:M16463; NID:g143059; PID:AAA22551.1; PID:g143099
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 67.1%; Score 4191.5; DB 2; Length 1155;
 Best Local Similarity 69.8%; Pred. No. 1.1e-264;
 Matches 829; Conservative 82; Mismatches 231; Indels 45; Gaps 9;

QY 1 MENNIO-NOCVPYNCLNPEVEILNEER-STGRPLDLSLSTRELLSEFVGVGVAFGL 58
 Db 1 MDNNINIECIPYCNLSNPEVGLSGRIETGYTPIDISLSTOFFLSEFVGVGVAFGL 60
 QY 59 FDLIWIPTSDSLFLLOLEQRIETLERNRAITLRLGLADSYETIIEALREWEAN 118
 Db 61 VDLIWIPTSDSLFLLOLEQRIETLERNRAITLRLGLADSYETIIEALREWEAN 120
 QY 119 PNAQLREDYRIRFANTDDALITAINFTLTSFPIPLSVVQAAHLHLRLDRAVSFG 178
 Db 121 PTPALREERNIOFDMNSALTAPLFAVQYQVPLSVVQAAHLHLRLDRAVSFG 180
 QY 179 GWGLDIATVNNHNLNLHRTKHCCLDYNQGLENLRTNTQWAFRNFQFRDLTLV 238
 Db 181 RWGFDAATINSYRNDLRLGNCTHDAVRYNTGLERWVGPDSDRWIRYNOFRRELTLV 240
 QY 239 LDIVALPNPDVRYPIQTSQSLREIYTSVIEDSPVSANIPNGNR---AEFGVRRP 294
 Db 241 LDIVSLFPNDSRTYPTVTSQTLREIYTNVLE-----NFGSFRALAQEGSIRSP 294
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 Db 295 HLMDFMNSLFTVETVRSQIVWGGH---LVSSRTAGNRINFPSPYGVF-NPGGAIWADED 354
 QY 352 PRFYRTLSDPVFRG---GFGNPHY-VLGLRGVAFQOQTNTHTRTFRNSGTSLSLDEIP 407
 Db 355 GQGYRTLSLTLRPPNIGINNQLSVLDCTEFAYCTSSNLPSAVYRKSGTVDSLDEIP 414
 QY 408 PQDNGAPMNDXSVLNLHVTIVRWPCEISDSWRAPMFSWTHRSATPTNTIDPRTQI 467
 Db 415 PQNNVPVPPROGFSHRUSHVSMFRSGFSNVSITRAPMFSWIHRSFNNIIPSSQITQI 474

QY 468 PLVKAHTLQSGTIVRVGPGFTGGDILRLRTSGGPAYTIIVNINQOLPORARIRYASTTN 527
 Db 475 PLTSTNLGSGTSVVGKPGFTGGDILRLRTSGQISTLVNITAPLSQYRVRIRYASTTN 534
 QY 528 LRIYTVAGERIFAQGFNKMTDGTDLPTFQSGSYATINTAFTFPMSSQSFVGTADTFSSG 587
 Db 535 LQFHTSIDGRFINQGNFSATSSGSLGSGSFRVGTFTPFNSGSSVFTLSAHVFNSSG 594
 QY 588 NEVYIDRELIPVATFAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVC 647
 Db 595 NEVYIDRELIPVATFAEYDLERAQKAVNELFTSSNQIGIKTDVTDYHIDQVSNLVC 654
 QY 648 LSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFKGINRQDLDRGWRGSDTITQGGDV 707
 Db 655 LSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFKGINRQDLDRGWRGSDTITQGGDV 714
 QY 708 FKENYVTLPGTDFECYPTLYQKIDESKLPYTRYQLRGYIEDSDLEIYLRINAKHET 767
 Db 715 FKENYVTLPGTDFECYPTLYQKIDESKLPYTRYQLRGYIEDSDLEIYLRINAKHET 774
 QY 768 VNVLTGSLNPLSVQSPTRKCGEPNRCAPHLWNPDDLDCSCRDGEKCAHHSHHSLDIDV 827
 Db 775 VNVLTGSLNPLSVQSPTRKCGEPNRCAPHLWNPDDLDCSCRDGEKCAHHSHHSLDIDV 808
 QY 828 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEKPLVGEALARKVRAEKKWRKREKLE 887
 Db 809 GCTDLNEDLDVWVIFKIKTQDGHARLGNLEKPLVGEALARKVRAEKKWRKREKLE 868
 QY 888 LETNIVYKEAKESVDALFVNSQYDRLQADTNIAHIAADKRVHSIREAYLPELSVIPGVN 947
 Db 869 WETNIVYKEAKESVDALFVNSQYDRLQADTNIAHIAADKRVHSIREAYLPELSVIPGVN 928
 QY 948 VDIFEEELKGRIFTAFYLDARNVIKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 1007
 Db 929 AAIFEEELKGRIFTAFSLYDAENVKNGDFNGLSCWNKGVHDVVEEQNNHRSVLVVPWE 988
 QY 1008 AEVSQEVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEVPNNVT 1067
 Db 989 AEVSQEVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEVPNNVT 1048
 QY 1068 CNDYTAQEEYGGAYTSNRNGYDYGESNVPADYASVYEKSYTDGRRNPCEENRGY 1127
 Db 1049 CNDYTAQEEYGGAYTSNRNGYDYGESNVPADYASVYEKSYTDGRRNPCEENRGY 1108
 QY 1128 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1174
 Db 1109 GDYTPLPAGYVTKLEYFPETDKWIEGEGTGFIVDSVELLMEE 1155

RESULT 15

S02134

Parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai ICI)
 N:Alternate names: delta-endotoxin ICI; entomocidal crystal protein
 C:Species: Bacillus thuringiensis
 A:Variety: strain aizawai ICI
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
 C:Accession: S02134; S04994
 R:Haider, M.Z.; Ellar, D.J.
 Nucleic Acids Res. 16, 10927, 1988

A:Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICI entomocidal crystal protein
 A:Reference number: S02134; MUID:89083518; PMID:3205732
 A:Accession: S02134
 A:Status: translation not shown
 A:Molecule type: DNA

A:Residues: 1-1155 <HA>

A:Cross-references: EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278

A:Experimental source: strain aizawai ICI

R:Haider, M.Z.; Ellar, D.J.

J. Mol. Biol. 208, 183-194, 1989

A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid chan

A:Reference number: S04994; MUID:89362455; PMID:2769751

A:Accession: S04994

A:Molecule type: DNA

A:Residues: 429-449, 'A', 451-724 <HAW>

A:Cross-references: EMBL:X161315

A:Experimental source: strain aizawai IC1

C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 67.1%; Score 4189.5; DB 2; Length 1155;

Best Local Similarity 69.8%; Pred. No. 1.5e-264;

Matches 828; Conservative 84; Mismatches 230; Indels 45; Gaps 9;

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QY 1 MNNQTO-NOCVYNCLNPEVEILNEER-STGRPLDLISLITRELLSEFVPGVGVAFGL 58
DB 1 MNNPNINFCIPYCLNSPEVEVLGGERIETGYTIDISLQFLLSEFVPGAGFVLGL 60
QY 59 FOLINGFITPDSWISFLQIEQILQRIETLERNRAITTLRLGLADSYEIIYEAALREWEAN 118
DB 61 VDIINGIFGPSQWDAFLVQIEQLINQRIEFPARNQAISRLGSLNLYQIYAESFREWEAD 120
QY 119 PNAQLREOVIRFRANTODALITANNFTLSFEPLISVYQAAANHLSLRLRDVSGQ 178
DB 121 PTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLLSVYQAAANHLSLRLRDVSGQ 180
QY 179 GGLDITATVNNHYRLINLIHRYTKHCLDITYNOGLENLRGNTTROWARENOFRDLTLTV 238
DB 181 RRGFDAAITNSRYNDLTRLIGNYTHAVRWYNTGLERWGPDSRDWIYRNQFRRELITLV 240
QY 239 LDIVALFPNYDYRTYPIQTSQLTREITSSVIEDSPVSANIPNGFNRA----EFGVRPP 294
DB 241 LDIVSLFPNYDSRTYPIRTVSQLTREITNPVLE-----NFDGSGFSAQOIEGSIKSP 294
QY 295 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGRNINPYSYGVF-NPGCAIWIADSD 351
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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 27, 2002, 20:27:55 ; Search time 157 Seconds

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2879.780 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

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Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4804.5	76.9	3531	10 US-09-873-873-9
				Sequence 5, Appli
				Sequence 1, Appli
				Sequence 25, Appli
				Sequence 9, Appli

5	4804.5	76.9	3531	10	US-09-873-873-11	Sequence 11, Appl
6	4804.5	76.9	3531	10	US-09-873-873-13	Sequence 13, Appl
7	4745.5	76.0	3534	10	US-09-873-873-27	Sequence 27, Appl
8	4647.5	74.4	3534	10	US-09-873-873-33	Sequence 33, Appl
9	4313.5	69.1	3579	10	US-09-873-873-29	Sequence 29, Appl
10	4211.5	67.4	4360	10	US-09-756-643-1	Sequence 1, Appli
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ALIGNMENTS

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; Sequence 5, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3522
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-826-660-5

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Qy 1141 GluLeuGluThrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
Db 3421 GAATTAGATCTTCCAGAAACCGATAAGGTATGATGAGATCGGAGAAACCGAAGGA 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCTGGACACGCTGGAATTACTCTTATGAGGAA 3522

RESULT 2

US-09-826-660-1
; Sequence 1, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3444
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-1

Alignment Scores:
Pred. No.: 0 Length: 3444
Score: 5879.00 Matches: 1117
Percent Similarity: 95.83% Conservative: 8
Best Local Similarity: 95.14% Mismatches: 23
Query Match: 94.15% Indels: 26
DB: 10 Gaps: 1

US-09-837-961-8 (1-1174) x US-09-826-660-1 (1-3444)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProThrAsnCysLeuAsnAsnProGluVal 20
Db 1 ATGGAGACACATACAGATCAGTGGTCCCTACACTGCCTCAACAATCTCGAGTA 60
Qy 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
Db 61 GAGATCTTCAACGAAGAGAGGTGCTGACTGGCAGTATGCGGTAGACATCTCCCTGCTCCT 120
Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 1174

Db 121 ACACGTTTCCTGCTGAGTTTGTTCACAGGTGTGGAGTTGGCTTGGCCCTCTTCGAC 180
Qy 61 LeuiletrpGlyPheleThrProSerAspTrpSerLeuPheLeuLeuGlnleGluGln 80
Db 181 CTCATCTGGGGCTTCATCACTCCATCTGATGTGGAGCTCTTCTCTCCAGATTGAACAG 240
Qy 81 LeuileGlnArgleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
Db 241 TTGATTGACAAAGGATTGAGACTTGGAAAGGAATCGGGCCCATCACTACCTCTGGTGC 300
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
Db 301 TTACACAGACGCTATCAGATCTACATGTAGACGACTGAGAGAGTGGAGACCAATCCTAC 360
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuile 140
Db 361 AATGCCCACTGAGAGAAGATGTCGTATACGCTTTGCTTAACACAGATGATCTTTGATC 420
Qy 141 ThrAlaIleAsnAsnPhenThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCCATCAACAACTACCCCTTACAGCTTCGAGATCCCTCTCTCTGGTCTATGTT 480
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
Db 481 CAAGCTGCTTAACCTGCACCTGTCTACCTACCTGCGGACGCTGTGCTGTTGGCAAGTTGG 540
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GGACTGGACATGCTACTGTCAACAATCACTCAACAGACTCATCAATCTGATTCATGCA 600
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TACACGAACATGTTTGGATACCTACATCAGGATTCGAGACCTGAGAGCTACTAC 660
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
Db 661 ACTCGCAATGGCCAGGTTCAATCACTAGTTTCAGGAGAGACTTACACTTACTGTGTAGAC 720
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
Db 721 ATAGTTGCTCTCTTCGAACTACGATGTTGCTGATTCATCCGATTCAACAGCTATCCCAA 780
Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
Db 781 CTTACAGGGAGATCTACACAGTTCACTCAGTTCATTGAAGACTCTCCAGTTTCTCGCAACATA 840
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProHisLeuMetAspPheMet 300
Db 841 CCCATGTTTCAACAGGCTGAGTTTGGAGTCAGACCCACCCCATCTCAITGACTTCATG 900
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
Db 901 AACTCTTTGTTGTTGACTGTCAGAGACTGTTAGATCCCAACTGTGTGGGAGACACTTA 960
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
Db 961 GTTAGCTCAGCAGACAGCTGGCCTGCAATGCTATCACTTTCCTAGTTACGGGGTCTTCAAT 1020
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
Db 1021 CCCGGGGGCCCATCTGGATTGAGATGAGATCCACGCTCTTCTATCGGACCTTGTCATCA 1080
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
Db 1081 GATCCTCTCTGCTCGCAGAGGCTTGGCAATCCCTCACTATGATCTGCTCTTAGGGGA 1140
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
Db 1141 GTGGCTTTCAACAACTGTAGATCAATCACACCCGACATTCAGGAACCTCCGGGACCAT 1200
Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
Db 1201 GACTCTCTAGATGAGATACCACTCAAGACCAACAGCGGGCCACTTGGATGACTACTCC 1260

Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
Db 1261 CATCTGCTGATCATGTACTTGTGCGCTGGCCAGGTGAGATCTCAGGTTCGACTCA 1320
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
Db 1321 TGGAGACACCAATGTTCTCTTGGACGATCTAGTAGCGTACCCCAACACACCATGTAT 1380
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCAGAGAGATCACTCAGATTCCTTGGTGAAGCACACACACTTCAGTCAGGAATCA 1440
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgThrSerGlyGlyPro 500
Db 1441 GTTCTAAGAGGGCGGGTTCAGGGAGGAGACATTCCTCGAGCCACTAGTGGAGAGCA 1500
Qy 501 PheAlaThrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
Db 1501 TTCGGTACACCATGTCAACATCAATGGCACTTCCCAAGGATCTGTCGAGATA 1560
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 GGTATGCTCTACTACCAATCTAAGAATCTAGCTTACGTTGCGAGTGAACGATCTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAGTTCAACAAGACAATGGATACCGGTGATCCACTTACATTCCTTCTTCTCC 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACGCCACTATCAACACCGGTTCACTTCCCAATGAGCCAGACAGCTTTCACAGTAGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACCTTCACTCAGGCACAGAACTGTACATTCACAGGTTTGAGTTGATTCAGT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCCACACTCGAGGAGAGCTGCTGACTTGGAAAGACACAGAGGGGTGATGCTCTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTCATCTGCTCCATCAGATTTGGCTCAAGACAGATGTGACTGACTATCACATCTCATCG 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTTCCAACTTGTGTAGTGCTCTCTGATGAGTTCTGTTGGATGAGAGAGAGAGTGG 1980
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
Db 1981 TCCGAGAGAGTCAACATGCTTAGCGACTTAGTGTAGCGGAACCTGCTTCAAGATCCC 2040
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
Db 2041 AACTTTCGGGATCAACAGCACTAGATCTGATGAGGGAGAGAGTGGAGATCAACC 2100
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATTCAAGAGAGTGTATGATGTTTCAAGGAGAACTATGTTACGCTCTTGGTACCTTTGAT 2160
Qy 721 GlucyTyrProThrTyrLeuTyrGlnLysIleAspGlnSerLysLeuLysProTyrThr 740
Db 2161 GAGTGCATCCCAATACCTTACCAAGATAGATGAATCGAAACTCAAAAGCTACACA 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuLeuArg 760
Db 2221 AGATACCACTGTGAGGTTTACATCGAGACAGTCAAGACTTCAGATCTACCTCATCAGA 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
Db 2281 TACAAGCCAAACATGAGACAGTCAATGTGCTGGGAGGGTTCACCTTGGCCACTTCA 2340

QY 781 ValGlnSerProileArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
|||||
Db 2341 GCCCAAGTCCATC----- 2355
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
|||||
Db 2356 -----GCCAAGTGGCCATCCTACACAC 2382
QY 821 pheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
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Db 2383 TTCTCTTGGACATAGAGCTTGGCTGTACCGACCTGACGAGACCTCGGTGTGGGTG 2442
QY 841 IlePheLysIleLysThrClnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
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Db 2443 ATCTTCAAGATCAAGACTCAAGATGCCATGCCAGCTAGGCAATCTGGAGTTCTAGAA 2502
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
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Db 2503 GAGAAACCACTTGTGGAGAAGCCCTCGTAGAGTGAAGAGGCTGAGAGAGTGGAGG 2562
QY 881 AspLysArgLysLeuGluLeuGluThrAsnIleValTyLysGluAlaLysGluSer 900
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Db 2563 GACAGAGAGAGAGTGGAAATGGGAACAACAACATTTGTACAAAGAAAGCCCAAGAAAGC 2622
QY 901 ValAspAlaLeuPheValAsnSerGlnTyTrpAspGlnLeuGlnAlaAspThrAsnIleAla 920
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Db 2623 GTTGACGCTCTGTGTGAACCTCAGTATGATAGCTCCAGCTGATACCAACATAGCT 2682
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyTrpLeuProGluLeu 940
|||||
Db 2683 ATGATTCATCTGCAGACAAACCGCTTCATAGCTTCGGAAGCTTACCTCTGAACTT 2742
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
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Db 2743 AGCTGATTCGCGGTGCAATCGCTATCTTTGAGAGTTAGAAAGGGCGCATCTTCACT 2802
QY 961 AlaPhePheLeuTyTrpAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
|||||
Db 2803 GCATTCCTCTGTATGATCGGAGGATGTCATCAGAATGGTGACTTCACAAATGGCCTA 2862
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
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Db 2863 TCCTGTGGAATGTGAAGGGCAGCTAGATGTAGAGAACAACAAATCACCGCTCTGTC 2922
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
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Db 2923 CTGTGTCTCTGATGAGTGGAGCAGAGTTTACAGAAGATTCCTGCTCTCTGCTGCT 2982
QY 1021 GlyTyTrileLeuArgValThrAlaTyLysGluGlyTyTrpGlyGluGlyCysValThrIle 1040
|||||
Db 2983 GGCTACATCTTCTGCTTACCGGCTACAAAGAGAGGATAGGAGAGGTTGCGCTCACATA 3042
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
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Db 3043 CAGCAGATTGAGAACACACCGCAGGAGTGAAGTTACGAACCTGCTCAGGAGGAGTGC 3102
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyTrpAlaAsnGlnGluGluTyTrpGlyGly 1080
|||||
Db 3103 TACCCCAACAACACCGTACTTGCATGACTACACTCGGACTCAAGAGGAGTATGAGGT 3162
QY 1081 AlaTyTrThrSerArgAsnArgGlyTyTrpAspGluThrTyTrpGlySerAsnSerSerValPro 1100
|||||
Db 3163 ACTTACACTTCTCGCAATCGAGGATAGGATGAGGCTATGAGAGCAACTCTTCTGTACCC 3222
QY 1101 AlaAspTyTrAlaSerValTyTrpGluLysSerTyTrpAspGlyArgArgAspAsnPro 1120
|||||
Db 3223 GCTGACTATCATCAGCCTATGAGGAGAGGCTTACACCGATGACCTAGGAGCAATCT 3282
QY 1121 CysGluSerAsnArgGlyTyTrpGlyAspTyTrpProLeuProAlaGlyTyTrpValThrLys 1140
|||||
Db 3283 TGCGAACTTAACAGAGGCTATGGGACTACACCGGTTACACCGGCTATGTACCCAA 3342
QY 1141 GluLeuGluTyTrpPheProGluThrAspLysValTrpIleGluLeuGly 1160

Db 3343 GAGTTAGTACTTTCAGAAACCGACAGGTTTGGATTGAGATTGAGAAACGGAGGA 3402
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
|||||
Db 3403 ACAITCATTTGTATAGCGTGGAGTTACTTCTGATGGAGGAA 3444
RESULT 3
US-09-873-873-25
; Sequence 25, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malivar, Thomas
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxin
; FILE REFERENCE: MEMO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-873-873-25

Alignment Scores:
Pred. No.: 0 Length: 3534
Score: 4812.50 Matches: 933
Percent Similarity: 84.16% Conservative: 66
Best Local Similarity: 78.60% Mismatches: 165
Query Match: 77.07% Indels: 23
DB: 10 Gaps: 9
US-09-837-961-8 (1-1174) x US-09-873-873-25 (1-3534)
QY 1 MetGluAsnAsnIleGln--AsnGlnCysValProTyAsnCysLeuAsnAsnProGlu 19
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Db 1 ATGGATAACAATCCGACATCAATGAATGCATCTTATAATTGTTAAGTAACCTGAA 60
QY 20 ValGluIleLeuAsnGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38
|||||
Db 61 GTAGAAGTATTAGTGGAGAAAGAAATAGAAACTGGTTACACCCCAATCATATTCCTTG 120
QY 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
|||||
Db 121 TCGCTTAACGCAATTTCTTTTGTAGTGAATTTGTCGCGTGTGATTTGCTTGAAGTACT 180
QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78
|||||
Db 181 GTGTATATATATGGGAATTTTGGTCCCTCTCAATGGGAGCGCATTCCTGTACAAAT 240
QY 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98
|||||
Db 241 GAACAGTTAATTAACCAAGAATAAGAAATTCGCTAGGAACCAAGCCATTTCTAGATA 300
QY 99 ArgGlyLeuAlaAspSerTyTrpGluIleTyTrpLeuAlaLeuArgGluTrpGluAlaAsn 118
|||||
Db 301 GAAGGACTAAGCAATCTTTATCAAAATTTACGCAATCTTTTAGAGAGTGGGAAGCAGAT 360
QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138
|||||
Db 361 CCTACTATCCAGCATTAAGAGAGAGATGCGTATTCATTCATGACATGACATGACAGTGC 420

Qy	486	ThrGlyGlyAspIleu	argThrSerGlyGlyProPheAlaTyrThrIleVal	Asn	507
Db	1483	ACGGGAGGAGATATCTTCGACGAACAAGTCGGAGACCATTTGCTTTATCTATCTATGTTAAAT	1542		
Qy	508	IleAsnGlyGlnLeu	ProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn	527	
Db	1543	ATTAATGGGCATATCCCAAAAGGTATCGTCCAGAATACGCTATGCTCTACTACAAAT	1602		
Qy	528	LeuArgIleTyrValThrVal	AlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr	547	
Db	1603	CTAAGAATATTACGTACCGTTCCAGGTCAACGGATTTTGTGTGCTCAATTTAAACAAACA	1662		
Qy	548	MetAspThrGlyAsp	ProLeuThrPheGlnSerPheSerTyrAlaIleThrIleAsnThrAla	567	
Db	1663	ATGGATACCGGTGAACCAATTAACATCCAACTCTTTAGTCAGCAACTATTAATACAGCT	1722		
Qy	568	PheThrProMetSerGln	SerSerPheThrValGlyAlaAspThrPheSerSerGly	587	
Db	1723	TTTACATTTCCCAATGAGCCAGAGTAGTTTCACAGTAGTGCTGATACTTTTAGTTCAGGG	1782		
Qy	588	AsnGluValTyrIle	aspArgPheGlnLeuIleProValThrAlaThrPheGluAlaGlu	607	
Db	1783	AATCAAGTTTATATAGACAGATTCAATTGATTCACAGTACTGCAACATTTGAAGCAGAA	1842		
Qy	608	TyrAspLeuGluArgAla	GlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle	627	
Db	1843	TATGATTTAGAAAGACACAAAAGCGGTGAATCGCTGTTTACTTCTATAAACCAAATA	1902		
Qy	628	GlyIleLysThrAsp	ValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys	647	
Db	1903	GGGATAAACACAGATGTGACGATTATCATATTGATCAAGTATCCAAATTTAGTGGATGT	1962		
Qy	648	LeuSerAspGluPheCys	LeuAspGluLysArgGluLeuSerGluLysValLysHisAla	667	
Db	1963	TTATCAGATCAATTTGCTTGATGAAGAAAGCGAATTTGTCGGAGAAGTCAAAACATCGC	2022		
Qy	668	LysArgLeuSerAsp	GluArgAsnLeuGlnAspProAsnPheLysGlyIleAsnArg	687	
Db	2023	AAGCGACTCAGTCATCAGCGGAATTTACTTCAAGATCCAAACTTCAAGGCAATCAATAGG	2082		
Qy	688	GlnLeuAspArgGly	TrpArgGlySerThrAspIleThrIleGlnArgGlyAspAspVal	707	
Db	2083	CACATAGACCGTGGTGGAGAGAGTAGTCGGATATACCATCCAAAGAGAGATGACGTA	2142		
Qy	708	PheLysGluAsnTyrVal	ThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu	727	
Db	2143	TTCAAGAAAAATTATCTCACACTACACAGTACCTTTGATGAGTGTCTATCCAAACATATTG	2202		
Qy	728	TyrGlyLysIleAsp	GluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr	747	
Db	2203	TATCAAAAAATCATCAATCAAAATTAAGCCTTTACCCTTTATCAATTAAGAGGGTAT	2262		
Qy	748	IleGluAspSerGln	AspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr	767	
Db	2263	ATCGAAGATAGTCAAGACTTAGAATCTATTTAATTCGTACAATGCCAAACATGAAACA	2322		
Qy	768	ValAsnValLeuGly	ThrGlySerLeuTrpProLeuSerValGlnSerProIleArgLys	787	
Db	2323	GTAAATGTCCAGGTACGGGTTCCTATTGGCCGCTTCAGCCCCAAAGTCCAAATCGGAAG	2382		
Qy	788	CysGlyGluProAsn	ArgCysAlaProHisLeuGluTrpAsnProAspLeuAspCysSer	807	
Db	2383	TGTGGAGACCGAATCATGATGCGCGCCACACCTTGAATGGAATCCTGACTTAGATTGTTGC	2442		
Qy	808	CysArgAspGlyGlu	LysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal	827	
Db	2443	TGTAGGSGATGGAGAAAGTGTCCCATCATTCGTGCATCAATTTCTCCTTAGACATGTATGA	2502		
Qy	828	GlyCysThrAspLeu	AsnGluAspLeuAspValTrpValIlePheLysIleLysThrGln	847	
Db	2503	GGATGTACAGCTTAAATGAGGACCTAGGTGATGGGTGATCTTTAGATTAAGATTAAGACGCA	2562		
Qy	848	AspGlyHisAlaArg	LeuGlyAsnLeuGluPheLeuGluLysProLeuValGlyGlu	867	

Qy	199	HisArgTyrThrIysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly	218
Db	601	GGCAACTATACAGATTATCTGCTACGCTGGTACAAATACGGGATTAGAACTGTATGGGGA	660
Qy	219	ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrVal	238
Db	661	CCGGATTCTAGAGATTGGGTAAAGTATATCAATTTAGAGAGAAATTAACACATACTGTA	720
Qy	239	LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrPheIleGlnThrSer	258
Db	721	TTAGATATCGTTGCTCTGTTCCCGAATTATGATAGTAGAAGATATCAATTCGAACAGTT	780
Qy	259	SerGlnLeuThrArgGlnIleTyrThrSerSerValIleGluAspSerProValSerAla	278
Db	781	TCCCAATTAAACAGAGAAATTTATACAAACCCAGTATTAGAA-----	822
Qy	279	AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro	294
Db	823	AATTTTCATGGTAGTTTTCGAGCTCGGCTCAGGSCATAGAAAGAACTATTAGGAGTCCA	882
Qy	295	HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr	314
Db	883	CAITTCATCGATATACTTAACAGTATAACCATCTATACGGTAGTCTCATAGGGGTATTAT	942
Qy	315	ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn	332
Db	943	TATGGTCAGGCAATCAATATATGCTCTCTCTGTAGGGTTTCGGGGCCAGAAATTCAC	1002
Qy	333	PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp	351
Db	1003	TTTCCGCTATATGGAATCTATGGGAATGAGCTCCACACACACATGATTTGTCTCACTA	1062
Qy	352	ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly	368
Db	1063	GGTCAGGGCGTATAGACATTTATCGTCCACTTTATATAGAGACCTTTTATATATAGG	1122
Qy	369	PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly	387
Db	1123	ATAAATAATCAACAACATATCTGTTCTTACGGGACAGAAATTTGCTTATGGAACTCTCA	1182
Qy	388	ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro	407
Db	1183	AATTGGCCATCCGCGTATACAGAAACGGAACGGTAGATTCGCTGATGAATACCG	1242
Qy	408	ProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr	427
Db	1243	CCACAGAAATAACAACGTGCCACCTAGGCAAGGATTTAGTCATCGATTAAAGCCATGTTCA	1302
Qy	428	PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetPheSer	447
Db	1303	ATGTTTCGTCAGCTTTAGTATAGTGTAAAGTAAATAGAGCTCCCAATGTTTCT	1362
Qy	448	TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle	467
Db	1363	TGGACGCACCGTAGTCAACCCCTACAAATACAAATGATCGGAGAGGATTACTCAATA	1422
Qy	468	ProLeuValIysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe	487
Db	1423	CCATGGTAAAGCACATACATCTCAGTCCAGTACTCTGTTGTAAGAGGCGCCGGGTTT	1482
Qy	488	ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn	507
Db	1483	ACGGAGGAGNATTCTTCACACACAAAGTGAGGACCAATTTCCTTATACTATTGTTAAT	1542
Qy	508	IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn	527
Db	1543	ATAAATGGCAAAATTACCCCAAGGATATCGTGCAGAAATACGCTATGTCCTCTACTACAAT	1602
Qy	528	LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnIysThr	547
Db	1603	CTAGAATTTACGTAAACGGTTGACGGTGAACGGATTTTTCCTGGTCAATTTAAACAAACA	1662
Qy	548	MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla	567

Db	1663	ATGGATACCGGTGACCCATTAACTCCAACTCTTTAGTTACGCAACTATAATACAGCT	1722
Qy	568	PhetThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly	587
Db	1723	TTTACATATCCCAATGAGCCAGAGTAGTTTTCACAGTAGGTGCTGATACCTTTAGTTAGG	1782
Qy	588	AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu	607
Db	1783	AATGAAGTTTATATAGACAGATTTGAATGTGATTCAGTTACTGCAACATTTGAAGCAGAA	1842
Qy	608	TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle	627
Db	1843	TATGATTTAGAAGACGACAAAGCGGTGAATGCCTGTTTACTTCTATPAACCAATA	1902
Qy	628	GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys	647
Db	1903	GGGATATAAACACATGTGACGGATTATCATATGTATCAAGTATCCAATTTAGTGGATGT	1962
Qy	648	LeuSerAspGluPheCysLeuAspGlnLysArgGlnLeuSerGluLysValLysHisAla	667
Db	1963	TTTATCAGATGAATTTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAAACATCG	2022
Qy	668	LysArgLeuSerAspGluArgAsnLeuGlnAspProAsnPheLysGlyIleAsnArg	687
Db	2023	AAGCGACTCAGTCATGAGCGGAATTTACTTCAAGATCCAACTTCAAAAGCATCAATAGG	2082
Qy	688	GlnLeuAspArgGlyTrrpArgGlySerThrAspIleThrIleGlnArgGlyAspAspVal	707
Db	2083	CAACTAGACCGTGGTGGAGAGAGTAGTACGGATATTACATCCAAAGAGGAGATGACGTA	2142
Qy	708	PhelysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu	727
Db	2143	TTCAAGAAATTAATGTCACACTACAGGTACCTTTGATGAGTGTCTATCCAAACATAATTG	2202
Qy	728	TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr	747
Db	2203	TATCAAAAATTCGATGAATCAAAATTAAGCGCTTTACCCGTTTATCAATTAAGAGGTAT	2262
Qy	748	IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr	767
Db	2263	ATCGAAGATAGTCCAGACTTAGAATCTATTAAATCCGTACATGCAAAACATCAACA	2322
Qy	768	ValAsnValLeuGlyThrGlySerLeuTrrpProLeuServAlGlnSerProIleArgLys	787
Db	2323	GTAATGTGCCAGGTACGGGTTTCCTTATGGCGCGCTTCAGCCCAAGTCCCAATCGGAAG	2382
Qy	788	CysGlyGluProAsnArgCysAlaProHisLeuGluTrrpAsnProAspLeuAspCysSer	807
Db	2383	TGTGGAGCGCGAATCGATGCGCGCCACACCTTGAATGGAATCCTGACTTAGATTGTTGG	2442
Qy	808	CysArgAspGlyGlnLysCysAlaHisSerHisHisPheSerLeuAspIleAspVal	827
Db	2443	TGTAGGATGGAGAAAAGTGTGCCATCATCTCGCATCATTTCTCTTAGACATTCATGTA	2502
Qy	828	GlyCysThrAspLeuAsnGlnAspLeuAspValTrrpValIlePheLysIleLysThrGln	847
Db	2503	GGATGTCACACTTAAATGAGGACCTAGGTGTATGGGTGATCTTTAAGATTAAGACGCAA	2562
Qy	848	AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluGluLysProLeuValGlyGlu	867
Db	2563	GATGGCACCAAGACTAGGGAATCTAGAGTTCTTCGAAGAGAAAACCATTAAGTAGGAGAA	2622
Qy	868	AlaLeuAlaArgValLysArgAlaGluLysLysTrrpArgAspLysArgGluLysLeuGlu	887
Db	2623	CGCGTAGCTCGTGTGAAAAGCGGAGAAAAAATGGAGAGCAACCGTGAATAATTGGAA	2682
Qy	888	LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn	907
Db	2683	TGGAAACAAATATCGTTTATAGAGGCGCAAGAGATCTGTAGATGCTTTATTTGTAAC	2742
Qy	908	SerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAspLys	927

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Db 2743 TCTCAATATGATCAATAACAGCGGATACCAATATTCGCCATGATTCATCGCGCAGATAAA 2802
Qy 928 ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsn 947
Db 2803 CGTGTTATAGCATTCGGAAGCTTATCTGCGAGCTGCTGTGATTCGGGTGTCAAT 2862
Qy 948 ValAspIlePheGluLeuLeuLysGlyArgIlePheThrAlaPhePheLeuTyrAspAla 967
Db 2863 GCGGCTATTTTGAAGAANTAGAGGCGGTATTTTCACGTGCATTCCTCCATATGATGCG 2922
Qy 968 ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly 987
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Qy 988 HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValValProGluTrpGlu 1007
Db 2983 CATGTAGATGTAGAGACAAACAAACACACCGACGTTCCGTCCTGTTGTCGGATGGGA 3042
Qy 1008 AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr 1027
Db 3043 GCAGAGTCTCACAGAAGTCTGCTGCTGTCGCGGTGCTGCTATATCTTCGTGTACACA 3102
Qy 1028 AlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluLeuGluAsnThr 1047
Db 3103 GCGTACAAAGAGGATATGAGAGGTTGCGTAACCATTCATGAGATCGAGAACAAATACA 3162
Qy 1048 AspGluLeuLysPheSerAsnCysValGluGluValTyrProAsnAsnThrValThr 1067
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Qy 1068 CysAsnAspTyrThrAlaAsnGlnGluTyrGlyGlyAlaTyrThrSerArgAsnArg 1087
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Qy 1088 GlyTyrAspGluThrTyrGlySerAsnSerSerValProAlaAspTyrAlaSerValTyr 1107
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Qy 1108 GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr 1127
Db 3331 GAAGAAATATCGTATACAGATGGACGACGAGAGAAATCCTGTGTGAATTTACAGAGGCTAT 3390
Qy 1128 GlyAspTyrThrProLeuProLagIleTyrValThrLysGluLeuGluTyrPheProGlu 1147
Db 3391 AGGGATTACACGCCCATACCACTGCTGTTATGTGACAAAGAAATAGAACTTCCCGAGAA 3450
Qy 1148 ThrAspLysValTrpIleGluLeuGlyGluThrGluGlyThrPheIleValAspSerVal 1167
Db 3451 ACCGATAAGGTATGGATTGAGATTGGAGAAACGGAAGAACATTTATCGTGGACGCGT 3510
Qy 1168 GluLeuLeuMetGluGlu 1174
Db 3511 GAATTACTCTTATGGAGAA 3531

RESULT 5
US-09-873-873-11
; Sequence 11, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 11
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
US-09-873-873-11

Alignment Scores:
Pred. No.: 0 Length: 3531
Score: 4804.50 Matches: 932
Percent Similarity: 84.08% Conservative: 66
Best Local Similarity: 78.52% Mismatches: 166
Query Match: 76.95% Indels: 23
DB: 10 Gaps: 9

US-09-837-961-8 (1-1174) x US-09-873-873-11 (1-3531)
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Qy 20 ValGluIleLeuAsnGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38
Db 61 GTAGAGTATTAGCTGGAGAAAGATAGAACTGGTTACACCCCATCGATATTTCTTCTTG 120
Qy 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
Db 121 TCGCTAACCAATTTCTTTTGTAGTGAATTTGTCGGGTCTGGATTTGTGTAGGACTA 180
Qy 59 PheAspLeuIleTrpClyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78
Db 181 GTTGATATATATGGGAATTTTGTGCTCCTCCTCAATGGGACCATTTCTTGTACAAAT 240
Qy 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98
Db 241 GAACACTTAATTAACCAAGATAGAGAAATTCGCTAGGAACCAAGCCATTTCTAGATTA 300
Qy 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118
Db 301 GAAGSACTAAGCAATCTTTATCAAAATTTACGCAAAATCTTTTAGAGAGTGGAGAGCAT 360
Qy 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138
Db 361 CCTACTAATCCACCATTAAGAGAGAGATCGGTATTCAATCAATCAATGACATGACATGCC 420
Qy 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158
Db 421 CTTACAACCGCTATTCTCTTTTTCAGTTCAAAATATATCAAGTCTCTCTTTTATCAGTA 480
Qy 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178
Db 481 TATGTTCAAGCTGCAAAATTTACATTTATCAGTTTTCAGAGATGTTTCAGTGTGTGGACAA 540
Qy 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgGluLeuAsnLeuIle 198
Db 541 AGGTGGGATTTGATCCCGGCTATCAATATAGTTCGTATTAATGATTAACTAGGCTTATT 600
Qy 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuAsnLeuArgGly 218
Db 601 GCAACTATACAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal 238
Db 661 CCGGATTCAGAGATGGGTAAAGTATATCAATTTAGAGAGAAATTAACACTAAGTGA 720
Qy 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258
Db 721 TTAGATATCGTTGCTGTTCCGGAATTTATGATAGAGAGATATCAATTCGACAGATT 780
Qy 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278

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781 TCCCAATTACAGAGAAATTTATACAAACCCAGTATTAGAA----- 822
QY AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294
Db AATTTTGATGGTATTTCCGAGCTCGGCTCAGGGCATAGAAAGATATTAGAGTCCA 882
QY HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314
Db CATTTGATGATATATTTACAGATATACCATCTATACGATGCTCATAGGGGTTATTAT 942
QY ValIrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332
Db TATTTGTCAGGGCATCAATAATAGGCTCTCTCGTAGGGTTTTTCGGGGCCAGATTCAC 1002
QY PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleThrPheAlaAspGluAsp 351
Db TTTCCGCTATATGGAAGTATGGGAATTCAGCTCCCAACAACAGTATTTGTTGCTCAACT 1062
QY ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368
Db GTTCAGGGCGGTATAGAACATTTATCGTCCCATTTATATAGAGACCTTTTAAATATAGGG 1122
QY PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387
Db ATAATAATCAACAACACTATCTGTTCTTGACGGGACAGAAATTTGCTATGGAACCTCTCTCA 1182
QY ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407
Db AATTTGCCATCCCTGTATACAGAAAAGCGGAACGGTAGATTCGGTGGATGAATACCG 1242
QY ProGluAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr 427
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QY PheValArgTrpProGlyGluIleSerGlySerAspSerTyrArgAlaProMetPheSer 447
Db ATGTTTCGTTACGGCTTTAGTATAGTAGTAGTAAAGTAAAGCTCCCAATGTTTCT 1362
QY TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGluIle 467
Db TGGACGACCGCTAGTGCACACCCCTACAAATACAAATTCATCGGAGAGGATTAACAAATA 1422
QY ProLeuValLysAlaHisThrLeuGlnSerGlyThrValValArgGlyProGlyPhe 487
Db CCATGGTAAACACACATACACTTCAGTCAGTACTACTGTTGTRAGAGGCCCCGGTTT 1482
QY ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507
Db ACGGGAGGAGATATCTTCGACGAACAAGTGGAGGACCAATTTGCTTATACTATTGTTAAT 1542
QY IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrAsn 527
Db ATAAATGGGCAATACCCCAAGATACGTCGCAAGATACGCTATGCTCTACTACAAAT 1602
QY LeuArgIleTyrValThrValAlaGlyArgIlePheAlaGlyGlnPheAsnLysThr 547
Db CTAGAATTTACGTAACGGTTGACGGTGAACGGATTTTCTGCTGCTCAATTTACAAAACA 1662
QY MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla 567
Db ATGGATACCGGTCACCCATTAACATCTTTAGTTAGTACGCAACTATTATATACAGCT 1722
QY PheThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly 587
Db TTTACATTCCTCAATGACCCAGAGTAGTTTTCACAGTAGTGTCTGATACCTTTTAGTTCAGGG 1782
QY AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu 607
Db ATGCAAGTTTTATATAGACAGATTTGAATGATTCACGTTACTGCAACATTTTGAAGCAGAA 1842
QY TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle 627

Db TATGATTATGAAGACACAAAAGCGGTGAATGCGTGTCTTACTTCTATAAACCAAAATA 1902
QY GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys 647
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QY LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla 667
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Db CAACTAGACCGTGGTGGAGAGGAGTACGGATATTACCATTCCAAAGAGGAGTACGTA 2142
QY PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu 727
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QY TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr 747
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QY IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr 767
Db ATCGAAGATAGTCAAGACTTAGAAATCTATTAAATTCGCTACAAATGCAAAACATGAACA 2322
QY ValAsnValLeuGluThrGlySerLeuTyrProLeuSerValGlnSerProIleArgLys 787
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QY CysGlyGluProAsnArgCysAlaProHisLeuGluTyrPasnProAspLeuAspCysSer 807
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QY CysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal 827
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QY LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn 907
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QY ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsn 947
Db CGTGTTCATAGCATTCGAGAGCTTATCTGCCGTGAGCTGTCTGTGATTCGGGTGTCAT 2862
QY ValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPheLeuTyrAspAla 967
Db GCGGCTATTTTGAAGAAATTAAGAGCGGTATTTTCACTGCATTCCTCTATATGATGCG 2922
QY ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly 987
Db AGAAATGTCATTAATAATGCTGATTTTAAATAGGCTTATCCTGCTGGAACGTGAAAGGG 2982

QY	1048	AspGluLeuLysPheSerAsnCysValGluGluGluValTyrProAsnAsnThrValThr	106
DB	3163	GAGCAACTGAAGTTTACCACTGCCTAGAAAGAGAAATCTATCCAAATAACACGGTAACG	3222
QY	1068	CysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGlyAlaTyrThrSerArgAsnArg	1087
DB	3223	TGTAATGATTATACTGTAATCAAGAAGAATACGAGAGTGGCTACACTCTCGTAATCGA	3282
QY	1088	GlyTyrAspGluThrTyrGlySerAsnSerSerValProAlaAspTyrAlaSerValTyr	1107
DB	3283	GGATAATACGAAGCT-----CCTCCGTACACAGCTGATTATCGCTCACTCTAT	3330
QY	1108	GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr	1127
DB	3331	GAAGAAAATTCGTATACAGATGGACGAAGAGAGAATCCTTGTGAATTTAACAGAGGGTAT	3390
QY	1128	GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu	1147
DB	3391	AGGGATTACAGCCCATCCAGTTGGTATGTCGACAAAGAATTAGAATACTTCCCGAGAA	3450
QY	1148	ThrAspLysValTyrPileGluLeuGlyGluThrGluGlyThrPheIleValAspSerVal	1167
DB	3451	ACCGATAAGGTATGGATTGGAGATTGGAGAAACGGAGGAACATTTATCGTGGACAGCGTG	3510
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DB	3511	GAATTACTCTTATGGAGGAA 3531	
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; Sequence 27, Application US/09873873			
; Patent No. US20020064865A1			
; GENERAL INFORMATION:			
; APPLICANT: Malvar, Thomas			
; APPLICANT: Gilmer, Amy Jelen			
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum			
; FILE REFERENCE: MECO:210--2			
; CURRENT APPLICATION NUMBER: US/09/873,873			
; CURRENT FILING DATE: 2001-08-20			
; PRIOR APPLICATION NUMBER: US 09/253,341			
; PRIOR FILING DATE: 1999-02-19			
; PRIOR APPLICATION NUMBER: US 08/922,505			
; PRIOR FILING DATE: 1997-09-03			
; PRIOR APPLICATION NUMBER: US 08/754,490			
; PRIOR FILING DATE: 1996-11-20			
; NUMBER OF SEQ ID NOS: 35			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 27			
; LENGTH: 3534			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Hybrid Delta-Endotoxin			
; NAME/KEY: CDS			
; LOCATION: (1)..(3531)			
US-09-873-873-27			
Alignment Scores:			
Pred. No.:		0	Length: 3534
Score:		4745.50	Matches: 923
Percent Similarity:		83.40%	Conservative: 67
Best Local Similarity:		77.76%	Mismatches: 174
Query Match:		76.00%	Indels: 23
DB:		10	Gaps: 9
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QY	20	ValGluLeuLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu	38

QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407
Db 1183 AATTGGCCATCCGCTGTATACAGAAAAGGACGGTAGGTTCCTCGTGAATGAATACCG 1242
QY 408 ProGlnAspAsnSerGlyAlaProTyrAsnAspTyrSerHisValLeuAsnHisValThr 427
Db 1243 CCACAGATACACACGTCGCCACTAGGCAAGGATTAGTCATCGATTAAAGCCATTGTCA 1302
QY 428 PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetPheSer 447
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QY 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467
Db 1363 TGGTATACATCGTAGTGTGAATTAATAATTAATTCGATCGGATGATTACTCAATA 1422
QY 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValAlaArgIleProGlyPhe 487
Db 1423 CCATTGGTAAAGCACATACACTTCAGTCAGGTACTACTGTGTGAAGAGGCCCGGGTTT 1482
QY 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValasn 507
Db 1483 ACGGAGAGAGATATCTTCGACGAAAGTGGAGGACCATTTGCTTATACATTGTTAAT 1542
QY 508 IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn 527
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QY 528 LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr 547
Db 1603 CTAGAATTTACGTTACGGTTGCAGGTACCGGATTTTGTGTCATTTAAACAACA 1662
QY 548 MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla 567
Db 1663 ATGATACCGGTGACCCATTAACATTCGAATCTTTAGTTACGCAACTATTAAATACAGCT 1722
QY 568 PheThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly 587
Db 1723 TTTCATCTCCCAATGACGACAGTAGTTTCACAGTAGGTGCTGTATCTTTAGTTACAGG 1782
QY 588 AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu 607
Db 1783 AATGAAGTTTATAGACAGATTTGAATGATTCAGTTACTGCAACATTTGAACAGAA 1842
QY 608 TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle 627
Db 1843 TATGATTTAGAAAGACACAAAGCGGTGAATCGCTGTTTACTTCTATAAACCAATA 1902
QY 628 GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys 647
Db 1903 GGGTAAACACAGATGTGACGGATTTCATATTGATCAAGTATCCAAATTAGTGGATTGT 1962
QY 648 LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla 667
Db 1963 TTATCAGATGAATTTGTCTGGATGAAAGCGAGAAATGTCCGAGAAAGTCAAAATCCG 2022
QY 668 LysArgLeuSerAspGluArgAsnLeuLeuGlnAspProAsnPheLysGlyIleAsnArg 687
Db 2023 AAGCGACTCAGTAGAGCGGAAATTTACTTCAAGATCCAAACTTCAAGAGGATCAATAGG 2082
QY 688 GlnLeuAspArgGlyTrpArgGlySerThrAspIleThrIleGlnArgGlyAspVal 707
Db 2083 CAACTAGACCGTGTGGAGAGGAGTAGCATATTACCATCCAAAGAGGAGATGACGTA 2142
QY 708 PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu 727
Db 2143 TTCAAAGAAAATTTATGTCACACTACCGGTACCTTTGTATGAGTGTCTATCCAAATATTG 2202
QY 728 TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr 747
Db 2203 TATCAAAAATCGATGAATCAAAAATTAAGCCCTTTACCCGTTTATCAATTAAGAGGAT 2262

QY 748 IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr 767
Db 2263 ATCGAAGATAGTCAAGACTTAGAAATCTATTAAATTCCTCAATGCAAAACATGAACA 2322
QY 768 ValAsnValLeuGlyThrGlySerLeuTrpProLeuSerValGlnSerProIleArgLys 787
Db 2323 GTAAATGTGCCAGGTACGGGTTCCTTATGGCGCTTTCAGCCCAAGTCCCAATCGAAG 2382
QY 788 CysGlyGluProAsnArgCysAlaProHisLeuGluTrpAsnProAspLeuAspCysSer 807
Db 2383 TGTGAGAGCGGAATCGATGCGCCACACACTTGAATGGAATCCTGACTTAGATTGTTTCG 2442
QY 808 CysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal 827
Db 2443 TGTAGGATGAGAAAAGTGTGCCCATCATTCGCGCATCAATTTCTCTTAGACATTGATGA 2502
QY 828 GlyCysThrAspLeuAsnGluAspLeuAspValTrpValIlePheLysIleLysThrGln 847
Db 2503 GGATGTACAGACTTAATAGAGACCTAGGTGTATGGGTGATCTTTAGATTAAAGCGAA 2562
QY 848 AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluLysProLeuValGlyGlu 867
Db 2563 CATGGCAGCAGACACTAGGGAATCTAGAGTTTCTCGAAGAGAAACCATTAGTAGGAGAA 2622
QY 868 AlaLeuAlaArgValLysArgAlaGluLysTrpArgAspLysArgGluLysLeuGlu 887
Db 2623 CGCTAGCTCGTGTGAAAAGAGCGAGAAAATGGAGAGACAAACGTTGAAAATTTGAA 2682
QY 888 LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValasn 907
Db 2683 TGGGAACAATAATCGTTTATAAGAGCGCAAAAGAACTGTAGATGCTTTATTGTAAAC 2742
QY 908 SerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAlaAspLys 927
Db 2743 TCTCAATATGATCAATTAACAAGCGATACGAATATTGCCATGATTCAATCGCGCAGATAA 2802
QY 928 ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValasn 947
Db 2803 CGTGTTCATACATCGAGAGAGCTTATCTGCTGAGCGTCTGTGATTCCGGGTGTCAAT 2862
QY 948 ValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPheLeuTyrAspAla 967
Db 2863 CGCGCTATTTTGAAGAATTAGAACGGCGTATTTTCACGTGCATTCCTCTATATGATCGG 2922
QY 968 ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly 987
Db 2923 AGAAATGTCATTAATAAATGGTGAATTTAATAATGGCTTATCTGCTGGAACGTGAAAGGG 2982
QY 988 HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValProGlyTrpGlu 1007
Db 2983 CATGTAGATGAGAGAGGATATGGAGAAAGGTTCGTAACCATTCATGAGATCGAGAACATA 3042
QY 1008 AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr 1027
Db 3043 GCAGAAGTGTCCACAAGAAGTTCGTGCTCGCGGTGCTGCTATATCTTCGTGTCACA 3102
QY 1028 AlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluIleGluAsnThr 1047
Db 3103 CGGTACAGAGGAGGATATGGAGAAAGGTTCGTAACCATTCATGAGATCGAGAACATA 3162
QY 1048 AspGluLeuLysPheSerAsnCysValGluGluValTyrProAsnAsnThrValThr 1067
Db 3163 GACCACTGAAGTTTACCACTGCGTAGAGAGAAATCTATCCAAATAACACGGTAACG 3222
QY 1068 CysAsnAspTyrThrAlaAsnGlnGluGlyTyrGlyAlaTyrThrSerArgAsnArg 1087
Db 3223 TGTAAATGATTATAGTAAATCAAGAAGATACGAGAGTGGTACACTTCTCGTAATCGA 3282
QY 1088 GlyTyrAspGluThrTyrGlySerAsnSerValProAlaAspTyrAlaSerValTyr 1107
Db 3283 GGATATAACGAAGCT-----CCTTCCGTAACGAGCTGATTATGCGTCACTAT 3330
QY 1108 GluGluLysSerTyrThrAspGlyArgAspAsnProCysGluSerAsnArgGlyTyr 1127

Db 3331 GAAGAAAAATCGTATACAGATGCGAAGAGAGAAATCCTGTGTAATTAACAGAGGTAT 3390
 QY 1128 GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu 1147
 Db 3391 AGGGATTACAGCGCACTACCACTGGTATGTGTGACAAAGAAATAGAAATCTCCCGAGAA 3450
 QY 1148 ThrAspLysValTrpIleGluLeuGlyGluThrGluGlyThrPheIleValAspSerVal 1167
 Db 3451 ACCGATTAAGTATGGAATGAGATTGAGAAACGGAAGGAACATTTATCGTGGACAGCGTG 3510
 QY 1168 GluLeuLeuLeuMetGluGlu 1174
 Db 3511 GAATTACTCCTTATGAGGAA 3531

RESULT 8

US-09-873-873-33
 ; Sequence 33, Application US/09873873
 ; Patent No. US20020064865A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Malvar, Thomas
 ; APPLICANT: Gilmer, Amy Jelen
 ; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
 ; FILE REFERENCE: MECO:210-2
 ; CURRENT APPLICATION NUMBER: US/09/873,873
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: US 09/253,341
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR APPLICATION NUMBER: US 08/922,505
 ; PRIOR FILING DATE: 1997-09-03
 ; PRIOR APPLICATION NUMBER: US 08/754,490
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 33
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Hybrid Delta-Endotoxin
 US-09-873-873-33

Alignment Scores:

Pred. No.: 0 Length: 3534
 Score: 4647.50 Matches: 907
 Percent Similarity: 82.48% Conservative: 72
 Best Local Similarity: 76.41% Mismatches: 185
 Query Match: 74.43% Indels: 23
 DB: 10 Gaps: 9

US-09-837-961-8 (1-1174) x US-09-873-873-33 (1-3534)

QY 1 MetGluAsnIleGln---AsnGlnCysValProTyrAsnCysLeuAsnProGlu 19
 Db 1 ATGGATAACAATCCGAACATCAATGAATGATTCCTTATTAATGTTTAAGTAACCCCTGAA 60
 QY 20 ValGluIleLeuAsnGluGluArg---SerThrGlyValArgLeuProLeuAspIleSerLeu 38
 Db 61 GTAGAGATTATAGTGGAGAAAGAAAGTAAGAACTGGTTACACCCCAATCGATTTCTCTTG 120
 QY 39 SerLeuThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
 Db 121 TCAGTAACGCAATTCCTTTGAGTGAATTTGTTCCCGGTGCTGGATTTGTTAGGACTA 180
 QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78
 Db 181 GTTGATATAATATGGGAATTTTGTGTCCTCTCAATGGGACGCAATTCCTGTACAAAT 240
 QY 79 GluGluLeuLeuGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeu 98
 Db 241 GAACAGTTAATTAACCAAGAAATAGAGAAATTCGCTAGGAACCAAGCCATTTCTAGATTA 300
 QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118

Db 301 GAAGGACTAAGCAATCTTTTATCAAAATTTACGCAAGATCTTTTAGAGAGTGGGAGCAGAT 360
 QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138
 Db 361 CCTACTAATCCAGCAATTAAGAGAAGATCGTATTTCATTAATCAATGATGAACAGAGTGC 420
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158
 Db 421 CTTACACCCCTATTCTCTTTTGCAGTTTCAAAATTTATCAAGTTCTCTTTTATCATGTA 480
 QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178
 Db 481 TATGTTCAAGCTCGAATTTACATTTATCATGTTTGAGAGATGTTTCAGTCTTGGACAA 540
 QY 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuLeuLeuLeu 198
 Db 541 AGTGGGGATTTGATGCGCGCACTATCAATAGTCGTTATATGATGATTTAACTAGCTTATT 600
 QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218
 Db 601 GGCACATATACAGATTATGCTGACCGCTGTCAATACGGGATTAGAACGTGATGGGGA 660
 QY 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrVal 238
 Db 661 CCGGATTTAGAGATTGGGTAAGTATATCAATTTAGAGAAGAAATTAACACTAAGTGA 720
 QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258
 Db 721 TTAGATATCCTGCTGCTCCGGAATTTATAGTAGTAGAAGATATCCATTCGAACAGTT 780
 QY 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278
 Db 781 TCCCAATTACAGAGAAATTTATACAAACCCAGTATTAGAA-----822
 QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294
 Db 823 AATTTGATGCTAGTTTTCGAGGCTCGCTCAGGCGCATAGAAAGAAAGTATTAGGAGTCCA 882
 QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGluThr 314
 Db 883 CATTTGATGATATACTTAACAGTATAACCATCTATACGATGCTCATAGGGGTATTAT 942
 QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332
 Db 943 TATTTGTCAGGCGCATCAATAATAGCTTCTCTGAGGTTTTCGGGGCCAGAAATTCAC 1002
 QY 333 PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp 351
 Db 1003 TTTCCGCTATATGGAACTATGGAAATGCGAGCTCCACACAACTATTTGCTCAACTA 1062
 QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368
 Db 1063 GGTCAAGGCGCTGATAGAACATTTATCGTCCACTTTATATAGAGACCTTTTAATATAGG 1122
 QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387
 Db 1123 ATAAATATCAACAACTATCTGTTCTTGACGGGACAGCAATTTGCTTAGGAACCTCTCA 1182
 QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407
 Db 1183 AATTTGCCATCCCTGTATACAGAAAAGCGAAGCGTAGATTTCGCTGGATGAATACCG 1242
 QY 408 ProGluAspAsnSerGlyAlaProTrpAsnAspTyrSerHisValLeuAsnHisValThr 427
 Db 1243 CCACAGAAATAACAACGTGCCACCTAGCAAGAGTTAGTCATCGATTAGCCATGTTCA 1302
 QY 428 PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaProMetPheSer 447
 Db 1303 ATGTTTCGTTTCAGGCTTTAGTAAATAGTAGTAAATATAATAGAGCTCTCTATGTTCTCT 1362
 QY 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467

Db 1363 TGGATACATCGTAGTGGCTGAATTTAATAATATAATTCATCGGATAGTATTACTCAATA 1422
QY 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe 487
Db 1423 CCATGGTAAAGACATACACTTACAGTCAGTACTACTGTGTGAAGAGGCCGGGTTT 1482
QY 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507
Db 1483 ACGGAGGAGATATCTTCGACGACACAGTGGAGGACCATTTGTCTTACTATTGTTAAT 1542
QY 508 IleAsnGlyGlnLeuProGluArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn 527
Db 1543 ATAAATGGCAATTTACCCCAAGGTATCGTCGAAGAATACGCTACCTACTACAAAT 1602
QY 528 LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr 547
Db 1603 CTAGAATTTACGTAACGGTTTCAGGTGAACGGATTTTGTCTGGTCAATTTAACAACA 1662
QY 548 MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla 567
Db 1663 ATGGATACCGGTGACCCATTAACATTCCTCAATCTTTAGTTACGCACTATTAAACAGCT 1722
QY 568 PheThrPheProMetSerGlnSerSerPheThrValGlyAlaAspThrPheSerSerGly 587
Db 1723 TTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGTGTGATCTTTAGTTCAGGG 1782
QY 588 AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu 607
Db 1783 AATGAGTTTATATAGACAGATTTGAATGTATCCAGTTACTGCAACACTCGAGGCTGAA 1842
QY 608 TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle 627
Db 1843 TATAATCTGAAAGAGCGCAGAGCGGTGAATCGCGTGTTCCTCTACAAACCACTA 1902
QY 628 GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys 647
Db 1903 GGGCTAAACAAATGAACGGATATCATATTGATCAAGTGTCCAAATTTAGTTACGTAT 1962
QY 648 LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla 667
Db 1963 TTATCGATGAATTTGTCTGGATGAAGCGAAGTGTCCGGAAGATCAACATCGC 2022
QY 668 LysArgLeuSerAspGluArgAsnLeuGlnLeuAsnPheLysGlyIleAsnArg 687
Db 2023 AAGCGACTAGTGAACGCAATTTACTCAAGATTCAAATTTCAAGACATTAATAGG 2082
QY 688 GlnLeuAspArgGlyTyrArgGlySerThrAspIleThrIleGlnArgGlyAspVal 707
Db 2083 CAACCAAGACGTGGTGGGCGGAAGTACAGGGATTCACCATCCAAAGGAGGATGAGTA 2142
QY 708 PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu 727
Db 2143 TTTAAAGAAAATACGTCACATATCAGTACCTTTGATGAGTGTATCCCAACATATTG 2202
QY 728 TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr 747
Db 2203 TATCAAAAATTCGATGAATCAAAATTAAGCCCTTTACCCGCTTATCAATTAAGAGGAT 2262
QY 748 IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr 767
Db 2263 ATCGAAGATAGTCAAGACTTAGAATCTATTAAATTCGCTACAAATGCAAAACATGAACA 2322
QY 768 ValAsnValLeuGlyThrGlySerLeuTyrProLeuSerValGlnSerProIleArgLys 787
Db 2323 GTRAAATGCCAGGTACGGGTTCTTATATGCGCGTTTCAGCCCAAAATCCCAATCGGAAG 2382
QY 788 CysGlyGluProAsnArgCysAlaProHisLeuGluTyrAsnProAspLeuAspCysSer 807
Db 2383 TGTGAGAGCGGAATCGATCGCGCCACACTTGAATGAATCCTGACTTAGATTGTTCG 2442
QY 808 CysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAspIleAspVal 827
Db 2443 TGTAGGATGGAGAAAAGTGTGCCCATCTTCGATCTTCCTTCTAGCAATGTATGTA 2502

QY 828 GlyCysThrAspLeuAsnGluAspLeuAspValTyrPvalIlePheLysIleLysThrGln 847
Db 2503 GGTATCAGACCTTAAATGAGACCTAGGTGTATGGTGATCTTTAAGATTAAAGCGCAA 2562
QY 848 AspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluLysProLeuValGlyGlu 867
Db 2563 GATGGCACCGAAGACTAGGAATCTAGAGTTTCTCGAAGAGAAACCATTTAGTAGAGAA 2622
QY 868 AlaLeuAlaArgValLysArgAlaGluLysLysTyrArgAspLysArgGluLysLeuGlu 887
Db 2623 CGCTAGTCTGTGAAAGAGCGGAGAAAATGAGAGACAAACGTGAAAAATTGGAA 2682
QY 888 LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn 907
Db 2683 TGGGAAACAAATATCGTTTATAAAGAGGCAAAAGAAATCTGATGCTTTATTTGTAAC 2742
QY 908 SerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAlaMetIleHisAlaAlaAspLys 927
Db 2743 TCTCAATATGATCAATTAACAAGCGATACGAATATTGCCATGATTCTCGCGCAGATAA 2802
QY 928 ArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIleProGlyValAsn 947
Db 2803 CGTGTTCATGCAATTCGAGAAAGCTTATCTGCTGAGCTGTCTGTGATTCCGGGTGCAAT 2862
QY 948 ValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPheLeuTyrAspAla 967
Db 2863 CGCGCTATTTTGAAGAAATTAGAAGGCGTATTTTCACTGCAATCTCCCTATATGATCG 2922
QY 968 ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTyrAsnValLysGly 987
Db 2923 AGAATGTCAATTAATAATGTCATTTTAATAATGCTTATCTCTGCGAAGCTGAAAGGG 2982
QY 988 HisValAspValGluGluGlnAsnHisArgSerValLeuValValProGluTyrPglu 1007
Db 2983 CATGTAGATGTAGAAGAACAAACCAACGTCGCGTCTGTGTTGTTCCGSAATGGAA 3042
QY 1008 AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr 1027
Db 3043 GCAGAAGTGTACAAAGAGTTCTGTCTGCGGGTGTGCTATATCTCTCGTGTGTACA 3102
QY 1028 AlaTyrLysGluGlyTyrGlyGluGlyCysValThrIleHisGluIleGluAsnThr 1047
Db 3103 CGGTACAGAGGAGGATATGGAAGAGTTGCGTAACCATTCATGAGATCGAAGAACATACA 3162
QY 1048 AspGluLeuLysPheSerAsnCysValGluGluValTyrProAsnAsnThrValThr 1067
Db 3163 GACGAACCTGAAGTTTAGCACTGCGTAGAAGAGAAATCTATCCAAATAACACGTAACG 3222
QY 1068 CysAsnAspTyrThrAlaAsnGlnGluTyrGlyGlyAlaTyrThrSerArgAsnArg 1087
Db 3223 TGTAAATGATTATCTGTAATATCAAGAGAAATACGAGGAGTGTGCTACACTTCTCGTAATCGA 3282
QY 1088 GlyTyrAspGluThrTyrGlySerAsnSerValProAlaAspTyrAlaSerValTyr 1107
Db 3283 GGATATAACGAGCT-----CCCTCCGTACCACCTGATTATGCTCACTCTAT 3330
QY 1108 GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr 1127
Db 3331 GAAGAAAAATCGTATACAGATGGACGAAGAGAAATCCTTGTGAATTTAACAGAGGCTAT 3390
QY 1128 GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu 1147
Db 3391 AGGATTTACAGCCACACACCTGAGTTGTTATGTGACAAAAGAAATAGAAATCTTCCCCAGAA 3450
QY 1148 ThrAspLysValTyrIleGluIleGlyGluThrGluGlyThrPheIleValAspSerVal 1167
Db 3451 ACCGATAGGTATGGATGGATGGAGAAACCGAAGAACATTTATCTGTCGACAGCGTG 3510
QY 1168 GluLeuLeuLeuMetGluGlu 1174
Db 3511 GAATTACTCCTTATGGAGGAA 3531

RESULT 9

US-09-873-873-29
 ; Sequence 29, Application US/09873873
 ; Patent No. US20020064865A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Malvar, Thomas
 ; APPLICANT: Gilmer, Amy Jelen
 ; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
 ; FILE REFERENCE: MRCO:210--2
 ; CURRENT APPLICATION NUMBER: US/09/873,873
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: US 09/253,341
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR APPLICATION NUMBER: US 08/922,505
 ; PRIOR FILING DATE: 1997-09-03
 ; PRIOR APPLICATION NUMBER: US 08/754,490
 ; PRIOR FILING DATE: 1996-11-20
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 29
 ; LENGTH: 3579
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Hybrid Delta-Endotoxin
 US-09-873-873-29

Alignment Scores:

Pred. No.: 0 Length: 3579
 Score: 4313.50 Matches: 844
 Percent Similarity: 78.42% Conservative: 97
 Best Local Similarity: 70.33% Mismatches: 226
 Query Match: 69.08% Indels: 33
 DB: 10 Gaps: 12

US-09-837-961-8 (1-1174) x US-09-873-873-29 (1-3579)

QY 1 MetGluAsnAsnLeuGln---AsnGlnCysValProTyrAsnCysLeuAsnAsnProGlu 19
 Db 1 ATGGATAACAATCCGAACATCAATGAATGATTCCTTATATTTGTTAAAGTAACCCGAA 60
 QY 20 ValGluLeuLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38
 Db 61 GTAGAAATATTAGTGGGAGAAAGAAATAGAACTGTTACACCCCAATCGATATTTCCTTG 120
 QY 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
 Db 121 TCGTACGCAATTTCTTTGAGTGAATTTGTTCCGGTGTGGATTTGCTTGGAGCTA 180
 QY 59 PheAspLeuLeuTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78
 Db 181 GTTCATATAATATGGGAATTTTGTGCTCTCAATGGGACGATTTCTTTGACAAAT 240
 QY 79 GluGlnLeuLeuGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeu 98
 Db 241 GAACATTAATTAACCAAGAAATAGAAATTCCTAGCAACCAAGCAATTTCTAGATTA 300
 QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118
 Db 301 GAAGACTACCAATCTTATCAATTTACCGAAGATCTTTTAGAGAGTGGGAAGCAGAT 360
 QY 119 ProAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138
 Db 361 CCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCAATGACATGAACAGTCC 420
 QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158
 Db 421 CTTACAACCGCTATTCTCTTTTGCAGTTCAAAATTAATCAAGTTCCTCTTTTTCAGTA 480
 QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln 178
 Db 481 TATGTTCAAGCTGCAATTTATCATTTATCAGTTTGTAGAGATGTTTTCAGTGTGGAACA 540

QY 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle 198
 Db 541 AGGTGGGATTTGATGCGCGACATCAATAGCTGTTATATGATTTAACTAGGCTTATT 600
 QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218
 Db 601 GGCACATATACAGATTATGCTGTAGCTGTGACAAATAGCGGATTAGACGTGTATGGGA 660
 QY 219 ThrAsnThrArgGlnTTPAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrVal 238
 Db 661 CCGATTCTAGAGATTGGTAAAGTATATCAATTTAGAGAGAAATTAACACTACTACTA 720
 QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258
 Db 721 TTAGATATCGTGTCTGTTCCCGAATTTATGATAGTAGAAGATATCAATTCGAACAGTT 780
 QY 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278
 Db 781 TCCCAATTAACAGAGAAATTTATACAAACCCAGTATTAGAA-----822
 QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294
 Db 823 AATTTGATGGTAGTTTTCGAGGCTCGCTCAGGCATAGAAAGAAAGTATTAGAGATCCA 882
 QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314
 Db 883 CATTTGATGGATATACTTAACAGTATACCATCTATACGGATCTCATAGGGGTTATTAT 942
 QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332
 Db 943 TATTGGTCAGGGCATCAAAATAATGGCTTCTCTCTAGGGTTTTCGGGGCCAGAAATTCAC 1002
 QY 333 PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTyrPheAlaAspGluAsp 351
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 QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368
 Db 1063 GGTCAAGCGGTGTATAGAACATTTATCGCCACTTTATATAGAGACCTTTTAAATATAGG 1122
 QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387
 Db 1123 ATAAATATCAACAACTATCTGTTCTTGACGGGACAGAAATTTGCTTATGGAACCTCCCA 1182
 QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407
 Db 1183 AATTGGCATCCGCTGTATACAGAAAGCGAGAGTAGATTGCTGCGATGAATACCG 1242
 QY 408 ProGlnAspAsnSerGlyAlaProTyrAsnAspTyrSerHisValLeuAsnHisValThr 427
 Db 1243 CCACAGAATAACAACGTGCCACCTAGGCAAGGATTTAGTCATCGATTAAAGCATGTTCA 1302
 QY 428 PheValArgTyrProGlyGluIleSerGlySerAspSerTyrArgAlaProMetPheSer 447
 Db 1303 ATGTTTCGTCAGCGTTTAGTAATAGTAGTCTAAAGTAAATAGAGCTCCCTATGTTCTCT 1362
 QY 448 TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467
 Db 1363 TGGTATACATCTGTAGTCAACTCTTACAAATCAATGATCCAGAGAGAAATTAATCAATA 1422
 QY 468 ProLeuValLysAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe 487
 Db 1423 CCTTTAGTGAAGGATTAGAGTTTGGGGGCGACCTCTGTCATTACAGGACCGAGGATTT 1482
 QY 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507
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 QY 508 IleAsnGlyGlnLeuProGlnArgThrArgAlaArgIleArgTyrAlaSerThrThrAsn 527
 Db 1543 ATTAATCAACCAATTTACCAGAAAGATACCGTTTAAGATTTCGTTACGCTCCAGAGGAT 1602
 QY 528 LeuArgIleTyrVal---ThrValAlaGlyGluArgIlePheAlaGlyGln-----543

Db 1603 GCACGAGTTATAGTATTAACAGGAGCGGCATCCACAGGAGTGGGAGCCAAAGTTAGTGA 1662
Qy 544 -----PheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
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Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrVal--- 579
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Qy 580 -----GlyAlaAspThrPheSerSerGlyAsnGluValTyrIleAspArg 594
Db 1783 GAACRACCTCTATTGGTCCAGGTTCTATTAGTAGCGGT---GAACCTTATATAGATAAA 1839
Qy 595 PheGluLeuIleProValThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGln 614
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Qy 615 LysAlaValAsnAlaLeuPheThrSerIleAsnGlnIleGlyIleLysThrAspValThr 634
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Qy 655 AspGluLysArgGluLeuSerGluLysValLysHisAlaLysArgLeuSerAspGluArg 674
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Qy 735 LysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeu 754
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Qy 915 AlaAspThrAsnIleAlaMetIleHisAlaAlaAspLysArgValHisArgIleArgGlu 934
Db 2800 GTGGATCAGAACATCGCAATGATTCATGCGCAGATAAAGCGCTTCATAGAATCCGGAA 2859
Qy 935 AlaTyrLeuProGluLeuSerValIleProGlyValAsnValAspIlePheGluLeu 954
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Db 2920 GAGGACGATTTTTCACGCGTATTCCTTATATGATCGGAGAAATGTCAATAAATGGC 2979
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Qy 1015 ArgValCysProGlyArgGlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGly 1034
Db 3100 CGTCTCTTCAGAGTGTGCTATATCTTCTGTCACAGCATATAAAGAGGGATATGGA 3159
Qy 1035 GluGlyCysValThrIleHisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsn 1054
Db 3160 GAGGCTCGCTAACATCCATCAGATCGAGACAAATACAGCAGACTGAAATTCAGAAC 3219
Qy 1055 CysValGluGluGluValTyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsn 1074
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Qy 1135 AlaGlyTyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGlu 1154
Db 3460 GCTGTTATGTAACAAGGATTTAGAGTACTTCCAGAGACCGATAAGGTATGATTGAG 3519
Qy 1155 IleGlyGluThrGluGlyThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3520 ATCGGAGAAACAGAGGAACATTCATCTGTGATAGCTGGAATTAATCTCTTATGAGGAA 3579

RESULT 10

US-09-756-643-1

; Sequence 1, Application US/09756643

; Patent No. US2001002639A1

; GENERAL INFORMATION:

; APPLICANT: Rice, Douglas
; APPLICANT: Carozzi, Nadine
; APPLICANT: Anderson, David
; APPLICANT: Rajasekaran, Kanniah
; APPLICANT: Rangan, Thirumale
; APPLICANT: Yemofsky, Richard
; APPLICANT: Lotstein, Richard
; APPLICANT: De Framond, Annick
; TITLE OF INVENTION: Insecticidal Cotton Plant Cells
; FILE REFERENCE: S-16768E

; CURRENT APPLICATION NUMBER: US/09/756,643
 ; CURRENT FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 08/218,697
 ; PRIOR FILING DATE: 1994-03-28
 ; PRIOR APPLICATION NUMBER: 07/759,969
 ; PRIOR FILING DATE: 1991-09-16
 ; PRIOR APPLICATION NUMBER: 07/274,452
 ; PRIOR FILING DATE: 1988-11-18
 ; PRIOR APPLICATION NUMBER: 07/122,109
 ; PRIOR FILING DATE: 1987-11-18
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 4360
 ; TYPE: DNA
 ; ORGANISM: Bacillus thuringiensis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (156)..(3623)
 ; US-09-756-643-1

Alignment Scores:

Pred. No.: 0 Length: 4360
 Score: 4211.50 Matches: 831
 Percent Similarity: 77.00% Conservative: 83
 Best Local Similarity: 70.01% Mismatches: 228
 Query Match: 67.45% Indels: 45
 DB: 10 Gaps: 9

US-09-837-961-8 (1-1174) x US-09-756-643-1 (1-4360)

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Db	816	CGGATTCTAGAGATTGGATAAGATAATACTAATTTAGAGAGAAATTAACACTACTGTA	875
Qy	239	LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer	258
Db	876	TTAGATATCGTTCTCTATTCCGAAGTATAGTAGTAAAGCTATCCAAATTCGACAGT	935
Qy	259	SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla	278
Db	936	TCCCAATTAACAGAGAAATTTATACAAACCAGTATTAGAA	977
Qy	279	AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro	294
Db	978	AATTTTGATGTAGTTTTCGAGGCTCGGCATAGAGGAGGAAAGTATTAGGAGTCCA	1037
Qy	295	HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr	314
Db	1038	CATTGTGATATATACAGTATACCATCTATACGGATGCTCATAGAGGAAATAT	1097
Qy	315	ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn	332
Db	1098	TATTGGTCAGGGCATCAATAAATGGCTTCTCCTGCTAGGGTTTCGGGGCCAGAAATTCAC	1157
Qy	333	PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleThrPheAlaAspGluAsp	351
Db	1158	TTTCCGCTATATGGAACTATGGAAATGCAGCTCCACAAACATATTTGTTCCTCACTA	1217
Qy	352	ProArgProPheThrArgThrLeuSerAspProValPheValArgGly-----Gly	368
Db	1218	GTTCAGGGCGGTATAGAACATTTATCTCCACTTATATAGAACACCTTTTATATATAGG	1277
Qy	369	PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly	387
Db	1278	ATAAATAATCAACAACATATCTGTTCTTACGGGACAGACAATTTGCTTATGGAACCTCTCA	1337
Qy	388	ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro	407
Db	1338	AATTGGCATCCGCTGTATACAGAAAAGCGGACGGTAGATTGCTGGTGAATGAATACCG	1397
Qy	408	ProGlnAspAsnSerGlyAlaProTyrAsnAspTyrSerHisValLeuAsnHisValThr	427
Db	1398	CCACAGATTAACACGTCGCCACCTAGCAAGGATTTAGTCATCGATTAGCCATGTTTCA	1457
Qy	428	PheValArgTrpProGlyGluIleSerGlySerAspSerTrpArgAlaPrometPheSer	447
Db	1458	ATGTTTCGTTTCAGGCTTTAGTAATAGTAGTAGTAAATAATAAGAGCTCTATGTTCTCT	1517
Qy	448	TrpThrHisArgSerAlaThrProThrAsnThrIleAspProGluArgIleThrGluIle	467
Db	1518	TGATACATCGTAGTCTGAATTAATAATAATAATTCCTCATCACAAATATACAAATA	1577
Qy	468	ProLeuValIleAlaHisThrLeuGlnSerGlyThrThrValValArgGlyProGlyPhe	487
Db	1578	CCTTTACAAAATCTACTAATCTTGGCTCTGGACACTCTGCTGTTAAGACACAGGATTT	1637
Qy	488	ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn	507
Db	1638	ACAGGAGGAGATATCTTCGAAGAACCTCACCTGGCCAGATTTCAACCTTAAGAGTAAT	1697
Qy	508	IleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIleArgTyrAlaSerThrThrAsn	527
Db	1698	ATTACTGCACCATTTATACAAAGATATCGGGTAAGAATTCGCTACGCTTCTACACAAAT	1757
Qy	528	LeuArgIleTyrValThrValAlaGlyGluArgIlePheAlaGlyGlnPheAsnLysThr	547
Db	1758	TTACAAATTCATACATCAATTCAGGAAGACCTATTAAATCAGGGGAATTTTTCAGCAAT	1817
Qy	548	MetAspThrGlyAspProLeuThrPheGlnSerPheSerTyrAlaThrIleAsnThrAla	567
Db	1818	ATCAGTAGTGGGAGTAATTACAGTCCGGAGGCTTTAGGACTCTAGGTTTACTACTCCG	1877

Qy	568	PheThrPheProMetSerGlnSerPheThrValGlyAlaAspThrPheSerSerGly	587
Db	1878	TTTAACTTTCAATGGATCAAGTGATTTACGTTAAGTGCTCATGCTCTCAATTCAGGC	1937
Qy	588	AsnGluValTyrIleAspArgPheGluLeuIleProValThrAlaThrPheGluAlaGlu	607
Db	1938	AATCAAGCTTTATATAGATCAATGAATTGTTCGGCAGAGAAGTACCTTTGAGCGCAGAA	1997
Qy	608	TyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeuPheThrSerIleAsnGlnIle	627
Db	1998	TATGATTTAGAAAGACACAAAAAGCGGTGAATAGCTGTATTACTTCTTCCAAATCAATC	2057
Qy	628	GlyIleLysThrAspValThrAspTyrHisIleAspGlnValSerAsnLeuValAspCys	647
Db	2058	GGGTAAACACAGATGTCGCGGATTCATATTGATCAAGTATCCAAATTTAGTTGAGTGT	2117
Qy	648	LeuSerAspGluPheCysLeuAspGluLysArgGluLeuSerGluLysValLysHisAla	667
Db	2118	TTATCTGATGAATTTGTCTGGATGAAAAAAGAAATGTCGAGAGAAAGTCAACATCGC	2177
Qy	668	LysArgLeuSerAspGluArgAsnLeuLeuGlnAspProAsnPheLysGlyIleAsnArg	687
Db	2178	ARGCGCTTATGTCATGCGCGAATTACTTCAAGATCCAAACTTTAGAGGATCAATAGA	2237
Qy	688	GluLeuAspArgGlyTyrArgLysSerThrAspIleThrIleGlnArgGlyAspVal	707
Db	2238	CAACTAGACCGTGCCTGGAGAGAGATCGGATATTACATCCAAGGAGCGCATGACGTA	2297
Qy	708	PheLysGluAsnTyrValThrLeuProGlyThrPheAspGluCysTyrProThrTyrLeu	727
Db	2298	TTCAAAAGAGAATTACCTTACGCTATTGGGTACCTTTGATGAGTGCCTATCCACGCTATT	2357
Qy	728	TyrGlnLysIleAspGluSerLysLeuLysProTyrThrArgTyrGlnLeuArgGlyTyr	747
Db	2358	TATCAAAAAATAGATGAGTCGAAATAAAGCGCTATACCCGTTACCAATTAAGAGGTAT	2417
Qy	748	IleGluAspSerGlnAspLeuGluIleTyrLeuIleArgTyrAsnAlaLysHisGluThr	767
Db	2418	ATCGACATAGTCAACACTAGAAATCTATTAAATTCGCTACATGCCAACACGAAACA	2477
Qy	768	ValAsnValLeuGlyThrGlySerLeuThrProLeuSerValGlnSerProIleArgLys	787
Db	2478	GTAATATGTCAGGTACGGGTTCCCTATTGGCGCTTTCAGCCCCCAAGTCCAATC	2531
Qy	788	CysGlyGluProAsnArgCysAlaProHisLeuGluThrAsnProAspLeuAspCysSer	807
Db	2531	-----	2531
Qy	808	CysArgAspGlyGluLysCysAlaHisSerHisHisPheSerLeuAspIleAspVal	827
Db	2532	-----GGAAATGTCCCATCATCCCATCAATTCCTCTCTGGACATTGATTT	2579
Qy	828	GlyCysThrAspLeuAsnGluAspLeuAspValTrpValIlePheLysIleLysThrGln	847
Db	2580	GGATGTACAGACTTAAATCAGGACTTAGTGCTGATGGGTGATTTCAAGATTAAGACGCA	2639
Qy	848	AspGlyHisAlaArgLeuGlnValAsnLeuGluPheLeuGluLysProLeuValGlyGlu	867
Db	2640	GATGGCCATGCAGACTAGGAANTCTAGAAATTCCTCGAAGAGAAACCATTTAGTAGAGAA	2699
Qy	868	AlaLeuAlaArgValLysArgAlaGluLysLysTrpArgAspLysArgGluLysLeuGlu	887
Db	2700	GCACTAGCTCGTGTGAAGACGCGAGAAAAAANTGGAGAGCAACCTGAAAAATTTGGAA	2759
Qy	888	LeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeuPheValAsn	907
Db	2760	TGGGAACAAATATTGTTTATAAAGAGCGCAAAAGAACTCTGTAGATGCTTTATTGTTAAAC	2819
Qy	908	SerGluTyrAspGluLeuGlnAlaAspThrAsnIleAlaValIleHisAlaAspLys	927
Db	2820	TCFCAATATGATAGATTACAGCGGATACCAACATCCGATGATTCATCGCGAGATAAA	2879

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Db	2880	CGCGTTCATACGATTCGAGAAGCTTATCTGCCTGAGCTGCTGTGATTCGCGGTGTCAT	2939
Qy	948	ValAspIlePheGluGluLeuLysGlyArgIlePheThrAlaPhePheLeuTyrAspAla	967
Db	2940	CGGCTATTTTGAAGAAATTAGAAGGCGGTATTTTCACATTCCTCCCTATATGATGCG	2999
Qy	968	ArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeuSerCysTrpAsnValLysGly	987
Db	3000	AGAAATGCTATRAAAATGCTGATTTTAATATGCTTATCTGCTGGAACGTGAAGGG	3059
Qy	988	HisValAspValGluGluGlnAsnAsnHisArgSerValLeuValProGluTrpGlu	1007
Db	3060	CATCATGATGTAGAAGAAACAAACACACCCTGCTGGTCTTGTGTTCGGAATGGAA	3119
Qy	1008	AlaGluValSerGlnGluValArgValCysProGlyArgGlyTyrIleLeuArgValThr	1027
Db	3120	GCAGAAGTGTCACAGAAGTTCGTGCTCTCCGGGTGCGGTATATCTCTCGTGTCA	3179
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Qy	1108	GluGluLysSerTyrThrAspGlyArgArgAspAsnProCysGluSerAsnArgGlyTyr	1127
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Qy	1128	GlyAspTyrThrProLeuProAlaGlyTyrValThrLysGluLeuGluTyrPheProGlu	1147
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Qy	1148	ThrAspLysValTrpIleGluIleGlyGluThrGluGlyThrPheIleValAspSerVal	1167
Db	3540	ACCGATAAGGTATGATGATTCGAGATCGAAGACGGAAGCAATTCATCGTGGACAGCGTG	3599
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RESULT 11			
US-09-851-194-1			
; Sequence 1, Application US/09851194			
; Patent No. US20020048799A1			
; GENERAL INFORMATION:			
; APPLICANT: Adang, Michael J			
; TITLE OF INVENTION: Insecticidal Protein Fragments			
; FILE REFERENCE: MP517-83D4			
; CURRENT APPLICATION NUMBER: US/09/851,194			
; CURRENT FILING DATE: 2001-05-08			
; PRIOR APPLICATION NUMBER: US 06/617,321			
; PRIOR FILING DATE: 1984-06-04			
; PRIOR APPLICATION NUMBER: US 08/477,973			
; PRIOR FILING DATE: 1995-06-07			
; PRIOR APPLICATION NUMBER: US 08/687,017			
; PRIOR FILING DATE: 1996-07-16			
; PRIOR APPLICATION NUMBER: US 08/682,169			
; PRIOR FILING DATE: 1996-07-16			
; PRIOR APPLICATION NUMBER: US 09/422,833			
; PRIOR FILING DATE: 1999-10-21			
; PRIOR APPLICATION NUMBER: US 09/612,811			

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; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4300
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (388)..(3924)
; OTHER INFORMATION:
; US-09-851-194-1

Alignment Scores:
Pred. No.: 0 Length: 4300
Score: 4148.00 Matches: 828
Percent Similarity: 76.21% Conservative: 85
Best Local Similarity: 69.12% Mismatches: 241
Query Match: 66.43% Indels: 44
DB: 10 Gaps: 14

US-09-837-961-8 (1-1174) x US-09-851-194-1 (1-4300)

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Db 448 GTAGAAGTATTAGGTGGGAGAAGAATAGAACTGGTTACACCCCAATCGATATTTCTCTG 507
QY 39 SerLeuThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
Db 508 TCGCTACGCAATTCCTTTGACGTGAATTTGTCCTCCGGTCTGGAATTTGCTTAGGACTA 567
QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78
Db 568 GTTGATATAATATGGGAATTTTGGTCCCTCTCAATGGGACGCATTTCTTTGACAAATT 627
QY 79 GluClnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeu 98
Db 628 GAACAGTTAATTAACCAAGAAGTATAGAAATTCGCTAGGAACCAAGCCATTTCTAGATTA 687
QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118
Db 688 GAAGSACTAAGCAATCTTTATCAAAATTTACGCAATCTTTTACAGAGTGGGAGACGAT 747
QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAla 138
Db 748 CCTACTAATCCAGCATTAAGAGAAGATGGGTATTCATTAATCAATGACATGACAGTGGC 807
QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuSerVal 158
Db 808 CTACACACCGCTATCTCTTTTTCAGTTCAAAATATCAAGTTCCTCTTTTATCAGTA 867
QY 159 TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyCln 178
Db 868 TATGTTCAAGCTGCAATTTACATTTATCAGTTTGTGAGAGATGTTTCAAGTCTTTGGACAA 927
QY 179 GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle 198
Db 928 AGTGGGGATTGTATGCGCGAGCTCAATAGTCTTATATGATTTTAACTAGGCTTATT 987
QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218
Db 988 GGCAACTATACAGATTATGCTGACGCTGACATACCGGATAGACGCTGATGGGA 1047
QY 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal 238
Db 1048 CCGGATCTAGAGATGGGTAAAGTAAATCAATTTAGAGAGAAATTAACACTAACGTGA 1107
QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258
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QY 259 SerClnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278
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QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294
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QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314
Db 1270 CATTTGATGATATACCTAAACAGTATACCATCTATACGATGCTCATAGGGGTATTAT 1329
QY 315 ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn 332
Db 1330 TATTTGGTCAGGCGATCAAAATAATGGCTTCCTCTAGGTTTTCGGGGCCAGAAATTCAC 1389
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QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368
Db 1450 GGTGAGGCGCTGTATAGAACATTTATCTCCACTTTATATAGAACCTTTTAATATAGGG 1509
QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387
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QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407
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QY 428 PheValArgTrpProGlyGluIleSerGlySerAspSerTyrArgAlaProMetPheSer 447
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QY 448 TrpThrHisArgSerGluAlaThrProThrAsnThrIleAspProGluArgIleThrGlnIle 467
Db 1750 TGGATACATCTAGTCTGTAATTAATAATAATAATATGCTCGGATAGTATTACTCAAAATC 1809
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QY 488 ThrGlyGlyAspIleLeuArgArgThrSerGlyGlyProPheAlaTyrThrIleValAsn 507
Db 1867 ACTGCTGGGACCTAGTTAGTAAATAGTAGTGGAAAT-----AAC 1908
QY 508 IleAsnGly-----GlnLeuPro-----GlnArgTyr 516
Db 1909 ATTCAGATAGAGGTTATTTGAGTTCCATTTCCATTTCCCATCCGATCTACCCAGATAT 1968
QY 517 ArgAlaArgIleArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGly 536
Db 1969 CGAGTTCGTGACGGTATGCTTCTGTAACCCGATTCACCTCAACGTTAATTTGGGTAAT 2028
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Db 2029 TCATCCATTTTTCCTCAATACAGTACCAGCTACAGTACGTCATAGTAAATCTCAATCA 2088
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QY 577 PheThrValGlyAlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGlu 596
Db 2140 AATATAGTGGTGTAGAAATTTTAGTGGGACTCCAGGAGTGAATATAGACAGATTTCGAA 2199
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QY 597 LeuIleProValThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAla 616
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DB 2260 GTGAATGCCGCTGTTACGCTCTCAAAACCACTAGGCTAAAAACAATTAACGGATTAT 2319
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DB 2860 CATTCGCATCATTTCTCTTAGACATTTGATGAGATGTACAGACTTAATGAGGACCTA 2919
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DB 3220 CTGCTGAGCTGTCTGTGATTCCGGGTGTCATCGCGCTATTTTGAAGAATTAGAGGG 3279

QY 957 ArgIlePheThrAlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPhe 976
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DB 3340 AATAATGGCTTATCCGCTGAGACGTAAGGCGATGTAGATGTAGAGAACAACAAC 3399
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QY 1037 CysValThrIleHisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysVal 1056
DB 3520 TCGGTAAACCAATTCATGAGATCCGAGAACATACAGACGAACTGAAGTTAGCAACTGCGTA 3579
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QY 1137 TyrValThrLysGluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGly 1156
DB 3808 TATGTGCACAAAGAATTAGAATACCTCCAGAAACCGTAAGGTATGAGATTGAGATTGA 3867
QY 1157 GluThrGluGlyThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
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RESULT 12
US-09-826-660-20
; Sequence 20, Application us/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-20

Alignment Scores:

Pred. No.:	0	Length:	3489
Score:	4042.50	Matches:	814
Percent Similarity:	74.46%	Conservative:	87
Best Local Similarity:	67.27%	Mismatches:	226
Query Match:	64.74%	Indels:	83
DB:	10	Gaps:	18
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Qy	21	GlulLeuAsnGluArg---SerThrGlyArgLeuProLeuAspIleSerLeuSer	39
Db	61	GTACTTCTTGATGAGAACGGATCTCAACTGGTAACCTAGCATTCGACATCTCACTGTCA	120
Qy	40	LeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPhe	59
Db	121	CTTGTCAGTTCTTGCTCCAACTTTTGTCCAGGGGTGGCTTCTTGTTGGACATCAT	180
Qy	60	AspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGlu	79
Db	181	GACTTTGTGTGGGCATGTGTGCCCATCTCAATGGGATGCCCTTCTGTACAGANTTGA	240
Qy	80	GlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArg	99
Db	241	CAGTTGATCATGATGAGAGGATAGCTGAGTTTGTCTAGGAATGCTGCCATTCGCAAT	300
Qy	100	GlyLeuAlaAspSerTyrgluIleTyriLeuAlaLeuArgGlnTrpGluAlaAsnPro	119
Db	301	GGATTTGGAAACACTTCACATCTATGTGGAGCCCTCAAGAAATGGGAAGAAGATCC	360
Qy	120	AsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeu	139
Db	361	AACAATCCAGCAACCCGTACGAGATCATTTGATCGCTTTCCGGATCTTGATGGCTACT	420
Qy	140	IleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyr	159
Db	421	GAAGGAGACATCTCGTTTCGAATCTCGGGCTTTGAAGTCGGTGTCTCCGTGTAT	480
Qy	160	ValGlnAlaAlaAsnLeuHisLeuSerLeuArgAspAlaValSerPheGlyGlnGly	179
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Qy	180	TrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuHis	199
Db	541	TGGGGATGCAACTATCAATGTCAATGAGAAGTACACAGACTCATCAGACACATGTAT	600
Qy	200	ArgTyrThrIysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThr	219
Db	601	GAGTATGCTGATCACTGTGCCACACCTACAACTCGTGGTCTCAACACACTTACCGAAGCT	260
Qy	220	AsnThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeu	239
Db	661	ACGTATCAAGATTTGGATCACTACAAATCGATTGAGGAGGATCTCACATTGACTGCTTG	720
Qy	240	AspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSer	259
Db	721	GACATTCGTGCTTCTTTCCAAACTATGCAACAGAGATATCCCATTCACACAGTGTGT	780
Qy	260	GlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerPro-----Val	276
Db	781	CAACTACAGGGAGGTACACTGATCCACTCATCTCAACTTCATATCCACAGTTACATCT	840
Qy	277	SerAlaAsnIleProAsnGlyPheAsnArgAlaGlu---PheGlyValArgProProHis	295
Db	841	GTTCGTGAGTTACCTACT---TTCAATGTGATGAAAGCTCAGCCATCAGGAATCCACAC	897
Qy	296	LeuMetAspPheMetAsnSerLeuPheValThrAlaGlu-----ThrValArgSerGln	313
Db	898	TTGTTTGATTCACACATCTTACCATCTTCACTGATTTGGTTTCAGTGTTCAGTCACCA	957

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Db 1978 GTTGAGTSCCTCTCTGATGAGTCTGTTGGATGAGAGAGGAGTTCGCGAGAGGTC 2037
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QY 805 AspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHisPheSerLeuAsp 824
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QY 845 LysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGluLysProLeu 864
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QY 865 ValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArgAspLysArgGlu 884
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QY 885 LysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSerValAspAlaLeu 904
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QY 925 AlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeuSerValIlePro 944
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Db 2920 GTGAAGGGCACGTAGATGTAGAGAGACAGACAACTACCCGCTCTGTCCTTGTGTTCTCT 2979
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RESULT 13
US-09-826-660-12
; Sequence 12, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-12
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Alignment Scores:
Pred. No.: 0 Length: 3468
Score: 4039.00 Matches: 813
Percent Similarity: 74.79% Conservative: 83
Best Local Similarity: 67.86% Mismatches: 236
Query Match: 64.69% Indels: 66
DB: 10 Gaps: 14
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Db	61	GTTCAGGTGCTGGGTGCAGAACGGATTGAGACTGGTTACACACCTATCGACATCTCGGTG	120
Qy	39	SerLeuThrArgPheLeuLeuSerGluPheValProGlyValIcylValAlaPheGlyLeu	58
Db	121	TCACATTACCAAAATCTCTTTTGTTCAGAGTTCGTGCCGGTGGATTCGTGCTTGGACTT	180
Qy	59	PheAspLeuIlePrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle	78
Db	181	GTCGATATCATTTTGGGAAATCTTTGTGCTCCTCTCAATGGGAGCGCTTCTTGTACAGAT	240
Qy	79	GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu	98
Db	241	GAGCACTTATCAACCCAMAGSATTGAAGAGTTCGTAGGAACACAGCCATCTCAAGGTT	300
Qy	99	ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn	118
Db	301	GAAGGCTCAGCAACCTTACCAGATTTACGCAGAACTCTTTTCGAGAGTGGGAGACGAC	360
Qy	119	ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla	138
Db	361	CCGACCAATCCTCCCTTAAGAGAGAGATCGCATTCATTCATGATGATGAACGACGCG	420
Qy	139	LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal	158
Db	421	CTGACGACCGCAATTCGCTCTTCGCCGTTTCAGAAATACCAAGTTCCCTTTATCCGCT	480
Qy	159	TyrValGlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGln	178
Db	481	TAGCTGCAGGCTGCCAACCTGCACCTTGTTCGGTCTCCGGGATGTCCTCGTGTTCGACA	540
Qy	179	GlyTrpGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle	198
Db	541	CGGTGGGGCTTTGATCGCGCACTATCAATAGTATCGGTATAATGATCTCACTAGGCTTAT	600
Qy	199	HisArgTrpThrLysHisCysLeuAspThrThrAsnGlnGlyLeuGluAsnLeuArgGly	218
Db	601	GGCAACTATACCGATTATGCTGTTCCTCGTACACACCGGGTCTCAACGTGTCTGGGGA	660
Qy	219	ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal	238
Db	661	CCGGATTCTAGATTTGGGTTCAGGTACAACCAAGTTTCAGCGAGAGTTGACACTAACTGC	720
Qy	239	LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer	258
Db	721	CTAGACATTGCTGCTCTTTCCTCAACTACGACTCTAGCGCGCTACCCAATCCGACTGTG	780
Qy	259	SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla	278
Db	781	TCACAAATTGACCGCGGAATCTACACAAACCCAGTCCCTCGAG-----822	
Qy	279	AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro	294
Db	823	AACTTCGACGGTAGCTTTTCAGGCTCGGCTCAGGCGCATAGAGAGAACATCGGCTCCA	882
Qy	295	HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr	314
Db	883	CACCTGATGGACATATTGAACAGTATPCAGATCTACACCGATGCGACCGGGTTATTATC	942
Qy	315	ValTrpGlyGlyHis-----LeuValSerSerArgAsnThrAlaGlyAsnArgIleAsn	332
Db	943	TACTGGTCAGGGCATCAGATCATGGCATCACCGGTGGGTCTCTGAGACCAAGATTCACT	1002
Qy	333	PheProSerTyrGlyValPhe---AsnProGlyGlyAlaIleTrpIleAlaAspGluAsp	351
Db	1003	TTCCCACTTACGGGACTATGGGCAATGCGCTCCACAAACAGGTATTGTGCTCACTC	1062
Qy	352	ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly	368


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QY 817 HisSerHisPheSerLeuAspPileAspValGlyCysThrAspLeuAsnGluAspLeu 836
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RESULT 14

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US-09-826-660-13
; Sequence 13, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-13
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Pred. No.: 0 Length: 3468
Score: 4039.00 Matches: 813
Percent Similarity: 74.79% Conservative: 83
Best Local Similarity: 67.86% Mismatches: 236
Query Match: 64.69% Indels: 66
DB: 10 Gaps: 14
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US-09-837-961-8 (1-1174) x US-09-826-660-13 (1-3468)

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QY 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38
DB 61 GTTGAGGTGCTGGGTGGAGACGGATTGAGACTGGTTACACACCTATCGACATCTCGTTG 120
QY 39 SerLeuThrArgPhePheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
DB 121 TCACATTACCAATTCCTTTTGTACAGTTCGTGCCGCTGCGGATTCGTGCTTGCATCT 180
QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIle 78
DB 181 GTCGATATCATTTGGGGAATCTTTGGTCCCTCTCAATGGGAGCGCTTCTTGTACAGATA 240
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QY 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98
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Db 241 GAGCACTATCAACCAAGAGATGAGAGTTCGTAGGAAACCAAGCACTCAAGGTTA 300
QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrGluAlaAsn 118
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Db 301 GAAGGCTCAGCAACCTTTACAGATTACGAGAACTCTTTCCAGAGTGGGAGACAGAC 360
QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138
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QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerVal 158
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QY 179 GlyTyrGlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIle 198
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Db 541 CGTGGGGTTTCATGCCCACTATCAATAGTCGTTATATGATCTGACTAGGCTTATT 600
QY 199 HisArgTyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGly 218
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QY 219 ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal 238
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QY 239 LeuAspIleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSer 258
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QY 259 SerGlnLeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAla 278
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QY 279 AsnIleProAsnGlyPheAsnArgAla-----GluPheGlyValArgProPro 294
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QY 295 HisLeuMetAspPheMetAsnSerLeuPheValThrAlaGluThrValArgSerGlnThr 314
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QY 352 ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly 368
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QY 369 PheGlyAsnProHisTyr---ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly 387
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QY 388 ThrAsnHisThrArgThrPheArgAsnSerGlyThrIleAspSerLeuAspGluIlePro 407
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QY 537 GluArgIlePheAlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPhe 556
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RESULT 15
US-09-826-660-14
; Sequence 14, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 3468
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. toxin gene
US-09-826-660-14
Alignment Scores:
Pred. No.: 0 Length: 3468
Score: 4039.00 Matches: 813
Percent Similarity: 74.79% Conservative: 83
Best Local Similarity: 67.86% Mismatches: 236
Query Match: 64.69% Indels: 66
DB: 10 Gaps: 14
US-09-837-961-8 (1-1174) x US-09-826-660-14 (1-3468)
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Db 1 ATGCACAAACATCCCAACATCAACGAGTGCATCTTACAACTCCCTGAGCAACCCCTGAG 60
QY 20 ValGluIleLeuAsnGluGluArg---SerThrGlyArgLeuProLeuAspIleSerLeu 38
Db 61 GTTGAGCTGCTGGTGGAGAACGGATTGAGACTGGTTACACACCTATCGACATCTCGTTG 120
QY 39 SerLeuThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeu 58
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QY 59 PheAspLeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIle 78
Db 181 GTCGATCATATTTGGGAAATCTTTGGTCCCTCTCAATGGGAGCGCTTCTTGTACAGATA 240
QY 79 GluGlnLeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeu 98
Db 241 GAGCAGTTAATTAACCAAGAATAGAGAATTCGTAGGAACCAAGCCATCTCAAGGTTA 300
QY 99 ArgGlyLeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsn 118
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QY 119 ProAsnAsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAla 138
Db 361 CCAGCAATCTCTCCCTTAAGAGAGAGATGCGCATTCATTCATTCATGACATGAACGCGC 420
QY 139 LeuIleThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuSerVal 158
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	Db	601	GGCAACTATACCGATTATGCTGTCTCGTGTGTAACAACACCGGCTCTCGAAGTGTCTGGGA	660
	Qy	219	ThrAsnThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrVal	238
	Db	661	CCGATTCCTAGAGNATGGGTACAGGTACACCAGTTCAGCGGAGAGTTGACAACTACTC	720
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	Db	1003	TTCCCACCTTACGGGACTATGGGCATGAGCTCCACACACACAGTATTGTTGCTCACTC	1062
	Qy	352	ProArgProPheTyrArgThrLeuSerAspProValPheValArgGly-----Gly	368
	Db	1063	GGTCAGGCGGTATAGAACCCTTGTCCAGCACTATATAGAGAGACCTTCAACATCGGC	1122
	Qy	369	PheGlyAsnProHisTyr--c-ValLeuGlyLeuArgGlyValAlaPheGlnGlnThrGly	387
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	Qy	488	ThrGlyAspIleLeuArgargThrSerGlyGlyPropheAlaTyrThrIleValasn	507

D	b	1450	ACTGAGCGGACTTGGTTTAGGCTGAATCTCTCCGGCAAC-----AAC	1521
Q	y	508	IleasnGly-----GlnLeuPro-----GlnArgTyr	516
D	b	1522	ATCCAGATAGAGGTATATTGAGTGCCCATTCACCTTCCCATCGACATCTACACGATAT	1581
Q	y	517	ArgAlaArgIleArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGly	536
D	b	1582	CGTGTGGTGAAGTATGCTCTGTTACCCCTATTCACTCAACGTCAATTGGGGTAAT	1641
Q	y	537	GluArgIlePheAlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPhe	556
D	b	1642	TCCCTCAATCTTTCCCAATACAGTACCAGCGACAGCTACATCCCTCGGATAATCCAATCT	1701
Q	y	557	GlnSerPheSerTyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSer	576
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Q	y	697	ThrAspIleThrIleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuPro	716
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Q	y	737	LysProTyrThrArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIle	756
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Job time : 315 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run On: November 27, 2002, 20:26:25 ; Search time 104 Seconds

(without alignments)
3461.909 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MENNIOQCVPYNCLNPEV.....IGETEGFIVDSVELLMEE 1174

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Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q-/cgn2_1/USPTO.spool/US03837961/runat_25112002_142416_5954/app_query.fasta_1.1351

-DB-issued_Patents_NA -QFMT=fastap -SUFFIX=ini -MINMATCH=0.1 -LOOPCL=0

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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

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Database :

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5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6244	100.0	3522	US-07-828-788A-9	Sequence 9, Appl
2	6244	100.0	3522	US-08-349-867-24	Sequence 24, Appl
3	6244	100.0	3522	US-08-239-476-24	Sequence 24, Appl
4	6244	100.0	3522	US-08-356-034-7	Sequence 7, Appl
5	6244	100.0	3522	US-08-598-305A-24	Sequence 24, Appl
6	6244	100.0	3522	US-08-639-923A-24	Sequence 24, Appl
7	6244	100.0	3522	US-08-933-891-7	Sequence 7, Appl
8	6244	100.0	3522	US-09-178-252-5	Sequence 5, Appl
9	6244	100.0	3522	PCT-US92-11337-9	Sequence 9, Appl
10	6244	100.0	3522	PCT-US95-05431-24	Sequence 24, Appl
11	6244	100.0	3522	5188960-7	Patent No. 5188960
12	6244	100.0	4020	PCT-US91-02560-1	Sequence 1, Appl

13	6049	96.9	3522	1	US-08-349-867-28	Sequence 28, Appl
14	6049	96.9	3522	1	US-08-239-476-28	Sequence 28, Appl
15	6049	96.9	3522	1	US-08-598-305A-28	Sequence 28, Appl
16	6049	96.9	3522	1	US-08-639-923A-28	Sequence 28, Appl
17	6049	96.9	3522	5	PCT-US95-05431-28	Sequence 28, Appl
18	5902	94.5	3444	1	US-08-349-867-22	Sequence 22, Appl
19	5902	94.5	3444	1	US-08-349-867-26	Sequence 26, Appl
20	5902	94.5	3444	1	US-08-239-476-22	Sequence 22, Appl
21	5902	94.5	3444	1	US-08-239-476-26	Sequence 26, Appl
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23	5902	94.5	3444	1	US-08-598-305A-26	Sequence 26, Appl
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26	5902	94.5	3444	5	PCT-US95-05431-22	Sequence 22, Appl
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28	5879	94.2	3444	4	US-09-178-252-1	Sequence 1, Appl
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34	5415	86.7	3504	1	US-08-291-368-3	Sequence 3, Appl
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37	4815.5	77.1	3531	3	US-08-754-490-13	Sequence 13, Appl
38	4815.5	77.1	3531	3	US-08-922-505A-13	Sequence 13, Appl
39	4815.5	77.1	3531	4	US-09-260-952A-13	Sequence 13, Appl
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41	4815.5	77.1	3531	4	US-09-253-331A-13	Sequence 13, Appl
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43	4812.5	77.1	3534	3	US-08-754-490-25	Sequence 25, Appl
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45	4812.5	77.1	3534	4	US-09-260-952A-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-07-828-788A-9

; Sequence 9, Application US/07828788A

; Patent No. 5273746

; GENERAL INFORMATION:

; APPLICANT: PAYNE, JEWEL M.

; APPLICANT: HICKLE, LESLIE A.

; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID R. SALIWANCHIK

; STREET: 2421 N.W. 41ST STREET, SUITE A-1

; CITY: GAINESVILLE

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/828,788A

; FILING DATE: 19920129

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SALIWANCHIK, DAVID R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: MA75

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3522 base pairs

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; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811a
; US-07-828-788A-9

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Alignment Scores:

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

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US-09-837-961-8 (1-1174) x US-07-828-788A-9 (1-3522)

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Qy 241 IleValAlaLeuPheProAsnTyrgluValArgThrTyrgluThrSerSerGln 260
Db 721 ATCGTGTCTCTTTTCCGAACATACGATGTAGAACATATCCAAATCAACGTCATCCCAA 780
Qy 261 LeuThrArgGluIleTyrgluSerSerValIleGluAspSerProValSerAlaAsnIle 280
Db 781 TTAACAAGGGAATTTATACAAGTTCAGTAATAGAGATTCCTCAGTTTCTCTATATA 840
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
Db 841 CCTAATGGTTTAAATAGGCGCAATTTGAGTTAGACGCCCACTCTTATGGACITTAG 900
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
Db 901 AATCTCTTTGTTGTAACGCGAGACTGTAGAACTCAAACTGTGTGGGAGACACTTA 960
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrglyValPheAsn 340
Db 961 GTTAGTTCACGAATACGCGTGGTAACCGTATAAATTTCCCTAGTACGCGGCTCTCAAT 1020
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrgluThrLeuSer 360
Db 1021 CCTGTGGCGCCATTTGGATTGCGATGAGGATCCACGTCCTTTTATCGGACATTATCA 1080
Qy 361 AspProValPheValArgGlyPheGlyAsnProHisTyrgluValLeuGlyLeuArgGly 380
Db 1081 GATCTGTTTGTCCGAGGAGGATTTGGGAATCTCATATATGTACTGGGCTTAGGGGA 1140
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
Db 1141 GTAGCATTTCAACAACCTGGTACGACACACACCCCAACATTTAGAAATAGTGGGACATA 1200
Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrg 420
Db 1201 GATTCTCTAGATGAATCCACCTCAGGATAATAGTGGGCACTTGAATGATATAGT 1260
Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
Db 1261 CATGTATTAAATCATGTTACATTTGTACGATGGCCAGGTGAGATTTCAGGAAGTATCA 1320
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
Db 1321 TGGAGAGCTCCAATGTTTCTTGGACGCGCGTAGTGCACCCCTACAAAATACAAATTGAT 1380
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCGGAGAGGATTACTCAAATACCATTTGGTAAAGCACATACACTTCAGTCAGGTACTACT 1440
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
Db 1441 GTTGTAAAGAGGCCCGGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGACCA 1500
Qy 501 PheAlaTyrgluThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrgluArgAlaArg 520
Db 1501 TTTGCTATATCTATTGTTAATATAAATGAGGCAATACCCCAAGAGTATCGTCGAGAAATA 1560
Qy 521 ArgTyrgluSerThrThrAsnLeuArgIleTyrgluValThrValAlaGlyGluArgIlePhe 540
Db 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTACGGTTGACGGTGAACGGATTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAATTTAAACAAACAAATGATACCGGTGACCCATTAACATTTCCAATCTTTAGT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACCAACTATTATACAGCTTTTACATTCCTCAATGAGCAGAGTGTTCACAGTAGGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrgluAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACTTTAGTTCAGGGAATGAAGTTTATATACAGACATTTGAATGATTCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrgluAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620

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Db 1801 ACTCCACATTGGAAGCAGATATGATTAGAAAGACACAAAAGCGGTGAATCGCGTG 1860
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTACTTCTATAAACCAAAATAGGATAAACAGATGACGGATTATCATATTGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAAATTAGTGGATTGTTTATCAGATCAATTTTCTCGGATGAAACCGGAATTG 1980
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
Db 1981 TCCGAGAAAGTCAACATGCGAAGCGACTCAGTATGATGAGCGGAATTTACTTCAAGATCCA 2040
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyIlePheGlySerThrAspIlePhe 700
Db 2041 AACTTCRAAGGCATCAATAGCAGCACTAGACCGTGGTGGAGAGGAATGACGGATATTACC 2100
QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAAGAGAGATGACGTATTCAAGAAATATGTCACACTACCAAGGTACCTTTGAT 2160
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QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTATCAATTAAGAGGGTATATCGAGATAGTCAAGACTTAGAAATCTATTGATCCGC 2280
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780
Db 2281 TATAATGCAAAACACGAACAGTAATGCTAGTACGGGTTCTTTATGCGCGCTTCA 2340
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800
Db 2341 GTCCAAAGTCCATCAGAAAGTGGAGAACCGAATCGATGCGCGCCACACCTTGATGG 2400
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHis 820
Db 2401 AATCCTGATCTAGATTGTTCTCGAGAGACGGGAAATGTGCACATCATTCGCATCAT 2460
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840
Db 2461 TTCTCCTTGACATTGATGTTGGATGTACAGACTTAATGAGGACTTAGATGATGGGTG 2520
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATATTCAGATTAAAGCGCAAGATGGCCATGCAAGACTAGGAAATCTAGAGTTTCTCGAA 2580
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880
Db 2581 GAGAAACCAATTAGTCGGGGAGCACTAGCTGCTGTAAGAGAGCAGAGAAATGAGAGA 2640
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2641 GATAAAGCTGAAAATTTGGAATTTGGAACAAATATTTGTTATAAAGAGGCAAAAGATCT 2700
QY 901 ValAspAlaLeuPheValAsnSerGluTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2701 GTAGATCTTATTGTAACTCTCAATATGATCAATTTACAAGCGGATAGCAATATTGCC 2760
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTCATCGGCAGATAACGTGTTTCATAGATTCGGGAGCGTATCTCCAGAGTTA 2820
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAAGATTAAGGGCGTATTTCCTACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnGlyLeu 980

Db 2881 GCATTCTTCTATATGATGCGAGAAATGCTATTAATAAACGGTGTATTTCAATAATGGCTTA 2940
QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
Db 2941 TCATGCTGGAACGTAAGGCGATGTAGATGTAGAAGAACAAACACCCGTTCCGGTC 3000
QY 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTTGTGTTCGGAATGGGAAGCAGAGTGTCAAGAAGTTCGTGCTGTCCGGTCTGT 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
Db 3061 GGCATATATCTTCTGTACACGCGTACAAGGAGGATATGAGAAGGTTCGGTAACCAAT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATCGAAGAACATACAGACGAACTGAAGTTTACAACTGCGTAGAAGAGATC 3180
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGly 1080
Db 3181 TATCCAAACACACGTAACGTTAATGATTATACTGCAATCAAGAGATACGGGGGT 3240
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100
Db 3241 GCGTACACTTCCGTAATCGTGGATATGACGAAACTTATGGAAGCAATCTCTGTACCA 3300
QY 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgAspAsnPro 1120
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Db 3361 TGTGAATCTAACACAGGATATGGGATATACACACCACTTACCGCTGCTATGTGACAAA 3420
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGlyGluThrGluGly 1160
Db 3421 GAATAGAGTACTTCCAGAAACGATAAGGTATGAGTTGAGATCGGAGAAACGAGGA 3480
QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTCTCGTGACGCGTGAATTAATCTCTTATGGAGAA 3522

RESULT 2

US-08-349-867-24
: Sequence 24, Application US/08349867
: Patent No. 5508264
: GENERAL INFORMATION:
: APPLICANT: Bradfisth, Gregory A.
: APPLICANT: Thompson, Mark
: APPLICANT: Schwab, George E.
: TITLE OF INVENTION: No. 5508264el Pesticidal Compositions
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David R. Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/349,867
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Saliwanchik, David R.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: MA86
: TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-349-867-24

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-349-867-24 (1-3522)

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Qy 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
Db 61 GAAATACATGACGAAGAACGACGACCGCGCCCTCGCGCTGGACATCAGCCCTGAGCCT 120
Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 121 ACACGTTCCCTTTGAGTGAATTTGTTCCAGGTGGAGTTGCGTTTGGATTATTGAT 180
Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
Db 181 TTAATATGGGTTTTATACCTCTCTGATTGGAGCTTATTTCTTTTACAGATTGAACAA 240
Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
Db 241 TTGATTGACAAAGAAATAGAAACATGTGAAAGAACCGGGCAATTACATTACGAGGG 300
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
Db 301 TTACAGATAGCTATGAAATTTATATTGAAGCACATTAAGAGAGTGGAAGCAATCCTAAT 360
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
Db 361 AATGCACAAATTAAGGAGAGATGCGTATTCGATTGCTAATACAGACGACGCTTTAATA 420
Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAAATAATTTACACTTACAAGTTTGAATCCCTCTTTTATCGGTCATGTT 480
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Db 481 CAAGCGGGAATTTACATTTTACATATTAAGAGACGCTGATCGTTTGGCGAGGTTGG 540
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GGACTGGATATAGCTACTGTTAATAATCATTTATATAGATTAAATAATCTTTATTCATAGA 600
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TATACGAACAATTTGTTGGACACATACAAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
Db 661 ACTGCACAATGGCAAGATTCATCAGTTTAGAGAGATTTAAACACTTACTGTATTAGAT 720
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
Db 721 ATCGTGTGCTCTTTTCCGAACATAGATGTTAGAACATATCAATTCAAACGTCCCAAA 780

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Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
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Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
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Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320
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Db 1561 CGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACTGCGGTTCAGGTGACGGATTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAATTTACAAAACAATGGATACCGGTGACCCCATTAACATTTCCAAATCTTTT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACGCACTATATATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCCAGTAGGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACTTTTACTTCAGGGAATGAAGTTTATATAGACACATTTGAATTCATTCAGATT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGAGCACAAAGCGGTGAATGCGGTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleIleThrAspValThrAspTyrHisIleAspGln 640

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Db 1861 TTTACTTCTATTAACCAATAGGATAAACAACAGATGTCACGGATTATCATATTGATCAA 1920
Qy ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAAATTTAGTGATGTTTATCAGATGAATTTCTCGGATGAAAGCGAAATG 1980
Qy SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGluAspPro 680
Db 1981 TCCGAGAAAGTCAACATGCGAAGCGACTCAGTGTAGCGGAAATTTACTTCAAGATCCA 2040
Qy AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
Db 2041 AACTTCAAGGCGATCAATPAGCACTAGACCGTGTGTTGGAGGAAAGTACGGATATTACC 2100
Qy IleGlnArgGlyAspValPheLysGluAsnTrpValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAGAGGAGATGACGTATTCAAGAAATATGTCACACTACCGAGTACCTTTGAT 2160
Qy GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTGTATCCAAAGTATTTATATCAAAATAGATGAGTGCAGAAATTAACCCCTATACT 2220
Qy ArgTyrGlnLeuArgGlyTyrIleLysAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTATCAATTAAGAGGATATATCGAGGATAGTCAAGACTTAGAAATCTATTGTATCCG 2280
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Qy SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000

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Db 3061 GGCTATATCCTTCGTGTACAGCGTACAGGAGGAGATATGAGAAAGTTGCGTAACCAAT 3120
Qy HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATCGAGAACATACAGACGAACCTGAAGTTTACCAACTGCGTAGAAGAGAACTC 3180
Qy TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGly 1080
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Db 3241 CGGTACACTTCCCGTAATCGTGGATATCGCAAACTTATGGAAGCAATCTCTGTATCCA 3300
Qy AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
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Qy CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
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Qy ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTATCGTGGACAGCGTGAATTAATCTCTTATGGAGGAA 3522

RESULT 3

US-08-239-476-24

: Sequence 24, Application US/08239476

: Patent No. 5527883

: GENERAL INFORMATION:

: APPLICANT: Thompson, Mark

: APPLICANT: Schwab, George E.

: TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in

: NUMBER OF SEQUENCES: 34

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: David R. Saliwanchik

: STREET: 2421 N.W. 41st Street, Suite A-1

: CITY: Gainesville

: STATE: Florida

: COUNTRY: USA

: ZIP: 32606

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/239,476

: FILING DATE:

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Saliwanchik, David R.

: REGISTRATION NUMBER: 31,794

: REFERENCE/DOCKET NUMBER: MA83

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (904) 375-8100

: TELEFAX: (904) 372-5800

: INFORMATION FOR SEQ ID NO: 24:

: SEQUENCE CHARACTERISTICS:

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; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-239-476-24

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Alignment Scores:

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Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

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US-09-837-961-8 (1-1174) x US-08-239-476-24 (1-3522)

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Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
Db 1 ATGGAAATATATATCAAAATCAATCGTACCTTACAAATGTTAAATATCTGAAGTA 60
Qy 21 GluIleLeuAsnGluGluSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
Db 61 GAAATACTGAACGAGAACCGACCGCCGCTGCCCTGGACATCAGCCTGAGCCT 120
Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 121 ACACGCTTCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTGGCTTGGATTTTGTAT 180
Qy 61 LeuIleTyrGlyPheIleThrProSerAspTyrPheLeuLeuGlnIleGluGln 80
Db 181 TTAATATGGGTTTTATAACTCTCTGATTTGGAGCTTATTTCTTTTACAGATTGAACA 240
Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
Db 241 TTGATTGAGCAAGAAATGAAACATTTGGAAGGAAACCGGCGCAATTTACTACATTACGAGGG 300
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrPheGluAlaAsnProAsn 120
Db 301 TTAGCAGATAGCTATGAAATTTATTTGAGCAGCACTAAGAGAGTGGGAGCAATCTTAAT 360
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
Db 361 AATGCACAAATTAAGGGAAGATGTGGTATTCGATTTGCTTAAATACAGACGACGCTTAATA 420
Qy 141 ThrAlaIleAsnAspPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAAATAATTTTACACTTACAGTTTGAATCCCTCTTTATTCGCTCTATGTT 480
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180
Db 481 CAAGCGCGCAATTTACATTTATCACTATTAAAGACGCTGTATCGTTGGGACAGGTTGG 540
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GGACTGGATATAGCTACTGTTAAATATCATTTATATAGATTAAATAATCTTTATTCATAGA 600
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TATACGAACAACTGTTTGGACACATACATCAAGTATAGAAATCTTAAGAGGTACTAAT 660
Qy 221 ThrArgGlnTyrAlaArgPheAsnGlnPheArgArgAspLeuThrValLeuAsp 240
Db 661 ACTGCACAAATGGCAGAGATCAATCAGTTTAGCAGAGATTTAACACTTACTCTATTAGAT 720
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
Db 721 ATCGTTGCTCTCTTTTCCGAACCTACGATGTAGAACATATCAAAATCAAAAGTCATCCCAA 780
Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
Db 781 TTAACAAGGGAATTTATACAAAGTTTCAGTAATTGAGGATTTCCAGTTTCTGCTAATATA 840

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Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProHisLeuMetAspPheMet 300
Db 841 CCTAATGGTTTTAATAGGCGGAATTTGGATTAGACCCGCCCATCTTATGGACTTTATG 900
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTyrGlyGlyHisLeu 320
Db 901 AATTCCTTTGTTGTTACTGCAGAGACTGTAGAGTCAAACTGCTGGGGAGACACTTA 960
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
Db 961 GTTAGTTACAGAAATACGGCTGGTAACCGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
Qy 341 ProGlyGlyAlaIleTyrPheAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
Db 1021 CCTGGTGGCGCCATTTGGATTGCAGATGAGATCCACGTCCTTTTATCGGCATATATCA 1080
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
Db 1081 GATCCTGTTTTGTCGGAGGAGATTTGGGAATCTTCATATGTACTGGGGCTTAGGGGA 1140
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
Db 1141 GTAGCATTTCAACAACTGGTACGAACACACCCGAACATTTAGAAATAGTGGACCATA 1200
Qy 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProTyrPheAsnAspTyrSer 420
Db 1201 GATTCCTAGATGAATCCCACTCAGGATAATAGTGGGCGACCTTGGAAATGATATAGT 1260
Qy 421 HisValLeuAsnHisValThrPheValArgTyrProGlyGlyLeuIleSerGlySerAsp 440
Db 1261 CATGTATTAAATCATGTTACATTTGTACGATGCCAGGTGAGATTTACAGAAATGATTC 1320
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
Db 1321 TGGAGAGCTCCAAATGTTTCTTGGACGACCGTAGTGCACCCCTACAAATACAAATGAT 1380
Qy 461 ProGluAlaArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCGGAGAGATTTACTCAATACCATTTGGTAAAGACACATACACTTTCAGTCAGGTACTACT 1440
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
Db 1441 GTTGTAAAGAGGCGCCGGTTTACGGGAGGAGATATCTTCGACGACAACTGGAGACCA 1500
Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
Db 1501 TTTCGTTTACTATTGTTAATAATAATGGGCAATTAACCCAAAGGTATCGTCAAGAAATA 1560
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 CGCTATGCTCTACTACAAATCTAAGAAATTTACGTAACTGTTGACAGGTGAACGGATTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGTGCAATTTAACAAACAAATGATACCGGTGACCCCATTAACATTCCTTTTACT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACGCAACTATTAAATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTTCACAGTAGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACCTTTTAGTTTCAGGGAATGAAGTTTATATAGACAGATTTGAATGATTCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCACAAATTTGAGCAGAGATATGATTTAGAAAGAGCACAAAGCGCGTGAATCGCGTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTATAAACCAATAGGGATAAAACAGATGTGACGGATTATCATATTGATCAA 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660

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Db 1921 GTATCCAATTTAGTGGATGTTTATCAGATGAATTTCTCGGATCAAAAGCGAATG 1980
Qy SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
Db 1981 TCCGAGAAGTCAACATGCGAAGGAGCTCAGTGATGAGCGAATTTACTTCAAGATCCA 2040
Qy AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrPargGlySerThrAspIleThr 700
Db 2041 AACITCAAGGCATCAATAGCCAACTAGACCGTGTGGAGAGAGTACCGATATACC 2100
Qy IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAAGAGGAGATGAGCTATTCAAGAAATATGTCACACTACCAGGTACCTTTCAT 2160
Qy GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProThrThr 740
Db 2161 GAGTGTATCCAACTGATTTATATCAAAATATAGATGAGTCAAAATTAACCCCTATACT 2220
Qy ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTATCAATTAAGAGGTATATCGAGATACTCAAGACTTAGAATCTATTGTATCGC 2280
Qy TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
Db 2281 TATATGCAAAACACGAAACAGTAATGCTAGTACGGGTCTCTTTATGGCGCTTCA 2340
Qy ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
Db 2341 GTCCAAAGTCCAAATCAGAAAGTGTGGAAACCGAATCGATCGCGCCACACCTTGAATGG 2400
Qy AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
Db 2401 AATCCTGATCTAGATTGTCTCTGACAGACGGGGGAAAAATGTGCACATCAITTCGCATCAT 2460
Qy PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
Db 2461 TTCTCCTTGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
Qy IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATATTCAAGATTAGACCAAGATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCC 2580
Qy GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
Db 2581 GAGAAACCATTAGTTCGGGAGCACCTAGCTCGTGTGAAGAGCAGAGAAAAATGGAGA 2640
Qy AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2641 GATAAACGTGAAAAATTGGAATTGGAACAAATATGTTTATAAAGAGGCAAAAGAACT 2700
Qy ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2701 GTAGATGCTTTATTGTAACTCTCAATATGATCAATATCAAGCGGATACGAAATATGCC 2760
Qy MetIleHisAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTTCATGCGCAGATAAACGTTTCATAGAATTCGGAGCGTATCTTCCAGATTA 2820
Qy SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATTCGGGTCGCTAAATGTAGACATTTTCGAAGAATTAAGAGCGGTATTTTCACT 2880
Qy AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATTCTTCCTATATGATGCGGAAATGTCATTAATAAACGGGTGATTTCATTAATGCTTA 2940
Qy SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
Db 2941 TCATGCTGGAACGTGAAGGGCATGTAGATGTAGAGAACAAAAACCAACCGGTTCGGTC 3000
Qy LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020

Db 3001 CTTGTGTTCCGAAATGGGAAGCAGAGATGTCAAGAAGATTCTGTCTGTCGGGTCT 3060
Qy GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGlyCysValThrIle 1040
Db 3061 GGCTATATCCCTTCGTGTCACAGCGTACAGGAGGATATGGAGAAGGTTCGTAACCAATT 3120
Qy HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATCGAACAATACAGACCAACTGAAGTTTACCACTGCGTAGAAGGAAGTC 3180
Qy TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
Db 3181 TATCCAAACAAACACCGTAACTGATGATTAATGATCTGCAAAATCAAGAAGATACGGGGT 3240
Qy AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100
Db 3241 CGGTACACTCCGTAATCGTGGATATACGAAACTTATGGAAACAATCTTCTTCTTACA 3300
Qy AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgAspAsnPro 1120
Db 3301 CCGTATTATGCTCACTCTATCAAGAAAAATCGTATACAGATGCGAGAGACCAATCT 3360
Qy CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3361 TGTGAATCTAACAGAGGATATGGGATACACACCACTACCACTACCACTATGTGACAAA 3420
Qy GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyCyluThrGluGly 1160
Db 3421 GAATTAGAGTACTTCCAGAACCGATAGGTATGATGATGATGATGATGATGATGATGATG 3480
Qy ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3481 ACATTCACTCGGACAGCGTGGAAATTAATCTCTTATGAGGAA 3522

RESULT 4

US-08-356-034-7
; Sequence 7, Application US/08356034
; Patent No. 5691308

GENERAL INFORMATION:

; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,110
; FILING DATE:
; APPLICATION NUMBER: 07/865,168
; FILING DATE: 09-APR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/451,261
; FILING DATE: 14-DEC-89
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/371,955
; FILING DATE: 27-JUN-89

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
REGISTRATION NUMBER: 21,023
REFERENCE/DOCKET NUMBER: MA43.C1.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811a
US-09-837-961-8

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Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

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US-09-837-961-8 (1-1174) x US-08-356-034-7 (1-3522)

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QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
DB 1 ATGGAGAATAATATCAAAATCAATCGTACCTTCAATTTGTTAAATATCCTGAAGTA 60
QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
DB 61 GAAATATTAAATGAGAAAGAGTAGTCTGCGACGATTACCGTTAGATATATCCTATCGCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
DB 121 ACACGCTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTCGGTTTGGATTATTTGAT 180
QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
DB 181 TTAATATGGGGTTTATAACTCCTTCTGATTGGAGCTTATTTCTTTACAGATTGAACAA 240
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
DB 241 TTGATTGAGCAAGAAGTAAGAAACATGGAAGAGGACCGGGCAATTACTACATTACGAGGG 300
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
DB 301 TTAGCAGATAGCTATGCAATTTATATTGAGCAGCTAAGAGAGTGGGAACCAATCCTAAT 360
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
DB 361 AATGCACAAATTAAGGAAGATGTGCGTATTCGATTTCGTAATACAGACGACCTTTAATA 420
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
DB 421 ACAGCAATTAATTAATTTACACTTACAGTTTGAATTCCTTTTATCGGCTCTATGTT 480
QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
DB 481 CAAAGCGGCAATTTACATTTATCATTATTAAGAGACGCTGTATCGTTTGGCAGGGTTGG 540
QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200

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DB 541 GGACTGGATATAGCTACTGTTAATAATCAATTAATAGATTAATAAATCTTATTCATAGA 600
QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
DB 601 TATACGAAACATGTTTGGACACATACATCAAGGATTAGAAAACCTTAGAGGTACTAAT 660
QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
DB 661 ACTCGACAATGGCAAGATTCAATCAGTTTAGCAGAGATTTAACACTTACTGTATTAGAT 720
QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
DB 721 ATCGTGTGCTCTTTTCCGACATACGATGTAGAACATATCCCAATCAACAGCATCCCCAA 780
QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
DB 781 TTAACAAGGGAAATTTATACAAAGTTCAAGTAATGAGGATTCACAGTTTCTGCTAATA 840
QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetaspPheMet 300
DB 841 CCTAATGTTTTAATAGGCGGAATTTGGAGTAGACCCGCCCATCTTATGGACTTTATG 900
QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
DB 901 AATTCCTTTGTTGTAACGACGACTGTTAGAGTCAACACGTGTGGGGGAGACACTTA 960
QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
DB 961 GTTAGTTACAGAAATACGCTGTAACCGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
DB 1021 CCTGTGGCGCCATTTGGATTGCAGATGAGATCCACGTCCTTTTATCGGCATTATCA 1080
QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
DB 1081 GATCCTGTTTTGTCGAGGAGGATTTGGGAATCTCATATTGTTACTGGGGCTTAGGGGA 1140
QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
DB 1141 GTAGCATTTCAACAACTGGTACGAACACACCGCAACATTTAGAAATAGTGGACCATTA 1200
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
DB 1201 GATTCTCTAGATGAATCCCACTCAGGATAATAGTGGGCACTTGGGAATGATTATAGT 1260
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGlyIleSerGlySerAspSer 440
DB 1261 CATGTATTAAATCATGTTACATTTGTACGATGCGCAGGTGAGATTTTCAGAGAGTATCA 1320
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
DB 1321 TGGAGAGCTCCAATGTTTCTTTGGACCGCACCGTAGTGAACCCCTACAAAATACAATTGAT 1380
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
DB 1381 CCGGAGAGGATTTACCAATACCATTTGGTAAAGACACATACACTTTCAGTCAGGTACTACT 1440
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
DB 1441 GTTGTAGAGGGCCCGGGTTTACGGGAGGAGATATCTTCGACGACCAAGTGGAGAGCA 1500
QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
DB 1501 TTTGCTTATCTATTGTTAATAATAATGGCAATTTACCCAAAGGTATCGTCAAGAATA 1560
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
DB 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAAAGGTTGCAAGTGAACGGATTTT 1620
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560

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Db 1621 GCTGGTCAATTTTACAAACAATGGATACCGGTGACCCATTACCAATCTTTTAGT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACCACTATTATACAGCTTTTACATTCOCATGACCCAGAGTAGTTTTCACAGAGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTCATCTTTTACTTCAGGGAATGAAGTTTATATAGACAGATTGAATTGATCCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTCCACATTTTGAAGCAGATATGATTTAGAAAGACACAAAAGCGGTGAATSCGCTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTATAAACCAATAGGATAAACAGATGTGACGGATTATCAATTTGATCA 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAAATTTAGTGGATTGTTTATCAGATGAATTTTCTGCGATGAAAGCGAGATTG 1980
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680
Db 1981 TCCGAGAAAGTCAACATGCCAAGCGACTCAGTGTATGACGGAATTTACTTCAAGATCCA 2040
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700
Db 2041 AACITCAAGGCATCAATAGGCACACTAGCCGCTGTTGGAGAGGAGTACCGATTATACC 2100
Qy 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAAGAGAGAGTACGATTTCAAGAAAATTTATGTCACACTACCGAGTACCTTTGAT 2160
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTGCCTATCCCAAGCTATTTATCAAAAATATAGATGAGTCGAAATTTAAACCCCTATACT 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTATCANTTAAGAGGTATATCGAGGATAGTCAGACTTAGAATCTATTGTATCCGC 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGluGlyThrGlySerLeuTyrProLeuSer 780
Db 2281 TATATGCAAAACACGAAACAGTAAATGTCTAGTACGGGTCTTTATGCGCGCTTCA 2340
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
Db 2341 GTCCAAAGTCCCAATCAGAAAGTGTGAGAACCGAATCGATGCGGCCACACTTGAATGG 2400
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
Db 2401 AATCTGTATCTAGATTGTTCTGTGAGACGCGGGGAAAATGTGCACATCATTTCGCATCAT 2460
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
Db 2461 TTCTCTTGAGCATTTGATGTTGAGTCTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2520
Qy 841 IlePheLysIleLysThrGlnAspClyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATATTCAAGATTAGACCCAGATGGCCATGCAAGACTAGGAAATCTAGAGTTTCTCGAA 2580
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
Db 2581 GAGAAACCATTAGTTCGGGAGCAGTACTGCTGTGAAAGAGCAGAGAAAAAATGGAGA 2640
Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2641 GATRAACGTGAAAAATTTGGAATTTGAAACAAATATTGTTTATAAAGAGCAAAAGAACT 2700
Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2701 GTAGATGCTTTATTGTAACTCTCAATATGATCAATATACAGCGGATACGAATATTGCC 2760

Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTTCATCGCGCAGATAAACGTTTCATAGAAATTCGGGAAGCGTATCTTCCAGAGTTA 2820
Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATTCCGGGTGTAATGTAGACATTTTTCGAAGAATTAAGAAGCGGTATTTTCTACT 2880
Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATCTTCTTATATGATCGCAGAAATGCAITAAAAACGGTGATTTCAATAATGGCTTA 2940
Qy 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
Db 2941 TCATGCTGACACGTCGAAAGGCATGTAGATGTAGNAGACAAAACAACACCGTTCGGTC 3000
Qy 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTGTGTTGTTCCGAATGGAAAGCAGAAAGTGCACAAAGATTCGTGCTCTCGCGGTCGT 3060
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
Db 3061 GGCATATCTCTCGTGTCCACGCGTACAGGAGGATATGGAGAAGTTGCGTAACCACT 3120
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValIleGluGluVal 1060
Db 3121 CATGAGATCGAACAATACAGACGAACTGAAGTTTACACTGCTAGAGAGGAAAGTC 3180
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
Db 3181 TATCCAAACAAACACGCTAACGTGTAATGATTAATCTGCAAAATCAAGAAGAAATACGGGT 3240
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
Db 3241 CGGTACACTTCCGTAATCGTGGATATGCAAACTTATGGAAGCAATCTTCTCTACCA 3300
Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
Db 3301 GCTGATTATGCTCACTCTATGAAGAAAATCGTATACAGATGGACGAGAGACAACTCT 3360
Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3361 TGTGAATCTAACAGAGGATATGGGATTAACACACACTACCACTGCGCTATCTGACAAA 3420
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
Db 3421 GAATTAGAGTACTTCCAGAACCCGATAAGGTATGGATTGAGATCGGAGAAACCGAAGGA 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCTGGACAGCGTGAATTAATCTCTTATGGAGAA 3522

RESULT 5

US-08-598-305A-24
; Sequence 24, Application US/08598305A
; Patent No. 5827514
; GENERAL INFORMATION:
; APPLICANT: BRADFISCH, Gregory A.
; APPLICANT: THOMPSON, Mark
; APPLICANT: SCHWAB, George E.
; TITLE OF INVENTION: No. 5827514el Pesticidal Compositions
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/598,305A
 FILING DATE: 08-FEB-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/349,867
 FILING DATE: 06-DEC-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sanders, Jay M.
 REGISTRATION NUMBER: 39,355
 REFERENCE/DOCKET NUMBER: M886.D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 352-375-8100
 TELEFAX: 352-372-5800
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3522 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-598-305A-24

Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-598-305A-24 (1-3522)

QY 1 MetGluAsnAsnIleGlnHsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
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 QY 21 GluIleuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 DB 61 GAAATACAGAACGAAGAACACACCGCGCGCTGCCGTGGACATCAGCCTTGAGCCTT 120
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 DB 121 ACAGTTTCCTTTGAGTGAATTTGTTCCAGGTGTGGAGTTCGGTTTGATTTGAT 180
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
 DB 181 TTAATATGGGGTTTATATACTCTTCTGATTGGAGCTTATTTCTTACAGATTGAACAA 240
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
 DB 241 TTGATTGGCAAGAAATGAAACATTGGAAGGAACCGGCAATTACTACTTACCAGGG 300
 QY 101 LeuAlaAspSerThrGluIleThrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 DB 301 TTACAGATAGCTATGAAATTTATATGAAGCACTAAGAGAGTGGGAAGCAATCCTAAT 360
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
 DB 361 AATCCACAATTAAGGGGAAGTGTGCGTATTGCGATTGCTTAATACAGACGCGCTTAAATA 420
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTrpVal 160
 DB 421 ACAGCAATAATAATTTTACACCTTACAAAGTTTGAATCCCTCTTTATCGGCTATGTT 480
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 DB 481 CAACGGCGGAATTTACATTTATCATATTAAAGACGCGCTATCGTTGGCGAGGTTGG 540
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuLeuIleHisArg 200

DB 541 GGACTGGATATAGTACTGTTAATAATCATATAATAGATTAAATCTTATTCATAGA 600
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 DB 601 TATACGAACCATTTGTCGACACATACAACTAGGATTAGAAACCTTAGAGGTTACTPAT 660
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
 DB 661 ACTCGACAATGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTrpProIleGlnThrSerSerGln 260
 DB 721 ATCGTGTCTCTTTTCCGACATACGATGTTAGAACATATCCAAATCAACGTCATCCCAA 780
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 DB 781 TTAACAAGGGAATTTATACAAGTTCAAGTAATTCAGGATTCCTCCAGTTTCTGCTAATA 840
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
 DB 841 CCTAATGGTTTAAATAGGGCGGAATTTGGAGTTAGACCGCCCACTTATGGACTTTATG 900
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
 DB 901 AATCTTTGTTTGAACGTCAGACACTGTTAGAACTCAAACTGTGGGGAGGACACTTA 960
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 DB 961 GTTAGTTCCAGAAATACGGCTGGTAACGTTAAATATTCCTAGTTACGGGGCTTCAAT 1020
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 DB 1021 CCTGGTGGCGCATTTGGATTCAGATCAGATCCACGTCCTTTTATCGGACATTATCA 1080
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
 DB 1081 GATCTGTTTTCGAGAGAGGATTTGGGAATCTCTCATTTATGTACTGGGCTTTAGGGA 1140
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 DB 1141 GTAGATTTTCAACAACTGGTACGAACCAACCCGACATTTAGAAATAGTGGGACCATTA 1200
 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
 DB 1201 GATTCCTCTAGATGAATCCOACTCAGGATAATAGTGGGCACTTGAATGATTATAGT 1260
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
 DB 1261 CATGTATTAAATCATGTTTACATTTGTACGATGGCCAGTGTGAGATTCAGGAAGTGTCA 1320
 QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 DB 1321 TGGAGAGCTCCAAGTTTCTTGGACGCGCTAGTGCACCCCTACAAATACATTTGAT 1380
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
 DB 1381 CGGAGAGGATTTACTCAAAATACCATTTGGTAAAGACACATACACTTCAGTCACTACT 1440
 QY 481 ValValArgGlyProGlyPheThrGlyAspIleLeuArgArgThrSerGlyGlyPro 500
 DB 1441 GTTGAAGAGGCGCGGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGACCA 1500
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
 DB 1501 TTTGCTTATACTATTGTTAATAATTAAGGGCAATTACCCCAAGGTATCTGCAAGATA 1560
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
 DB 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTACCGTTGCGAGGTGAACGGATTTT 1620
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560

Db 1621 GCTGGTCAATTTAACAACAATAGATACCGGTGACCATTAACATCCAACTCTTTAGT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TAGCAACTATTATACAGCTTTTACATCCCATGACCCAGAGTAGTTTCCAGTAGGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTGAATTGATCCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCACATTGGAAGCAGATATGATTAGAAAAGACACAAAAAGCGGTGAATCGCGTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTATAACCAATAGGATATAAACAAGATGACGGATTATCATATTGATCAA 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAAATTTAGTGGATTGTTATCAGATCAATTTTGTCTGGATGAACGAGAAATG 1980
Qy 661 SerGlnLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGluAspPro 680
Db 1981 TCCGAGAAAGTCAACATGCGAAGCACTCAGTGTATGACGGGAATTTACTTCAAGATCCA 2040
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIlePhe 700
Db 2041 AACTTCAAGGCATCATAGCCACTAGACCGTGGTGGAGAGGAATGACCGATTATACC 2100
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAAAATATGTGCACACTACCGAGTACCTTTGAT 2160
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTGCATCCAGAGTATTTATATCAAAAAATAGATGATGCGAAATTAACCCCTATACT 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTATCAATTAAGAGGGTATATCGAGATAGTCAAGACTTAGAAAATCTATTGATCCG 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780
Db 2281 TATATGCAAAACACGAACAGTAAATGTGTAGTACGGGTTCTTTATGCGCGCTTCA 2340
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Db 2341 GTCCAAAGTCCAAATCAGAAAGTGGAGAACCGAATCGATCGCGCCACACACTTGAATGG 2400
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
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Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840
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Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATATTCAGATTAAAGCCAGATAGGCGCATCGAAGCTAGGAATCTAGAGTTTCTCGAA 2580
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880
Db 2581 GAGAAACCATTTAGTCGGGAGGACACTAGTCTGTGAAAAGAGCAGAGAAAAATGGAGA 2640
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Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2701 GTAGATGCTTTATTTGTAACCTCTCAATATGATCAATTAACAAGCGGATACCAATATTGCC 2760

Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTTCATGCGGAGATAAAACGGTTCATAGAAATTCGGGAGCGGTATCTTCCAGAGTTA 2820
Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATCCGGGTGTAATATGTAGACATTTTCGAAGAATTAAGAAGCGGTATTTCCT 2880
Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATTCTCTTATATGATGCGAGAAATGCTATTAACAAACGGTGTATTCATATAATGGCTTA 2940
Qy 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
Db 2941 TCATGCTGGAACGGTAAGGCGCATGTAGATGTAGAAGAACAAACACACCGTTCGCGTC 3000
Qy 1001 LeuValValProGluTyrPgluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTTCTGTTCCGGATGGGAAGCAGAGTGTCAAGAAGTTCGTGCTGTCCGGGTGCT 3060
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGlyCysValThrIle 1040
Db 3061 GGCTATATCTCTGTCACAGCGTACAAAGGAGGATATGGGAAGGTTCGTGCTGTCCGGGTGCT 3120
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATTCGAGAACAATACAGACGAACTGAAGTTTAGCACTGCGTAGAAGAGAGTC 3180
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
Db 3181 TATCCAAACACACGGTAACGTGTAAATGATTATCTGCAATCAAGAGATATACGGGGGT 3240
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
Db 3241 GCGTACACTTCCCGTAATCGTGGATATGACGAAACTATGGAAGCAATTCCTCTGTACCA 3300
Qy 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
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Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
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Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160
Db 3421 GAATTAGAGTACTTCCCGAAGAACCGATAAGGTATGGATTGAGATCGGAGAAACGAGGA 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCTGGACGCGTGGAAATTTACTCTCTTATGGAGAA 3522

RESULT 6

US-08-639-923A-24
: Sequence 24, Application US/08639923A
: Patent No. 5840554
: GENERAL INFORMATION:
: APPLICANT: Thompson, Mark
: APPLICANT: Schwab, George E.
: TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
: Pseudomonas fluorescens
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David R. Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,923A
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,476
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Salliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-639-923A-24

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Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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US-09-837-961-8 (1-1174) x US-08-639-923A-24 (1-3522)

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DB 1 ATGGAATAATATATCAAAATCAATCGCTACCTACAAATGTTTAAATATCCTGAAGTA 60
QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeu 40
DB 61 GAATATCTGAACGAGAACGACGACCGCGCGCTGCGCTGGACATCAGCCTGAGCCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheasp 60
DB 121 ACAGCTTCCCTTTTGAGTCAATTTGTCACAGTGTGGAGTGTGCTTTGGATTATTGAT 180
QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
DB 181 TTAATATGGGGTTTATAACCTCTCTGATTGGAGCTTATTTCTTTACAGATTGACAA 240
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
DB 241 TTGATTGACGAAAGAAATAGAACAATTGGAAGAACCGGGCAATTACTACATTACGAGGG 300
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
DB 301 TTACAGATAGCTATGAAATTTATATGACACTAGAGAGTGGGAGCAATCCCTAAT 360
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
DB 361 AATGCACAAATTAAGGAAGATGTCGATTTCGATTGCTAATACAGAGCGCTTTAATA 420
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTrpVal 160
DB 421 ACAGCAATAATAATTTTACACTTTACAAAGTTTGAAGTTTCCCTTTATCGTCTATGTT 480
QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
DB 481 CAACGGCGGAATTTACATTTATCTACTATTAAGACACGCTGTATCGTTGGCGAGGTGG 540
QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuHisArg 200

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DB 541 GGACTGGATATAGCTACTGTTAATATCAATATATAGATTATAATCTTTATTATAGA 600
QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
DB 601 TATACGAAACATGTTTGGACACATACAAATCAAGATTAAGAACTTAAGAGGTACTAAT 660
QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
DB 661 ACTCGACAATGGCGAAGATTCAATCAGTTTAGAGAGATTTAACACTTACTGTATTAGAT 720
QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
DB 721 ATCGTGTCTCTTTTCCGAACATACCATGTTAGAATATCCAAATCAACACGTCATCCCAA 780
QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
DB 781 TTAACAAGGAAATTTATACAAGTTTCAGTAATTAGAGATTCCTCCAGTTCTCTAATATA 840
QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetaspPheMet 300
DB 841 CCTAATGTTTTAATAGGCGGAATTTGGAGTTAGACGCCCATCTTATGGACTTTATG 900
QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
DB 901 AATCTTTGTTTGAACGAGACTGTTAGAAGTCAAACTGTGGGAGGACACTTA 960
QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
DB 961 GTTAGTTTCAAGAAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGCTTCAAT 1020
QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
DB 1021 CCTGTTGGCGCAATTTGGATTGCAGATGAGATCCACGCTCTTTTATTCGACATTATCA 1080
QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
DB 1081 GATCCTGTTTTCGCGAGAGGATTTGGGAATCTCTAATATGTTACTGGGCTTAGGGGA 1140
QY 391 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
DB 1141 GTAGCATTTCAACAACTGGTACGAACACACACCGCAACATTTAGAAATAGTGGGACATA 1200
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
DB 1201 GATTCTCTAGTAAATCCCACTCAGGATAATAGTGGGCGACCTTGGAGATGATTATAGT 1260
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
DB 1261 CATGTATTAAATCATGTTACATTTGTACGATGGCCAGGTGAGATTTCAGGAAGTGATTCA 1320
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
DB 1321 TGGAGAGCTCCAATGTTTCTTGGACGCAACCGTAGTGCACCCCTACAAATACAAATTGAT 1380
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
DB 1381 CCGAGAGGATTACTCAAAATACCATTGGTAAAGCACATACACTTCAGTCAAGGTACTACT 1440
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
DB 1441 GTTGTAGAGGGCCCGGGTTTACGGGAGGAGATATTCTTCGACCAACAGTGGAGGACCA 1500
QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
DB 1501 TTTCTTATATACTATTGTTAATAAATGGCAATACCCCAAGAGTATCTGTCGAGAGATA 1560
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
DB 1561 CGTATGCCCTCTACTCAAAATCTAAGAATTACGTAACGGTTCGAGGTGAACGGATTTT 1620
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560

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Db 1621 GCTGGTCAATTTACAAACAAATGATCCGGTGGACCCCAATTAACATCCAAATCTTTTACT 1680
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACGCAACATTAATACAGCTTTTACATCCCAATGACCCAGAGTAGTTTCACAGTAGT 1740
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATCTTTTAGTTCAGGGAATCAAGTTTATATAGACAGATTTGAATGATCCAGTT 1800
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAAGCAGATATGATTTAGAAAGACACAAAGCGGTGAATCGCGTG 1860
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTTAACCAATAGGGAATAAAGACAGATGTGACGATTATCATATTGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAAATTTAGTGGATTTGTTTATCAGATGAATTTGTCTGGATGAAGCGAATGT 1980
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680
Db 1981 TCCGAGAAAGTCAACATGCGAAAGCGACTCAGTGATGAGCGGAATTTACTTCAAGATCCA 2040
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrAspGlySerThrAspIleThr 700
Db 2041 AACITCAAGGCATCAATAGGCACTAGACCGTGTGGAGGAAGTAGCGGATTTACC 2100
QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAAGAAATTTATGTCACACTACCAGGTACCTTTGAT 2160
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
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QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840
Db 2461 TTCTCCTTGGACATTCATGTTGGATGTACAGACTTAATGAGGACTTAGATGTATGGGGTG 2520
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
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QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
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Db 2701 GTAGATGCTTTATTGTAACTCTCAATATGATCAATTAACAGCGGATACGAATATTGCC 2760

QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrIleuProGluLeu 940
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QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
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Db 2881 GCATTCCTCTATATGATCGGAGAAATGCAATTAATAAACGTCATTTCAATATATGGCTTA 2940
QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGluAsnHisArgSerVal 1000
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QY 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
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QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
Db 3181 TATCCAAACACACGCTAACGTGTAATGATTATATCTGCAAAATCAAGAATAACGGGGT 3240
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QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
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QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyLeuThrGluGly 1160
Db 3421 GAAATTAGAGTAGTCTCCAGAAACCGATAAGGTATGGATTGAGATCGGAGAAACGGAAGA 3480
QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCTGGAGACGCTGGAATTAATCTCTTATGGAGAA 3522

RESULT 7

US-08-933-891-7

; Sequence 7, Application US/08933891

; Patent No. 6096708

; GENERAL INFORMATION:

; APPLICANT: Payne, Jewel M.

; APPLICANT: Sick, August J.

; TITLE OF INVENTION: No. 6096708el Bacillus thuringiensis Isolate

; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding

; TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik & Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: US

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/933,891
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/356,034
 ; FILING DATE:
 ; APPLICATION NUMBER: US/08/210,110
 ; FILING DATE:
 ; APPLICATION NUMBER: 07/865,168
 ; FILING DATE: 09-APR-92
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/451,261
 ; FILING DATE: 14-DEC-89
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/371,955
 ; FILING DATE: 27-JUN-89
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, Roman
 ; REGISTRATION NUMBER: 21,023
 ; REFERENCE/DOCKET NUMBER: MA43.C1.D1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (904)375-8100
 ; TELEFAX: (904)372-5800
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3522 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: BACILLUS THURINGIENSIS
 ; STRAIN: ATZAWAI
 ; INDIVIDUAL ISOLATE: PS811
 ; IMMEDIATE SOURCE:
 ; LIBRARY: LAMSDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
 ; CLONE: 811A
 ; US-08-933-891-7

Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-837-961-8 (1-1174) x US-08-933-891-7 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
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 Qy 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 Db 61 GAAATATTAATGAAGAAGAAGTACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 120
 Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 Db 121 ACACGTTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTGCGTTGGATTAATTGAT 180
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
 Db 181 TTAATATGGGGTTTATAACTCCTTCTGATTGGAGCTTATTTCTTTACAGATTGAACAA 240
 Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
 Db 1321 TGGAGAGCTCCCAATGTTTCTTGGAGCGCCCGGTAGTGCANCCCCCTACAAATCAATTGAT 1380

Db 241 TTGATTGACAAAGAATAAGAAACATTTGAAAGGAACCGGGCAATTACTACATTACGAGGG 300
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 Db 301 TTAGCAGATAGCTATGAATTTATATTGAAGCACTAAGAGAGTGGGAAGCAATCTTAAT 360
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
 Db 361 AATGCACAATTAAGGGAAGATGCGTATTGCAATTTGCTAATACAGACGCGCTTTAATA 420
 Qy 141 ThrAlaIleAsnAsnProPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 Db 421 ACAGCAATAAATAATTTTACACTTACAAGTTTGAATCCCTCTTTTATCGGTCTATGTT 480
 Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 Db 481 CAAGCGCGGAATTTACATTTATCACTATTAAAGAGAGCGTGTATCGTTTGGCAGGGTTGG 540
 Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
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 Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 Db 601 TATACGAAACATTTGTTGACACATACAAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
 Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
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 Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
 Db 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATATCCAAATTCACATCCTCCCAA 780
 Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
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 Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
 Db 901 AATTCCTTTGTTAACTGCAGAGACTGTAGAAAGTCAAACTGTGTGGGAGGACACTTA 960
 Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 Db 961 GTTAGTTCACGAATACGGCTGGTAACCGTATAAAATTTCCCTAGTTACGGGGTCTCAAT 1020
 Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProCArgProPheTyrArgThrLeuSer 360
 Db 1021 CCGTGGCGCCCATTTGGATTGCAGATGAGGATCCACGCTCTTTTATCGGACATTATCA 1080
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 Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 Db 1141 GTAGCAATTTCACAAACTGGTAGACACACCCGCAACATTTAGAAATAGTGGGACCATTA 1200
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 Db 1201 GATTCCTAGATCAATCCCACTCAGGATAATAGTGGGCACTTGAATGATTATAGT 1260
 Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
 Db 1261 CATGTATTAATCATGTTTACATTTGTACGATGGCCAGGTGAGATTTCAGGAAGTGAATCA 1320
 Qy 441 TrpArgAlaProMetPheSerThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 Db 1321 TGGAGAGCTCCCAATGTTTCTTGGAGCGCCCGGTAGTGCANCCCCCTACAAATCAATTGAT 1380

Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCGGAGAGGATTACTCAAAATACCAITGGTAAAGACACATACACTTCAGTCAGTACTACT 1440
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
Db 1441 GTTGTAAAGAGGCCCGGGTTTACGGAGAGAGATATCTTCGAGCAACAAGTCGAGGAGCA 1500
Qy 501 PheAlaTyrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
Db 1501 TTTGCTTATACTATTGTTAATAAATGGCAATTACCCCAAGGTATCGTCAGAATA 1560
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Db 1561 CGCTATGCTCTACTACAAATCAAGATTTACGTAACGGTTGCAGGTGAACGATTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAATTTAAACAACAATGATACCGGTGACCAATTAACATTCCAATCTTTTACT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACCGAATATTATACAGCTTTTACATTCCTCAATGACCGAGTAGTTTCACAGTAGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACTTTTAGTTTCAGGAATCAAGTTTATATAGACAGATTTGAATGATCCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGlyTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAAGCAGATATGATTTAGAAAGAGACACAAAGCGGTGAATCGCGTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
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Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAATTTAGTGGATTGTTTACAGATGAATTTTGTCTGGATGAAGAAGCAAGTTG 1980
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Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700
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Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAATATATGTCACACTACAGGTACCTTTGAT 2160
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Db 2701 GTAGATGCTTTATTGTTAAACTCTCAATATGATCAATTACAAGCGGATACGAATATTGCC 2760
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Db 2761 ATGATTCATGCGGCAGATAAACGTGTTATGAATTCGGGAAGCGTATCTTCCAGAGTTA 2820
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Db 2941 TCATCTGGAAGCTGAAAGGGCATGTAGATGTAGAAGAACAAACAACACCGTTCGGTC 3000
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Db 3001 CTTGTGTTCCGGAATGGAGACCAAGTGTCAAGAAGTTCGTCGTCTGTCGGGTCTGT 3060
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGlyGlyCysValThrIle 1040
Db 3061 GGCATATATCTCTGTCACAGCGTACAGGAGGATATGAGAGAGTTGCGTAACCAT 3120
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
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Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGlyGly 1160
Db 3421 GAATTAGAGTACTTCCAGAGAAACCGATAAGGTATGGATTGAGATCGGAGAAACGGAAGA 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3481 ACATTTCATCGTGGACGGTGGAAATTTACTCTTATGGAGGAA 3522

RESULT 8

US-09-178-252-5

: Sequence 5, Application US/09178252
 : Patent No. 6218188
 : GENERAL INFORMATION:
 : APPLICANT: Cardineau, Guy A.
 : APPLICANT: Stelman, Steven J.
 : APPLICANT: Narva, Kenneth E.
 : TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
 : FILE REFERENCE: MA-714XC2
 : CURRENT APPLICATION NUMBER: US/09/178,252
 : CURRENT FILING DATE: 1998-10-23
 : EARLIER APPLICATION NUMBER: 60/065,215
 : EARLIER FILING DATE: 1997-11-12
 : EARLIER APPLICATION NUMBER: 60/076,445
 : EARLIER FILING DATE: 1998-03-02
 : NUMBER OF SEQ ID NOS: 27
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 5
 : LENGTH: 3522
 : TYPE: DNA
 : ORGANISM: Bacillus thuringiensis
 US-09-178-252-5

Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-837-961-8 (1-1174) x US-09-178-252-5 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
 Db 1 ATGGAGATAAATTTCAAAATCAATCGGTACCTTCAATTTGTTAAATATCTCGAATGA 60
 Qy 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 Db 61 GAAATATTAATGAAGAAAGAGTACTGCGAGATTTACCGTTAGATATATCCCTATCGCT 120
 Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 Db 121 ACACGTTTCCTTTGAGTGAATTTGTTCCAGGTGTGGAGTTGCGTTTGGATTATTGAT 180
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80
 Db 181 TTAATATGGGGTTTATTAACCTCTCTGATTGGAGCTTAITTTCTTTACAGATTGAACA 240
 Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
 Db 241 TTGATTGACAAAGATAAGAACATTTGGAAGGACCGGGCAATTTACTACATTAGAGGG 300
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 Db 301 TTAGCAGATAGCTATGAAATTTATATTGAAGCATTGAAGAGATTGAAGAGTGGAAATCCTAAT 360
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
 Db 361 AATGCACAAATTAAGGAGAGATGTGGCTATTCGATTGTGTAATACAGACGACGCTTAATA 420
 Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 Db 421 ACAGCAATAAATAATTTTACACTTACAAGTTTGAATCCCTCTTTTATCGGCTATGTT 480
 Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 Db 481 CAAGCGCGCAATTTTACATTTATCACTATTAAAGACGCTGTATCGTTTGGCGAGGGTTGG 540
 Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
 Db 541 GGACTGGATAGCTACTGTTTAATAATCATTTATATATAGATTAAATAAATCTTATTATAGA 600

Qy 201 TyrThrIlyHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 Db 601 TATACGAACATTTGTTGGACACATCAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
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 Db 721 ATCGTTGCTCTTTTCCGAACCTAGATGTTAGAACATATCCAAATTCAAAGCTCATCCCA 780
 Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 Db 781 TTAACAAGGGAATTTATACAGTTCAAGTAATTTAGAGATTCTCCAGTTCTGCTAATAATA 840
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 Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
 Db 901 AATTCCTTTCTGTAACCTGCAGAGACTGTTAGAAGTCAAACTGCTGGGAGGACACTTA 960
 Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
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 Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
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 Db 1081 GATCCTGTTTTTCTCGAGGAGGATTTGGAAATCTCTCAATTATCTACTGGGGCTTAGGGA 1140
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 Db 1201 GATTCCTAGATGAATCCACCTCAGGATATAGTGGGGCACCTTGGAAATGATTATAGT 1260
 Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
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 Db 1561 CCGTATGCTCTACTACAAATCTAGAAATTTACGTACGGTTGCGAGGTGAACGGATTTT 1620
 Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
 Db 1621 GCTGGTCAATTTAACAACAACATGGATACCGGTGACCCCATTAACATTCATCTTTTACT 1680
 Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580


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QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
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QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
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QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
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QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
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QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
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QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
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QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
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QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCTGGACAGCGTGAATTAATCTCTTATGGAGGAA 3522
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RESULT 9

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PCT-US92-11337-9
; Sequence 9, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11337
```

?: FILING DATE: 19921231
?: CLASSIFICATION:
?: PRIOR APPLICATION DATA:
?: APPLICATION NUMBER: 97/828,788
?: FILING DATE:
?: ATTORNEY/AGENT INFORMATION:
?: NAME: SALIWANCHIK, DAVID R.
?: REGISTRATION NUMBER: 31,794
?: REFERENCE/DOCKET NUMBER: WA75
?: TELECOMMUNICATION INFORMATION:
?: TELEPHONE: 904-375-8100
?: TELEFAX: 904-372-5800
?: INFORMATION FOR SEQ ID NO: 9:
?: SEQUENCE CHARACTERISTICS:
?: LENGTH: 3522 base pairs
?: TYPE: NUCLEIC ACID
?: STRANDEDNESS: double
?: TOPOLOGY: linear
?: MOLECULE TYPE: DNA (genomic)
?: HYPOTHETICAL: NO
?: ANTI-SENSE: NO
?: ORIGINAL SOURCE:
?: ORGANISM: BACILLUS THURINGIENSIS
?: STRAIN: AIZAWAI
?: INDIVIDUAL ISOLATE: PS811
?: IMMEDIATE SOURCE:
?: LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
?: CLONE: 811A
?: PCT-US92-11337-9

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-837-961-8 (1-1174) x PCT-US92-11337-9 (1-3522)

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QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
DB 61 GAATATTAATAGAGAAAGAGACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
DB 121 ACAGCTTCCCTTTTGGAGTAAATTTGTCACAGTGTGGAGTTGGCTTTGGATTATTGAT 180
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QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
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QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
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QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
DB 421 ACAGCAATAATAATTTTACACTTACAAAGTTTGAAGTCCCTCTTTATCGTCTATGTT 480
QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180

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QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
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QY 221 ThrArgGluTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
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DB 721 ATCGTTGCTCTTTTCCGAACATGATGTTAGAACATATCAAAATTCAAACGTCATCCAA 780
QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
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QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
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QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
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QY 481 ValValArgGlyProGlyPheThrGlyAspIleLeuArgArgThrSerGlyGlyPro 500
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QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
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Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
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Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATTCCTCTATATGATGCGAGAAATGTCAATAAACGGTGATTTCAATATATGGCTTA 2940
Qy 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
Db 2941 TCATGCTGGAACGTCGAAGGCGATGTAGATGTAGAAGACAAACACACCGTTCGGTC 3000
Qy 1001 LeuValValProGluTyrPheGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTTGTTGTTCCGGATGCGAGCAGAAAGTGTCAAGAAGTTCGTGTCTCTCCGGGTGCT 3060
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
Db 3061 GGCATATCTCTCTGTGTACAGCGGTACAGGAGGATATGGAGAGGTTGCGTAACCAAT 3120
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATCGAAGCAATACAGACGAACTGAAGTTTACCACTGCGTAGAAGAGAGTC 3180
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyTyrGlyGly 1080
Db 3181 TATCCAAACAAACACGGTAACGTGAATGATATATCTGCAAAATCAAGAAGAAATACCGGGGT 3240
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
Db 3241 GCGTACACTTCCCGTATPCGTGGATATGACGAAACTTATGGAAGCAATCTTCTGTACCA 3300
Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
Db 3301 GCTGATTATGCGTCAGTCTATGAGAAAAATCGTATACAGATGGACGAGAGACAATCCT 3360
Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3361 TGTGAATCTAACAGAGGATATGGGATTTACACACCACTTACCAGCTGGCTATGTGCACAAA 3420
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValThrIleGluIleGlyGluThrGluGly 1160
Db 3421 GAATTAGAGTACTTCCCAAGAACCGATGAAGGTATGGATTGAGATCGGAGAAACGGAAGGA 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCGTGGACAGCGTGAATTTACTCTCTATGGAGGAA 3522

RESULT 10

PCT-US95-05431-24

; Sequence 24, Application PC/TUS9505431

; GENERAL INFORMATION:

; APPLICANT: Street address: 5501 Oberlin Drive

; APPLICANT: City: San Diego

; APPLICANT: State/Province: California

; APPLICANT: Country: US

; APPLICANT: Postal code/zip: 92121

; APPLICANT: Phone number: (619) 453-8030

; APPLICANT: Telex number:

; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; Fax number: (619) 453-6991

ADDRESSEE: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05431
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA83
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (904) 375-8100
 TELEFAX: (904) 372-5800
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3522 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-US95-05431-24

Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-09-837-961-8 (1-1174) x PCT-US95-05431-24 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
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 QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 DB 61 CAATACTGACGAAGAAGACGACGCCGCCGCCCTGCGCTGGACATCAGCCTGAGCCTT 120
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 DB 121 ACAGTTTCCTTTTGAAGTGAATTTGTTCCAGGTGCGGAGTTGCGTTGGATTATTTGAT 180
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80
 DB 181 TTAATATGGGGTTTATAACTCCCTCTCATTTGGAGCTTATTTCTTTTACAGATTGAACAA 240
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
 DB 241 TTGATTGACCAAGATACAAACATTTGAAAGGAACCGGCAATTTACTACATTACGAGGG 300
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 DB 301 TTAGCAGATAGCTATGAATTTATATTGAGCAGCTAAGAGAGTGGGAGCAAAATCCTAAT 360
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
 DB 361 AATCCAAATTAAGGAGAGATGCGTATTCGATTTCGTAATACAGACGACGCTTTAATA 420
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 DB 421 ACAGCAATAATAATTTTACACTTACAAGTTTGAAGTTTCCCTCTTTATCGGTCTATGTT 480

QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 DB 481 CAAGCGCGGAATTTACATTTATCACTATTAGAGAGCGCTATCGTTGGCAGGCTTG 540
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgIleAsnLeuIleHisArg 200
 DB 541 GGACTGGATATAGCTACTGTTTATATCAATTAATATAGATTATAAATCTTATTCATAGA 600
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 DB 601 TATACAAACATTTGTTGGACACATACAAATCAAGGATTAGAAAACCTTAAGAGTACTAAT 660
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 DB 661 ACTCGACAATGGCAAGATTCAATCAGTTTAGAGAGATTTAACACTTCTCTATTAGAT 720
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
 DB 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGAACATATCCAAATCAACGTCATCCCCAA 780
 QY 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280
 DB 781 TTACAAGGGAATTTATACAAGTTTCAGTAATGAGGATTCCTCAGTTTCTGCTAATAFA 840
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
 DB 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCTCTTATGGACCTTATG 900
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
 DB 901 RAATCTTTGTTGTAACCTGCAGAGACTGTTAGAAGTCAAACTGTGTGGGAGACACITTA 960
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 DB 961 GTTAGTTTCCAGAAATACGCTGGTAAACGCTATAAATTTCCCTAGTTACGGGCTCTCAAT 1020
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 DB 1021 CCTGTGGCGCATTTGGATTGCAGATGAGGATCCACCTCTCTTTTATCGGACATTATCA 1080
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
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 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 DB 1141 GTAGCATTTCAACAACTGGTACGAACACACCCCAACATTTAGAAATAGTGGGACCATTA 1200
 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
 DB 1201 GATTTCTAGATGAATCCACCTCAGGATAATAGTGGGCGCACCTTGGAAATGATTATAGT 1260
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
 DB 1261 CATGTATTAAATCATGTTTACATTTGTACATGGCCAGGTGAGATTTACAGGAGTGATTCA 1320
 QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 DB 1321 TSGAGCTCCAAATGTTTCTTGGACGCAACCGTAGTGCACCCCTACAAATACAATTGAT 1380
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
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 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
 DB 1441 GTTGTAGAGGCCCGGGTTTACGGGAGGAGATATTCTTCGACCAACAAGTGGGAGGACCA 1500
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
 DB 1501 TTTGCTTATACTATTGTTAATATAAATGGGCAATTTACCCCAAGGTATCGTGCAGAAATA 1560
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540

1561 CGCTATGCCCTACTACAAATCTAAGAATTTACGTACGCTGCAGCTGAACGATTTT 1620
541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
1621 GCTGGTCAATTTAACAAACAATGGATACCGGAGACCCATTAAACATTCCTTGTAGT 1680
561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
1681 TAGGCAACTATTATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGG 1740
581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
1741 GCTGATACTTTAGTTCAGGGAATGAAGTTTATATACACAGATTGTAATTCATCCAGTT 1800
601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
1801 ACHGCAACATTTCAAGCAGAAATGATTTTGAAGAGACACAAAAGCGGTGAATCGCGTG 1860
621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
1861 TTTACTTCTATAAACCAATPAGGATAAAACAGATGTCGCGGATATCATATATGATCAA 1920
641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspCysLeuArgGluLeu 660
1921 GTATCCAATTTAGTGGATTTGTTATCAGATGAATTTTGTCTGATGAAAAGCGAGAATTG 1980
661 SerGluLysValLysHisAlaLysArgLeuSerAspCysLeuArgAsnLeuLeuGlnAspPro 680
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681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrPArgGlySerThrAspIleThr 700
2041 AACTTCAAGGCATCAATAGGCACACTAGACCGTGGTTGGAGAGAGACTACGGATATACC 2100
701 IleGluArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
2101 ATCCAAGAGAGAGATGACGTATTCAAAGAAATATTGTCTCACATACCAGTACTTTGAT 2160
721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspCysLeuSerLysLeuLysProTyrThr 740
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2221 CGTTATCAATTAGAGGGTATATCGAGGATAGTCACAGACTTAGAATTCATTTGATCCGC 2280
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2401 AATCCTGATCTAGATTGTTCTCAGAGAGGGGAAAAATGTCACATCATTCGATCAT 2460
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2461 TTTCTCTTGGACATTTGATGTTGATGTACAGACTTAATGAGGACTTAGATGGGTG 2520
841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
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2581 GAGAAACCATTTAGTCCGGGAGCAGCTAGCTGCTGTTGAAGAGACAGAGAAAAATGGAGA 2640
881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900

2641 GATAAAGCTGAAAAATTTGGAATTTGGAACAAATATTTTATTATAAGAGGCCAAAGAACTCT 2700
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921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
2761 ATGATTCATCGGCAAGATAAAACGTTTCATAGAAATTCGGGAAGCGTATCTTCAGAGTTA 2820
941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
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2881 GCATTCCTCTATATGATCGAGAAATGTCAATTAATAAACCGTGATTTCAATAATGGCTTA 2940
981 SerCysTyrAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
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1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
3001 CTGTGTTGTTCCGGAATGGGAAGCAGAAAGTGTCAACAAGCTTCGTGCTCTCCGGGTCT 3060
1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
3061 GGTATATCTTCGTGTACAGCTACAGAGGGATATGGAAGGTTTCGCTAAACCAT 3120
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1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
3301 GCTGATTCGCGTCACTCTATGAAGAAAAATCGTATACAGATGACGAGAGACAACTCCT 3360
1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
3361 TGTGAATCTAACAGAGGATATGGGATACACACCACTACCACTGCTGGCTATGTGACAAAA 3420
1141 GluLeuGluTyrPheProGluThrAspLysValThrIleGluIleGlyGluThrGluGly 1160
3421 GAATTAGATFACPTCCAGAACCGATAAGGTATGGATGATGATGATGATGATGATGATGAT 1174
1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
3481 ACATTCACTGTCGACGCGTGGAAATCTACTCTTATGGAGGAA 3522

RESULT 11
5188960-7
; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL-SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/451,261
; FILING DATE: 14-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 371,955
; FILING DATE: 27-JUN-1989
; SEQ ID NO:7;

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; LENGTH: 3522
5189960-7

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-837-961-8 (1-1174) x 5189960-7 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
Db 1 ATGCGAGAATAATATCAAAATCAATGGTACCTTACAAATGCTTTAAATAATCCCTGCAAGTA 60

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Db 61 GAAATATTAATGAAGAAGAAGTACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 120

QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 121 ACAGCTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTGGCTTTGSGATTATTTGAT 180

QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80
Db 181 TTAATATGGGTTTATAACTCCTTCGTATGGAGCTTATTTCTTTTACAGATTGACAA 240

QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
Db 241 TTGATTGAGCAAAAGATAGAAACATTGGAAGAGAACCGGCAATTTACTATACGAGG 300

QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
Db 301 TTACAGATAGCTATGAATTTATTTAGACACTAGAGAGTGGGAGCAAAATCCCTAAT 360

QY 121 AsnAlaGlnLeuArgGluAspValArgPheAlaAsnThrAspAspAlaLeuIle 140
Db 361 AATGCACAATTAAGGAAGATGTCGGTATTCGATTCTTAATACAGACGAGCTTTAATA 420

QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAATAATTTTACACTTACAAGTTTGGAAATCCCTCTTTTATCGTCTATGTT 480

QY 161 GlbAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
Db 481 CAGCGCGGATTTACATTTATCTATTTAGAGACCGCTGTATCGTTTGGCAGGGTTGG 540

QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GGACTGGATATAGCTACTGTTAATATCAATTAATAGATTAATTAATCAATCAATGATA 600

QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
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QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
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QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
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QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
Db 781 TTAACAAGGGAATTTATACAAGTTCAGTAAATTCAGGATTTCTCCAGTTTCTGCTAATA 840

QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
Db 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTATGACTTTATG 900

QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyClyHisLeu 320
Db 901 AATCTTTGTTTCTTAACCTGCAGAGACTGTTAGAAGTCAAACTGTGCGGGAGGACACTTA 960

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QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
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Db 1201 GATTCTCTAGATGAATCCCACTCAGSATAATAGTGGGCACTTGGAAATCATTAAGT 1260

QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
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QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
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QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
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QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTTACTTATATAACCAATAGGATAAACAAGATGTCGAGGATTTATCATATTGATCAA 1920

QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAATTTAGTGGATTTGTTTATCAGATGAATTTTGTCTGATGAAAGCCAGAAATTG 1980

QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
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Db 1981 TCCGAGAAAGTCACACATCGCGAAGCGACTCAGTGATGAGCGAAATTACTTCAAGATCCA 2040
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Db 2041 AAC TTC AAGG CAC TCA A TAG CCA C T A G C C G T G T T G A G A G A A G T A C C G A T A T T A C C 2100
Qy 701 IleGlnArgGlyAspAspValPheLysGlnAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAATTAATGATCACAATACCAGGTACCTTTGAT 2160
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTGTCTATCCAACTATTATATCAAAAAATAGATGATGCGAAATTAACCCCTATACT 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTATCAATTAAGAGGTATATCGAGGATAGTCAGAGCTTAGAAATCTATTGTATCGCC 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
Db 2281 TATATGCAAAACAGCAACAGTAATGTGTAGTACGGGTCTTTATGGCGCTTTCA 2340
Qy 781 ValGlnSerProLysArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
Db 2341 GTCCAAAGTCCAAATCAGAAAGTGTGGAGAACGAATCGCGCCACACCTTGAATGG 2400
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
Db 2401 AATCCTGATCTAGATGTCTCTGTCGACAGACGGGAAAAATGTGCACATCATTCGCATCAT 2460
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
Db 2461 TTCCTTGGACATGTATGTTGGATGTACACACITTAATGAGGACTTAGATGTATGGGTG 2520
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATATTCAAGATTAAAGACCAAGATGGCCATCGACAGCTAGGAATCTAGAGTTTCTCGAA 2580
Qy 861 GluLysProLeuValGlyLysAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
Db 2581 GAGAAACCATTTAGTCGGGGAAGCACTACTCTGTGTGAAAGAGCAGAGAAAAATGGAGA 2640
Qy 881 AspLysArgGluLysLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2641 GATAACCTGAAAAATTCGAATTCGAACAATAATGTGTTTAAAGAGCGCAAGAAATCT 2700
Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2701 GTAGATGCTTTATTTGTAACCTCTCAATATGATCAATTTACAAGCGGATACGAATATGCC 2760
Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTATCGCGCAGATAAACGGTGTTCATAGATTCGGGAAGCGTATCTTCCAGAGTTA 2820
Qy 941 SerValIleProGlyValAsnValAspIlePheGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATTCGGGTGTAAATGTAGACATTTTCGAAGAAATTAAGGCGGTATTTTCACT 2880
Qy 961 AlaPheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATTCCTCTATATGATCGCAAGAAATGCTATTAACACGGTGTATTCATATAGGCTTA 2940
Qy 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
Db 2941 TCATGCTGGAACGGTGAAGGCGCATGTAGATGTAGAAGAACAAAAACACCCCGTTCGGTC 3000
Qy 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTTGTTGTCGGGAATGGGAACGACAGAGTGTCACAAAGTTCGTGTCTGTCGGGTGCT 3060
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040

Db 3061 GGCTATATCCTTCGTGTCACACGCTACAGGAGGATATGGAGAGGTTCGCTAACCAT 3120
Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATCGAGAACATACAGACCACTGAAGTTTAGCAACTGCGTAGAAGAGAGTC 3180
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluLysGly 1080
Db 3181 TATCCAAACACACACGTAACGTGTAATGATTATATCTCAAAATCAAGAAGATACGGGGT 3240
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100
Db 3241 CGGTACACTTCCTGTAATCGTGGATATGACGAAACTTATGGAGCAATCTTCTGTACA 3300
Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgAspAsnPro 1120
Db 3301 GCTGATTATGGCTAGTCTATCAAGAAAAATCGTATACAGATGGACGAGACAACTCT 3360
Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3361 TGTGAATCTAACAGAGGATATGGGATACACACACTACCACTGGCTATGTGACAAA 3420
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyLeuThrGluGly 1160
Db 3421 GAATTAGAGTACTTCCAGAAACCGATAAGGTATGATGATGATGATGATGATGATGAT 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCGTGGACAGCGTGAATTAATCTCTTATGAGGAA 3522

RESULT 12

PCT-US91-02560-1
; Sequence 1, Application PC/TUS9102560
; GENERAL INFORMATION:
; APPLICANT: Gawron-Burke, Cynthia
; APPLICANT: Chambers, Judith A.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryIF and cryIX
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze et al, c/o A.S. Nadel
; STREET: 1601 Market Street, 38th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02560
; FILING DATE: 19910415
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510327
; FILING DATE: 16-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-27 U1
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4020 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Gouble
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 478..4002

PCT-US91-02560-1

Alignment Scores:

Pred. No.: 0 Length: 4020
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-09-837-961-8 (1-1174) x PCT-US91-02560-1 (1-4020)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
 DB 478 ATGGAGAATAATATCAAAATCAATCGGTACCTTACAATGTTTAAATCCTGAAGTA 537
 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 DB 538 GAAATATTAAATGAAGAAGAGTACTGGCAGATTACCGTTAGATATATCCTTATCGTT 597
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 DB 598 ACACGTTTCCITTTGAGTGAATTTGTTCCAGGTGGGAGTTGCCGTTTGGATTATTGAT 657
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
 DB 658 TTAATATGGGTTTATAACTCTCTGATTGGAGCTTATTTCTTTACAGATTGAACAA 717
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
 DB 718 TTGATTGAGCAAGAATAAGAACATTTGGAAGAGAACCGGGCAATTTACTACATTACGAGG 777
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 DB 778 TTACAGATACGTATCAATTTATATTGAACACATAAGAGAGTGGAGCAATTCCTAAT 837
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle 140
 DB 838 AATGCACAAATTAAGGGAAGATGTGCTATTCGATTGTCTAATACAGACGACGCTTTAATA 897
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 DB 898 ACAGCAATTAATAATTTTACACTTACAAGTTTGAAGTTTCCCTCTTTATCGGTCTATGT 957
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 DB 958 CAAGCGGCAATTTACATTTATCACTATTACAGACGCTGTATCGTTGGCAGGCTGG 1017
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
 DB 1018 GGACTGGATATAGCTACTGTTAATAATCATTTATATAGATTAAATAATCTTATTCATAGA 1077
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 DB 1078 TATACGAACAATTTGTTGGACACATACATAATCAAGATTAGAAAACCTTAAGAGGTACTAAT 1137
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
 DB 1138 ACTGCACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTTAACAATTTACTGTATTAGT 1197
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
 DB 1198 ATCGTGTCTTTTCCGAATACGATGTTAGAACATATCAATTCAAATTCAAACGTCATCCAA 1257
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 DB 1258 TTACAAGGGAAATTTATACAAAGTTCAGTAATGAGGATTTCCAGTTTCTGCTAATATA 1317
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
 DB 1318 CCTAATGTTTATAGCGCGGAATTTGGAGTTAGACCGCCCATCTTATGGACTTTATG 1377
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320

DB 1378 AATTCITTTGTTGTAACCTCCAGAGCTGTAGAAGTCAAACTGTGTGGGAGACACTTA 1437
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 DB 1438 GTTAGTTCACGAATACGCTGTAAACCGTATAAATTTCCCTAGTATACGGGCTCTCAAT 1497
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 DB 1498 CCGTGTGGCGCCATTGGATTGCAGATGAGATCCACGTCCTTTTATCGCATATATCA 1557
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
 DB 1558 GATCCTGTTTTCGTCGAGGAGATTGGGAATCCTCATTTATGTACTGGGGCTTAGGGGA 1617
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 DB 1618 GTAGCATTTCAACAAACTGGTACGAACACACCCGGAACATTTAGAAATAGTGGACCA 1677
 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
 DB 1678 GATTCCTAGATGAATCCACCTCAGGATAATAGTGGGCACTTGGGAATGATTATAGT 1737
 QY 421 HisValLeuAsnHisValThrPheValArgTyrProGlyGluIleSerGlySerAspSer 440
 DB 1738 CATGTATTAAATCATGTTACATTTGTACATGGCCAGGTGAGATTTACAGAAAGTGA 1797
 QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 DB 1798 TGGAGAGCTCCAATGTTTCTTGGACGACCGTAGTGCACCCCTACAAATACAAATGAT 1857
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
 DB 1858 CCGGAGAGGATTAACAAATACCATTTGTTAAAGACACATACACTTCAGTCAGGTACTACT 1917
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
 DB 1918 GTTGTAGAGGCGCGGCTTTACGGGAGGAGATATCTTCGACGACAAAGTGGAGAGCA 1977
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
 DB 1978 TTTGCTTATACTATTGTTAATAATAAATGGCAATTAACCCAAAGGTATCGTGCAGAAATA 2037
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
 DB 2038 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAACGGTTGCGAGGTGAACGGATT 2097
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
 DB 2098 GCTGCTCAATTTACAAACAATGATACCGGTGACCCCATTAACATTCCTTTAGT 2157
 QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
 DB 2158 TACGCACTATTATACAGCTTTTACATTCGCAATGAGCCAGAGTAGTTTCCAGTAGGT 2217
 QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
 DB 2218 GCTGATACTTTTAGTTCAGGAATGAAGTTTATATAGACAGATTGGAATTGATTCAGTT 2277
 QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
 DB 2278 ACTCAACATTTGAAGCAGATATGATTTAGAGAGCACAAGGCGGTGAATGCCGTG 2337
 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
 DB 2338 TTTACTTCTATAAACCAAAATAGGGATAAAACAGATGTGACGGATTATCATATTGATCAA 2397
 QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
 DB 2398 GTATCCAAATTTAGTGGATTGTTTATCATGATGATTTTGTCTGTGGATGAAGGAGAAATG 2457
 QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680

Db 2458 TCCGAGAAAGTCAAACATGCGAAGCGACTCAGTCGATGAGCGGAATTTACTTCAAGATCCA 2517
Qy 681 AsnPhelYsGlyIleAsnArgGlnLeuAspArgGlyIleThrAspIleThr 700
Db 2518 AACATCAAGGCAATCAATAGCAACTAGACCGTGGTGGAGAGAAATACCGATATTACC 2577
Qy 701 IleGlnArgGlyAspValPheLeuYsGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2578 ATCAAAGAGAGATGACGATTTCAAGAAAATTTATGTCACATACACAGTACCTTTGAT 2637
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2638 GAGTGTATCCACAGCTATTTATATCAAAAAATAGATGATGCGAAATTAACCCCTACT 2697
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2698 CGTTATCAATTAAGAGGATATTCGAGATAGTCAAGACTTAGAAATCTATTTCATCCGC 2757
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780
Db 2758 TATAATCAAAACACGAAACAGTAATGTCTAGTACGGGTTCTTTATGCGCCCTTTCA 2817
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr 800
Db 2818 CTCGAAAGTCCAAATCAGAAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTGAATGG 2877
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
Db 2878 AATCCTGATCTAGATTTGCTCGAGAGAGCGGGAATAATGTGCACATCATTCGCATCAT 2937
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840
Db 2938 TTCTCTTGGACATGTATGTTGGATGTACAGACTTAATGNGGACTTAGATGTATGGGTG 2997
Qy 841 IlePheYsIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2998 ATATTCAAGATTAAAGCGCAAGATGGCCATGCAAGACTAGGAAATCTAGAGTTTCTCGAA 3057
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880
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Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 3118 GATAACGTCGAAAATTTGGAATTTGGAACCAAAATATTGTTTATAAGAGGCAAAAGAAATCT 3177
Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 3178 GTAGATGCTTTATTTGTAACCTCTCAATATATGATCAATTAAGCGGATACGAATATTGCC 3237
Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 3238 ATGATTCATCGGCAGATAACGTTGTCATAGAAATTCGGAAGCGTATCTTCCAGAGTTA 3297
Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 3298 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAGAAATTAAGGCGGTATTTTCACT 3357
Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 3358 GCATTTCTTCATATGATGCGGAGAAATGTCAATTAAGGCGGTATTTCAATATGGCTTA 3417
Qy 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
Db 3418 TCATGCTGGAGCGTAAGGCGATGTAGATGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3477
Qy 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3478 CTGTGTTCTCGGAATCGGAGAGAGAGAGTGTACAGAAAGTTCGTCTGTCTCGGGTCTGT 3537
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
Db 3538 GGTATATCTCTGTCGACAGCGTACAGAGGGGATATGAGAGAGTTCGTAACCAT 3597

Qy 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluGluVal 1060
Db 3598 CATGAGATCGAGAAACAATACAGACGAATGAAGTTTAGCAACTCGTAGAAGAGAGTC 3657
Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
Db 3658 TATCCAAACACACAGCGTAACGTGTAAATGATTATATCTGCAAAATCAAGAGAAATACGGGGT 3717
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
Db 3718 GCGTACACTTCCCGTAATCGTGGATATGACGAAACTTATGAGCAATCTCTGTACCA 3777
Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgAspAsnPro 1120
Db 3778 GCTGATTATGCTGCTATGTAAGAAAAATCGTATACAGATGACGAGAGAGCAATCCT 3837
Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3838 TGTCATCTAACAGAGGATATGGGGATACACACACTACCGCTGGCTATGTGCAAAA 3897
Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
Db 3898 GAATTAGAGTACTTCCAGAGAAACGATAAGGTATGATTGAGATCGGAGAAACGAGGA 3957
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3958 ACATTCATCTGGACAGCGTGAATTTACTCTTATGGAGAA 3999
RESULT 13
US-08-349-867-28
; Sequence 28, Application US/08349867
; Patent No. 5508264
; GENERAL INFORMATION:
; APPLICANT: Bradfisch, Gregory A.
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,867
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-349-867-28
Alignment Scores: 0 Length: 3522
Pred. No.:

Score:	6049.00	Matches:	1143
Percent Similarity:	97.79%	Conservative:	5
Best Local Similarity:	97.36%	Mismatches:	26
Query Match:	96.88%	Indels:	0
DB:	1	Gaps:	0
US-09-837-961-8 (1-1174) x US-08-349-867-28 (1-3522)			
QY	1	MetGluAsnAsnIleGlnAsnGluCysValProTyrAsnCysLeuAsnAsnProGluVal	20
DB	1	ATGGAATAATATTCAAATCAATGCGTACCTTACAAATGTTTAAATCAATCCTGAAGTA	60
QY	21	GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu	40
DB	61	GAATACTGAACGAGAACGACACCGCCGCGCTGGACATCAGCCTGAGCCCT	120
QY	41	ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp	60
DB	121	ACAGCTTCCCTTTGAGTGAATTTGTTCCAGTGTGGAGTTGCGTTGGATTATTTCAT	180
QY	61	LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGluIleGluIn	80
DB	181	TTAATATGGGTTTATAACCTCTCTGATTGGAGCTTATTCTTTTACAGATTGAACAA	240
QY	81	LeuIleGluInArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly	100
DB	241	TTGATTGAGCAAGAAATAGAAACATTGGAAGGAAACCGGGCAATTACTACATTAGCAGGG	300
QY	101	LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn	120
DB	301	TTACGATACCTATGAAATTTATATTGAACACTAAGAGAGTGGGAAGCAATCCTAAT	360
QY	121	AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAsnAlaLeuIle	140
DB	361	AATCGCAATTAAGGAGAGATGCGTATTCGATTTCGTAATACAGACGCGCTTTAATA	420
QY	141	ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal	160
DB	421	ACAGCAATAAATAATTTACACTTTACAGTTTGAAGTTTGAATCCCTCTTTATCGTCTATGTT	480
QY	161	GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp	180
DB	481	CAAGCGGCGAATTTACATTTTATCACTATTATAGACGCGTGTATCGTTTGGCAGGGTTGG	540
QY	181	GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgIleLeuAsnLeuIleHisArg	200
DB	541	GGACTGGATATAGTACTGTTTAATATCATTTATATAGATTATTAATATCTTTATTTCATAGA	600
QY	201	TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn	220
DB	601	TATACGAACATTTGTTGGACACATACAAATCAAGGATTAGAAACTTAAGAGGTACTAAT	660
QY	221	ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp	240
DB	661	ACTCGCAATGGGCAAGATTCATCACTTTTAGGAGAGATTAAACACTTACTGTATTAGAT	720
QY	241	IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln	260
DB	721	ATCGTGTCTCTTTTCCGAATACGATGTTAGAACATATCCAAATTCAAACGTCATCCCAA	780
QY	261	LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle	280
DB	781	TTAACAAGGGAATTTATACAAAGTTTCAATTTGAGGATTCTCCAGTTTCTGCTAATAATA	840
QY	281	ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet	300
DB	841	CCTAATGGTTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTATGGACTTTATG	900
QY	301	AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu	320
DB	901	AATTCCTTTGTTGTAACGTCAGAGACTGTGTAGAAAGTCAAACTGTGTGGGAGGACACTTA	960
QY	321	ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn	340

DB	961	GTTAGTTCCAGAAATACGCTGGTAACCGTATAAATTTCCCTAGTTACGGGCTCTCAAT	1020
QY	341	ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer	360
DB	1021	CCTGGTGGCGCAATTTGGATTTCAGATCAGGATCCACGCTCTTTTATCGGACATTATCA	1080
QY	361	AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly	380
DB	1081	GATCCTGTGTTTGTCCGAGAGGATTTGGGAATCCTCATTTATGTACTGGGCTTGAAGGA	1140
QY	381	ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle	400
DB	1141	GTAGCATTTCAACAACTGGTACGAACCAACCCCAACATTTAGAAATAGTGGGACCATTA	1200
QY	401	AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer	420
DB	1201	GATTCCTAGATGAATCCCACTCAGGATAATAGTGGGCACTTGGAAATGATTATAGT	1260
QY	421	HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer	440
DB	1261	CATGTATTAATCATGTGTACATTTGTAGATGGCCAGGTGAGATTTCAGGAAGTGATTCA	1320
QY	441	TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp	460
DB	1321	TGGAGAGCTCCAAATGTTTCTTGGACGCCGCTAGTGCACCCCTACAAATACAAATTGAT	1380
QY	461	ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr	480
DB	1381	CCGGAGAGGATTACTCAAAATACCATTGTTGTAAGAGGAGATTTCTTCACGAAACAAAGTGGAGGACCA	1440
QY	481	ValValArgGlyProGlyPheThrGlyAspIleLeuArgArgThrSerGlyGlyPro	500
DB	1441	GTTTAAAGAGGCGCGGGTTTACGGGAGGAGATTTCTTCACGAAACAAAGTGGAGGACCA	1500
QY	501	PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle	520
DB	1501	TTTCTGTATACATTTGTTAATTAATTAATGGGCAATTAACCCCAAGAGTATCTGTCAGAAATA	1560
QY	521	ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe	540
DB	1561	CGCTATGCTCTACTACAAATCTAAGATTTACGTAACGGTTGCAGGTGAACGGATTTT	1620
QY	541	AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer	560
DB	1621	GCTGGTCAATTTAACAACAAATGATACCGGTGACCATTAACATTCCTTTTAGT	1680
QY	561	TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly	580
DB	1681	TACGCACTATTATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCCAGTAGGT	1740
QY	581	AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal	600
DB	1741	GCTGATCTTTTACTTTCAGGGAATGAAGTTTATATAGACAGATTGAAATTCATCCAGTT	1800
QY	601	ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu	620
DB	1801	ACTCCAACATTTGAAGCAGAAATGATTTAGAAAGACACAAAAGGGGGTGAATGCGGTG	1860
QY	621	PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln	640
DB	1861	TTTACTTCTATAAACCAATAGGATGAACAGATGTGAGGATTTATCATTCGATCGTGA	1920
QY	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
DB	1921	GTGTCCAATTTAGTTACGTATTTCGATCAATTTGTTCTGGATGAACGAGAGATTG	1980
QY	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro	680
DB	1981	TCGAGAAAGTCAACATGCGAAGCGACTCAGTGATGAACGCAATTTACTCCAAGATTCA	2040
QY	681	AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr	700

Db 2041 AATTTCAAGACATTAAATAGCAACACGAGCGTGGTGGGGGAGTAGTACAGGGATTACC 2100
Qy 701 lleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAGGAGGGGATGACGCTATTAAAGAAATACGTCACACTATCAGGTACCTTTGAT 2160
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTCTCATCAACATATTTGTATCAAAAATCGATGAATCAAAATAAAGCCATTACC 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluLysTyrIleuLeuArg 760
Db 2221 CGTTATCAATTAAGAGGTATATCGAAGATAGTCAAGACTTAGAAATCATTAATTCGC 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer 780
Db 2281 TACAATGCAAAACATGAACAGATAATGTGCCAGGTACGGGTTCCTATTGGCGGCTTCA 2340
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyrP 800
Db 2341 GCCCAAGTCCAAATCGGAAGGTGGAGAGCGAATCGATGCGCGCCACACCTTGAATGG 2400
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
Db 2401 AATCCTGACTTAGATTGTTCTGTAGAGGTAGGAGAAAGTGTGCCCATCATTCGCATCAT 2460
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal 840
Db 2461 TTCTCTTAGACATGATGTAGAGGTAGTACAGACTTAAATGAGGACCTAGGTGTATGGGTG 2520
Qy 841 llePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATCTTAAAGATTAAAGCAAGATGGCAGCGCAAGACTAGGGAATCTAGAGTTCTCGAA 2580
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysTyrArg 880
Db 2581 GAGAAACCATTTAGTAGAGAACGCTAGCTGCTGTGTAAGAGCGGAGAAAAAATGGAGA 2640
Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2641 GACAAACGTGAAAAATGGAATGGGAAGCAAAATATCGTTTAAAGAGCGCAAAAGAAATCT 2700
Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
Db 2701 GTAGATGCTTTATTGTAACCTCAATGATGATCAATACAGCGGATAGCATATGGC 2760
Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTATCGCGCAGATAAAGCTGTATAGCATTCGAGAGCTTATCTGCTGAGCTG 2820
Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATTCCGGGTGCAATCGGCTATTTTGAAGATTAGAGGGCGGTATTTTCAC 2880
Qy 961 AlaPheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
Db 2881 GCATTCCTCCATATGATCGGAGAAATGTCATTAATAAAGGTGATTTTATATAGCTTA 2940
Qy 981 SerCysTyrAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000
Db 2941 TCCTGTGGAACGTGGAAGGGCATGTAGATGTAGAAGAACAAACCAACCCGCTTCGGTC 3000
Qy 1001 LeuValValProGluTyrPheGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 3001 CTGTGTTTCCGGAATGGGAAGCAGAGGTGTACAGAAAGTTCTGCTGTCTCCGGTCTG 3060
Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
Db 3061 GGCTATATCTCTGCTACAGCGTACAGAGGGGATATGGAGAGGTTCGCTAACCAT 3120
Qy 1041 HisGluIleGluAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3121 CATGAGATCGAGAACAAATACAGACGAACCTGAAGTTTAGCAACCTGTGTAGAAGGAAGTA 3180

Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
Db 3181 TATCCAAACACACCGTACGTGTATGATTAATACGCCACTCAAGAGAAATATGAGGT 3240
Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
Db 3241 ACGTACACATCTCGTAATCGAGGATATGACGGAGCCTATGAAAGCAATTTCTTCTGTACCA 3300
Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgAspAsnPro 1120
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Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160
Db 3421 GAATTAGACTACTTCCAGAAAACCGATAAGGTATGATGATGAGATCGAGAACGGAAGA 3480
Qy 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3481 ACATTATCTGTGACACGCTGGAATTACTTCTTATGGAGAA 3522

RESULT 14

US-08-239-476-28
; Sequence 28, Application US/08239476
; Patent No. 5527883

GENERAL INFORMATION:

; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; TITLE OF INVENTION: Pseudomonas fluorescens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESS: David R. Saliwanchik
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA83
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-239-476-28

Alignment Scores:

Pred. No.: 0 Length: 3522
Score: 6049.00 Matches: 1143
Percent Similarity: 97.79% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 26
Query Match: 96.88% Indels: 0

DB: 1 Gaps: 0
US-09-837-961-8 (1-1174) x US-08-239-476-28 (1-3522)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
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Db 1 ATGGAAATATATCAAAATCAATCGGTACCTTACAATTTTAAATAATCTCTGAAGTA 60
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QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
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Db 61 GAATACTGAACGAAGAACCCAGCCGCGCTGGACATCAGCCTGAGCCT 120
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QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
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Db 121 ACACGTTTCCTTTTGTAGTGAATTTGTCCAGGTGTGGAGCTTGGTTTGGATTATTGAT 180
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QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80
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Db 181 TTAATATGGGGTTTTATACTCCTTCTGATTGGAGCTTATTCTTTTACAGATTGAACAA 240
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QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
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QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
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QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuAsnLeuArgGlyThrAsn 220
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QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
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Db 661 ACTCGACAATGGCAAGATTCATCATGTTTAGGAGAGATTTACACTTACTGTATTAGAT 720
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QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
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QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGluThrValTrpGlyGlyHisLeu 320
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Db 1021 CCTGGTGGCCCATTTGCAATTCAGATCCAGATCCACGCTCTTTTATCGGACATTAACA 1080
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QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
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QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
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Db 1441 GTTGTAAAGGGCCCGGTTTACGGGAGGAGATATTCTTCGACGAAACAAGTGAGGACCA 1500
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QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
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Db 1501 TTTGCTTATACTATTGTTAATAATATGGAATTAACCCAAAGGATATCGTCAAGAATA 1560
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Db 1561 CGCTATGCTCTACTACAATCTAAGAATTTAGTAAAGTTCAGGTTCAGGTGAACGATTTT 1620
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QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
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Db 1621 GCTGTCAATTTTAAACAAACAATGGATACCGGTGACCCATTAACATTCCAATCTTTAGT 1680
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Db 1681 TAGCAACATTAATAACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGT 1740
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QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
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Db 1801 ACTGCAACATTTGAAGCAGATATGATTTAGAAAGACACAAAAGCGGTGAATGGCTG 1860
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QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
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Db 1861 TTTACTTCTATAACCAATAGGATAAAACAGATGTGACGGATTTATCATATCGATCGA 1920
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QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
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Db 1921 GTGTCCAATTTAGTTACGTATTTATCGGATGAATTTTGTCTGGATGAAGAGCGAGATTTG 1980
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QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
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QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
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Db 2101 ATCCAAGAGGGATGACGTATTTAAAGAAAATACGTCACACATCATCAGGTACCTTTGAT 2160
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QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
Db 2761 ATGATTTCATCGCGCAGATAAAGCGTTTCATAGCATTCGAGAAGCTTATCTGCTGAGCTG 2820
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2821 TCTGTGATTCGGGTGTCATTCGGCTATTTTGAAGAATTAGAAGCGGTATTTTCTACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAspGlyLeu 980
Db 2881 GCATCTCCCTATATGATCGCAGAAATGTCATTAATAATGGTGATTTAATAATGGCTTA 2940
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QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
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QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080
Db 3181 TATCCAAACACACGGTAACGTGAATGATTATCTCGGACTCAAGAAGAATATGAGGGT 3240

QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
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QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
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QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
Db 3481 ACATTCATCGTGACAGCGTGAATTAATCTTCTATGGAGAA 3522

RESULT 15

US-08-598-305A-28
; Sequence 28, Application US/08598305A
; Patent No. 5827514
; GENERAL INFORMATION:
; APPLICANT: BRADFISCH, Gregory A.
; APPLICANT: THOMPSON, Mark
; APPLICANT: SCHWAB, George E.
; TITLE OF INVENTION: No. 5827514el Pesticidal Compositions
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,305A
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,867
; FILING DATE: 06-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA86.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-598-305A-28
Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6049.00 Matches: 1143
Percent Similarity: 97.79% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 26
Query Match: 96.68% Indels: 0

DB: 1 1 Gaps: 0
US-09-837-961-8 (1-1174) x US-08-598-305A-28 (1-3522)
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QY 21 GluileLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
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QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheCysLeuPheAsp 60
DB 121 ACACGTTTCTTGGTGAATTTGTTCAGGTTGGGAGTTGCGGTTGGATTATTTGAT 180
QY 61 LeuileTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuLeuGlnIleGluGln 80
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QY 81 LeuileGluGlnArgileGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
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DB 361 AATGCCAATTAAGGAGAGATGTCGATTTCGATTTCGTAATACAGACGAGCTTAAATA 420
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluileProLeuLeuSerValTrpVal 160
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QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrile 400
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QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
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QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
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QY 761 TyrAsnAlaLysHisGluThrValasnValLeuGlyThrGlySerLeuThrProLeuSer 780
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Db 3481 ACATTTCATCGTGACAGCGTGGGAATTACTTCTTATGGAGAA 3522

Search completed: November 28, 2002, 02:20:26
Job time : 306 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 27, 2002, 20:22:40 ; Search time 485 seconds
(without alignments)
5451.229 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNIQOVCPYNCLNPEV.....IGETGTFIVDSVELLMEE 1174

Scoring table:

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	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-LOPEXT=0 -UNITS=bits -SPART=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCAL=LOCAL -OUTFMT=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6244	100.0	3522	12	Lepidopteran-activ
2	6244	100.0	3522	14	Delta endotoxin ge
3	6244	100.0	3522	19	Plasmid pMVC2243 B
4	6244	100.0	3522	20	Wild-type B.t cryI
5	6244	100.0	3522	22	B. thuringiensis t
6	6244	100.0	4020	12	crYIF gene. Bacil
7	6238	99.9	3522	16	crYIF toxin with l
8	6237	99.9	3522	17	Codon-reworked Cry
9	6049	96.9	3522	16	CryIF/436 chimeric
10	6049	96.9	3522	17	CryIF/436 chimeric
11	6049	96.9	3522	19	Plasmid pMVC2254 c
12	5902	94.5	3444	16	CryIF/cryIA(b) chi
13	5902	94.5	3444	16	CryIF/cryIA(b) chi
14	5902	94.5	3444	17	CryIF/cryIA(b) chi
15	5902	94.5	3444	17	CryIF/cryIA(b) cod
16	5902	94.5	3444	19	Plasmid pMVC2244 c
17	5902	94.5	3444	19	Plasmid pMVC2523 c
18	5879	94.2	3444	20	Plant-optimised cr
19	5879	94.2	3444	22	CryIF/cryIA fusion
20	5674	90.9	3450	16	CryIA(c)/cryIF/cry
21	5674	90.9	3450	17	CryIA(c)/cryIF/cry
22	5674	90.9	3450	19	Plasmid pMVC2239 B
23	5595	89.6	3558	22	B. thuringiensis c
24	5409	86.6	3504	17	CryIF class toxin
25	4815.5	77.1	3531	19	Bacillus thuringie
26	4815.5	77.1	3531	24	DNA encoding B. th
27	4812.5	77.1	3534	19	Bacillus thuringie
28	4812.5	77.1	3534	24	DNA encoding B. th
29	4804.5	76.9	3531	19	Bacillus thuringie
30	4804.5	76.9	3531	24	DNA encoding B. th
31	4745.5	76.0	3534	19	Bacillus thuringie
32	4745.5	76.0	3534	24	DNA encoding B. th
33	4706.5	75.4	3531	19	Bacillus thuringie
34	4706.5	75.4	3531	24	DNA encoding B. th
35	4647.5	74.4	3534	24	DNA encoding B. th
36	4636.5	74.3	3534	19	Bacillus thuringie
37	4391.5	70.3	3629	10	Bacillus thuringie
38	4385.5	70.2	4438	12	Modified CryIA(b)
39	4373	70.0	4999	7	Sequence encoding
40	4346.5	69.6	3582	24	Bacillus thuringie
41	4346.5	69.6	14946	24	Maize ubiquitin pr
42	4346.5	69.6	15503	24	Plasmid pEW3 encod
43	4344.5	69.6	3531	8	Sequence of gene e
44	4342	69.5	3623	9	Sequence encoding
45	4342	69.5	3623	9	Sequence encoding

ALIGNMENTS

RESULT 1
AAQ10182
ID AAQ10182 standard; DNA; 3522 BP.
XX AAQ10182;
AC AAQ10182;
XX 20-MAR-1991 (first entry)
DT
DT
DE Lepidopteran-active toxin D gene.
XX
KW Lepidopteran-active toxin D; pest control; ss.
OS
OS Bacillus thuringiensis PS81L (NRRL B-18484).
XX
XX EP405810-A.
XX
PD 02-JAN-1991.
XX

Qy	561	TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly	580
Db	1681	TACGCAACTATTAAATACAGCTTTTACATTTCCCAATGAGCAGAGTAGTTTCACAGTAGGT	1740
Qy	581	AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal	600
Db	1741	GCTGATACTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTGTAATTTGATTCAGTT	1800
Qy	601	ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu	620
Db	1801	ACTGCAACATTTGAACGCAATATGATTTAGAAAGAGCACAAAAGCGGTGATGCGCTG	1860
Qy	621	PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln	640
Db	1861	TTTACTTCTATAAACCAATAGGATAAACACAGATGTGACGGATTATCATATTGATCAA	1920
Qy	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
Db	1921	GTATCCAATTTAGTGATTGTTTATCAGATGAATTTTGCTGGATGAAGCGGAATTG	1980
Qy	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro	680
Db	1981	TCGGAGAAAGTCAACATCGCAAGCGACTAGTGATGAGCGGAATTTACTTCAAGATCCA	2040
Qy	681	AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrPArgGlySerThrAspIleThr	700
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Qy	721	GluCysTyrProThrTyrIleuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr	740
Db	2161	GAGTGCTATCCAACTGATTATATCAAAAATAGATGAGTGGAAAATTAAACCCCTATACT	2220
Qy	741	ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg	760
Db	2221	CGTTATCAATTAAGAGGTATATCGAGGATAGTCAAGACTTTAGAATCATTTTGTGATCCGC	2280
Qy	761	TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer	780
Db	2281	TATAATGCAAAACACGAAACAGTAAATGTGCTAGGTAACGGTCTTTATGGCCGCTTCA	2340
Qy	781	ValGlnSerProIleargLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr	800
Db	2341	GTCCAAAGTCCAAATCAGAAAGTGTGGAGAACCGAATCGATGCGCGCCACACCTTGATGG	2400
Qy	801	AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis	820
Db	2401	AACTCTGATCAGATTGTCTTCAGACAGCGGGAAAAATGTGCACATCATTCGCCATCAT	2460
Qy	821	PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrpVal	840
Db	2461	TTCTCCTTGGACATTGATGTTGCGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG	2520
Qy	841	IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu	860
Db	2521	ATATTCAAGATTAAAGCGCAAGATGGCCATGCAAGACTAGSAAATCTAGAGTTTCTCGAA	2580
Qy	861	GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrpArg	880
Db	2581	GAGAAACCATTAGTTCGGGGAACACTAGCTCGTGTCAAAAGAGCAGAGAAAAATGCGACA	2640
Qy	881	AspLysArgGluLysLeuGluLeuThrAsnIleValTyrLysGluAlaLysGluSer	900
Db	2641	GATAAACGTGAAAAATTGGAATTGGAACCAAAATTTGTTTATAAGAGGCAAAAGAACTCT	2700
Qy	901	ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla	920
Db	2701	GTAGATGCTTTATTGTAACTCTCAATAATGATCAATTACAGCGGATACGAATATTGGC	2760

QY	921	MetIleHisAlaalaAspLysArgValHisArgIleArgGluAlaTyrIleuProGluLeu	940
DB	2761	ATGATTTCATCGGCAGATAAACGTGTTTCATAGAATTCGGGAACGATATCTTCACAGAGTTA	2820
QY	941	SerValIleProGlyValAsnValaspIlePheGluGluLeuLysGlyArgIlePheThr	960
DB	2821	TCTGGATTCCGGGGTAAATATAGACATTTTCGAAGAATTAAAGGGCGTATTTTCACT	2880
QY	961	AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
DB	2881	GCATTCTTCCTATATGATCGCGAGAAATGTCATTAATAACGGTGATTTCAATAATAGGCTTA	2940
QY	981	SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal	1000
DB	2941	TCATCTGGAACGTCGAAGCGCATGTAGATGTAGAAGACAAACAACACCCGTTCCGGTC	3000
QY	1001	LeuValValProGluTrpGluAlaGluValSerGlnGluValargValCysProGlyArg	1020
DB	3001	CTTGTTGTTCGGGAATGGGAACGAGAGTGTACACAAGAAGTTCTGCTCTCCGGGTCGT	3060
QY	1021	GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle	1040
DB	3061	GGCTATATCTTCGTCACGCGTACAGAGGAGGATATGGAGAAGGTTCCGTAACCATT	3120
QY	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
DB	3121	CATGAGATCGAGAACAATACAGACGAAGTGAAGTTTAGCAACTCGCTAGAGAGGAATC	3180
QY	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly	1080
DB	3181	TATCCAAACAACACGCGTAACGTGTATGATTTACTGCAAAATCAAGAAGAATACGGGGT	3240
QY	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
DB	3241	GGGTACACTCCCGTAATCGTGGATATGACGAACATATAGGAAGCAATCTTCTGTACCA	3300
QY	1101	AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro	1120
DB	3301	GCTGATTATGCGTCAGTCCTATGAAGAAAATCGTATACAGATGACAGAGAGACATCCT	3360
QY	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
DB	3361	TCTGAATCTAACAGAGGATATGGGATTCACACCACTACCAGCTGGCTATGTGCAAAA	3420
QY	1141	GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly	1160
DB	3421	GAATTAGAGTACTTCCAGAAACCGTAAGTATGATTTGAGATCGGAACCGAGGA	3480
QY	1161	ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu	1174
DB	3481	ACATTTCATCGTCAGACGCGTGAATTAATCTCTTATCGAGGAA	3522
RESULT	2		
AAQ47291			
ID	AAQ47291	standard; DNA; 3522 BP.	
XX			
AC	AAQ47291;		
XX			
DT	28-JAN-1994	(first entry)	
XX			
DE		Delta endotoxin gene.	
XX			
KW		Endotoxin; Bacillus; lice; insecticide; sheep; ss.	
XX			
OS	Bacillus thuringiensis PS8II (Clone A).		
XX			
Key		Location/Qualifiers	
FT	mat_peptide	1..3522	
FT		/*tag= a	
FT		/product= delta endotoxin.	
XX			
PN	W09314641-A.		
XX			

PD 05-AUG-1993.
 XX PF 31-DEC-1992; 92WO-US11337.
 XX PR 29-JAN-1992; 92US-0828788.
 XX (MYCO) MYCOGEN CORP.
 XX Hickie LA, Payne J;
 XX WPI: 1993-258266/32.
 DR P-PSDB; AAR39754.
 XX Controlling biting lice on sheep - comprises administering
 PT Bacillus thuringiensis toxins to host
 XX Disclosure; Page 42-43; 64pp; English.
 CC Many strains of Bacillus thuringiensis (B.t) produce insecticidal
 CC delta endotoxins. A number of these endotoxins have been found to
 CC be toxic to Damlinia ovis, the biting louse of sheep. The B.t.
 CC isolates which produce these toxins can be grown and the delta
 CC endotoxin which is produced can be recovered by standard procedures.
 CC The genes encoding these endotoxins can also be transferred to a
 CC suitable host via a recombinant vector and the resulting
 CC transformants used in methods to control lice.
 XX
 SQ Sequence 3522 BP; 1156 A; 589 C; 782 G; 995 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0
 US-09-837-961-8 (1-1174) x AAQ47291 (1-3522)
 QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
 DB 1 ATGGAGAATAATATTCACAAATCAATCGGTACCTTCAATATGTTAAATATCCTGAAGTA 60
 QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 DB 61 GAAATATTAAATGAACAAGAGTACTGCGAGATTACCGTTAGATATATCCCTATCCCTT 120
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 DB 121 ACACGTTTCCTTTTGAGTGAATTTATATTCAGGTGTGGAGTTGCGTTTGGATTATTGAT 180
 QY 61 LeuIleTyrGlyPheIleThrProSerAspTyrSerLeuPheLeuGlnIleGluGln 80
 DB 181 TTAATATGGGGTTTATATCTCTCTGATTTGAGAGCTTATTTCTTTACAGATTGAACAA 240
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
 DB 241 TTGATTTGACAAAGAATAAGAAATTTGGAAGAAAGAACCGGGCAATTACTACATTACGAGG 300
 QY 101 LeuAlaAspSerTyrGluIleThrIleGluAlaLeuArgGluThrGluAlaAsnProAsn 120
 DB 301 TTAGCAGATAGCTATGAATTTATATTTGAAGCACTTAAGAGAGTGGGAAGCAATCCTAAT 360
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
 DB 361 ATGCAACAATTAGGGAAGATGTGGTATTCGATTTCGTTAAATACAGACCGCTTTAATA 420
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 DB 421 ACAGCAATAAATAATTTTACACTTACAGCTTTGAATCCCTTTTATCCGGTCTATGTT 480
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180

DB 481 CAAGCGCGGAATTTACATTTAICACTATTAAAGAGACGCTGATCGTTTGGCAGGGTTGG 540
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuLeuAsnLeuIleHisArg 200
 DB 541 GGACTGGATAGTACTGTTAATAATCATATAATAGATTAAATAATCTTATTCATAGA 600
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 DB 601 TATACGAACATTTGTTGGACACATACAACTAAGGATTAGAAAACCTTAAGAGTACTAAT 660
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
 DB 661 ACTCGACAATGGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTTAGAT 720
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
 DB 721 ATCGTTGCTCTTTTCCGAACACTAGATGTAGAACATATCCAAATCAACGTCATCCCAA 780
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 DB 781 TTAACAGGGAATTTATACAGTTTCAGTAATTCAGAGATTCCTCAGTTTCTGCTAATA 840
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
 DB 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTATGGACTTATG 900
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
 DB 901 AATTCTTTGTTTAACTGAGAGACTGTAGAAAGTCAAACTGTGTGGGAGACACTTA 960
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 DB 961 GTTAGTTCAGAAATACGCTGTTAAACCGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 DB 1021 CCTGTGGCGCCATTGTTGATTCAGATGAGGATCCACGCTCTTTTATCGGACATTATCA 1080
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
 DB 1081 GATCCTGTTTGTTCGAGAGGATTGGAATTCCTCATTTACTTGGGGCTTAGGGGA 1140
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 DB 1141 GTAGCAATTCACAAACTGTTAGACACCAACCCGACCAATTTAGAAATAGTGGACCA 1200
 QY 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyValaProTrpAsnAspTyrSer 420
 DB 1201 GATTCCTAGATGAATCCACCTCAGGATAATAGTGGGACCTTGGAAATGATTATAGT 1260
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
 DB 1261 CATGTATTAAATCATGTTTACATTTGACGATGCCAGTGAGATTTTCAGAAAGTATTCA 1320
 QY 441 TrpArgAlaProMetPheSerTyrThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 DB 1321 TGGAGAGCTCCAAATGTTTTCCTGGAGCACCGCTAGTGCACCCCTACAAATACATTGAT 1380
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
 DB 1381 CGGAGAGGATTACTCAAAATACCAATGTTGTAAGACACATACACTTCCAGTCAGTACTACT 1440
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
 DB 1441 GTTGTAAAGAGGCCCGGGGTTTACGGAGGAGATATTTCTTCGACGAACAAGTGGAGACCA 1500
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
 DB 1501 TTTGCTATACATTGTTGTTAATAATGGCAATTTACCCCAAGGTTATCGTCAAGAAATA 1560
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
 DB 1561 CGCTATGCTCTACTACAAATCTAGAATTTACGTAAACGGTTGACGGTGAACGGATTTT 1620

QY	541	AlaGlyGlnPheAsnLysThrKetaspThrGlyAspProLeuThrPheGlnSerPheSer	560
Db	1621	GCTGGTCAATTTAAACAAACAATGGATACCGGTGACCCATTAAACATTCCAAATCTTTTAGT	1680
QY	561	TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly	580
Db	1681	TACGCAACTATTAAACAGCTTTACATTTCCCAATGCCAGAGTAGTGTTCACAGTAGT	1740
QY	581	AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal	600
Db	1741	GCTGATACTTTTAGTTACGGGATGAAGTTTATATAGACAGATTGAATTGATTCAGT	1800
QY	601	ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu	620
Db	1801	ACTGCACATTTGACACAGAAATATGATTTAGAAAGACAAAAGGCGGTGAATCGCGCTG	1860
QY	621	PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln	640
Db	1861	TTTACTTCTATAAACCAATAGGGATAAAACAGATGTGACGGATTATCATATTGATCAA	1920
QY	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
Db	1921	GTATCCAATTTAGTGGATTGTTTATACAGATGAATTTTCTCGGATGAAAAGCGAGAA	1980
QY	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro	680
Db	1981	TCCGAGAAAGTCAACATCCGAGGCGACTCAGTGATGACCGGAATTTACTTCAAGATCCA	2040
QY	681	AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr	700
Db	2041	AACTTCCAAAGGCATCAATAGCAACATAGACCGTGTGTGGAGAGAAAGTACGGATATTACC	2100
QY	701	IleGluArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp	720
Db	2101	ATCCAAGAGAGATGACGTATTCAAAGAAATATGTCACACTACAGAGTACCTTTGAT	2160
QY	721	GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr	740
Db	2161	GAGTGTATCCAAACGTATTTATATCAAAATAATAGATGAGTCCGAATTAANAACCCATAC	2220
QY	741	ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg	760
Db	2221	CGTTATCAATTAAGAGGGTATATCGAGGATAGTCAAGACTTTAGAAATCTATTGATCCGC	2280
QY	761	TyrAsnAlaLysHisGlnThrValAsnValLeuGlyThrGlySerLeuTyrProLeuSer	780
Db	2281	TATATGCAAAACACGAACACATAATGTGTAGTACGGGTTCTTTATGGCCGCTTTCA	2340
QY	781	ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyr	800
Db	2341	GTCCAAGTCCAATCAGAAAGGTGCGAGAACCGAATCGATCGCGCCACACCTTGAAATGG	2400
QY	801	AsnProAspLeuAspCysSerCysArgaspGlyGluLysCysAlaHisSerHisHis	820
Db	2401	AACTCCGTATCTAGATTGTTCTTCGACAGACGGGAAAAATGTGCACATCATTCGCATCAT	2460
QY	821	PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTyrVal	840
Db	2461	TTCTCCTTGACATGAATGTGGATGTACAGACTTAATAGGAGACTTAGATGATGGGGT	2520
QY	841	IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu	860
Db	2521	ATATTCAAGATTAAAGACGCAAGATGCCATGCAAGACTAGGAAATCTTAGAGTTTTCGAA	2580
QY	861	GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg	880
Db	2581	GAGAAACCAATTAGTCGGGGAACCATAGCTCGTGTGTGAAGAGACAGAGAAAAATGGAGA	2640
QY	881	AspLysArgGluLysLeuGlnLeuGlnThrAsnIleValTyrLysGluAlaLysGluSer	900
Db	2641	GATAACCGTGAANAATGGAAATTTGAACAAATATGTTTATAAAGAGGACAAAGAAATCT	2700

Qy	901	ValaspAlalLeupheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleala	920
Db	2701	GTAGATCGCTTTATTTCGTAAACTCTCAATATGATCATTAACACGCAGATACGAATAATTGCC	2760
Qy	921	MetileHisAlaAlaAspLysArgValHisArgIleAtrgGluaIaTyrlLeuProGluLeu	940
Db	2761	ATGATTCAATCGGCACATAAACGTTCATAGAATCCGGGAAGCGTATCTTCCAGTGTTA	2820
Qy	941	SerVallleProGlylValAsnValasPillePheGluGluLeuLysGlyArgIlePheThr	960
Db	2821	TCTGTGATCCGGGTCTAAATGTAGACATTTTCGAAGAATTAAGAAGCGGTATTTTCACT	2880
Qy	961	AlaPhePheLeuTyrRspAlaArqasnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
Db	2881	GCATCTCTCATTATGATCGGAAGAATGCAATTAAGAAGCGTGATTTCAATAATGGGTTA	2940
Qy	981	SerCysTrpAsnVallysGlyHisValAspValGluGlnAsnAsnHisArgSerVal	1000
Db	2941	TCATGCTGGAACGTGAAGGCGATGTAGATGTAGAAGAACAAACAACCACCGTTCGGTC	3000
Qy	1001	LeuvalValProGluTrpGluAlagluValSerGlnGluValArgValCysProGlyArg	1020
Db	3001	CTTGTTGTTCCGGAATGGGAAGCAGAAGTGTCCACAAGAAGTTCCTGTCTGTCCGGGTCTG	3060
Qy	1021	GlyTyrIleLeuArgValThralTatYrLysGluGlyTyrGlyGluGlyCysValThrIle	1040
Db	3061	GGCTATATCCTTCGTCTCACACGTFACAGAGGAGGATATGAGARAGGTTCGCTAACCAATT	3120
Qy	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
Db	3121	CATGAGATCGAGAACAATACACAGCAACTGAAGTTTAGCAACTCGCTAGAGAGAGAAATC	3180
Qy	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly	1080
Db	3181	TATCCAACACACAGGTACGTGTATGATGATATCTGCAATCAAGARAATACGGGGGT	3240
Qy	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
Db	3241	GCSTACACTTCCCGTAATCGTGGATGATGACGAACAATTTATGAAGCAATTTCTCTGTACCA	3300
Qy	1101	AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro	1120
Db	3301	CGTGATTATGCGTCAGTCTATGAAGAAAATCGTATACAGATGGACGAAAGAGACAATCCCT	3360
Qy	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
Db	3361	TGTGAATCTAACAGAGATATGGGATTACACACACTTACCAGCTGGCTATGTGACAAAA	3420
Qy	1141	GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly	1160
Db	3421	GAATPAGATGACTTCCAGAAAACCGATAGGTATGGATTGAGATCGGAAGAAACGGAAGGA	3480
Qy	1161	ThrPheIleValAspSerValGluLeuLeuMetGluGlu	1174
Db	3481	ACATTATCGTGGACAGCGTGGNAATTACTCCTTATGGAGGAA	3522
RESULT	3		
AAVG2081	ID	AAVG2081 standard; DNA; 3522 BP.	
XX	AC	AAVG2081;	
XX	XX		
XX	XX		
DT	13-JAN-1999	(first entry)	
XX	XX		
DE	DE	Plasmid pMYC2243 Bt endotoxin DNA fragment.	
XX	XX	Bt toxin; lepidoptera; pest; cryIIF; chimeric; core toxin; cryIA(c);	
KW	KW	synergism; plant; primer; endotoxin; ss.	
XX	XX		
OS	XX	Synthetic.	
XX	XX		
PX	PN	US5827514-A.	

PD 27-OCT-1998.
 XX
 XX 08-FEB-1996; 96US-0598305.
 PF
 XX 06-DEC-1994; 94US-0349867.
 PR
 XX 08-FEB-1996; 96US-0598305.
 PR
 XX (MYCO) MYCOGEN CORP.
 PA
 XX Bradfisch GA, Schwab GE, Thompson M;
 PI
 XX WPI: 1998-593944/50.
 DR
 XX P-PSDB; AAW6708.
 DR
 XX
 PT Composition for biological control of lepidopteran pests -
 PT comprising cells expressing two chimeric Bacillus thuringiensis
 PT crystal proteins
 XX
 XX Example 5; Column 53-58; 75pp; English.
 PS
 XX This sequence encodes a Bt endotoxin which is used in a method for
 CC controlling lepidopteran pests. The method involves the use of cells
 CC that express the Bacillus thuringiensis delta-endotoxins cryII chimeric
 CC core toxin-containing protein and CryIA(c) chimeric core toxin-containing
 CC protein in a combination that have synergistically enhanced activity,
 CC against e.g. corn earworm (Heliothis zea).
 XX
 XX Sequence 3522 BP; 1150 A; 601 C; 786 G; 985 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0

US-09-837-961-8 (1-1174) x AAV62081 (1-3522)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
 Db 1 ARGAAAAATATATTCAAAATCAATGGTACCTTACAAATTTGTTAAATAATCCTGAAGTA 60
 Qy 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 Db 61 GAAATACCTGAACGAAGACGACGACCGCGCGCTGGGACATCAGCCTGAGCCTT 120
 Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 Db 121 ACAGCTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTGGGTTGGATTATTGAT 180
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80
 Db 181 TTATATGGGCTTTATPACCTCTTCGATTGGAGCTATTTCCTTTACAGATTGACAA 240
 Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
 Db 241 TTGATTGACAAAGAAATAGAAACATTTGAAAGGAAACCGGCAATTACTACATTACGAGG 300
 Qy 101 LeuAlaAspSerTrpGluIleTrpIleGluAlaLeuArgGluTrpGluAlaAspProAsn 120
 Db 301 TTACGAGATAGCTATGAAATTTATTTAGACCTATGAGAGTGGGAGCAATTCCTAAT 360
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
 Db 361 AATGCACAATTAAAGGAAGATGGCGTATTCGATTATGCTATATACAGAGCCTTAATA 420
 Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 Db 421 ACAGCAATAAATAATTTTACACTTACAAAGTTTGAAGTCCCTCTTTATCGTCTATGTT 480
 Qy 161 GlnAlaAlaAsnLeuHisSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 Db

Db 481 CAAGCGGCGAANTTTACATTTATCACTATTAGAGAGCGGTGATTCGTTGGGCGAGGTTGG 540
 Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
 Db 541 GGACTGGATATAGCTACTGTTAATAATCATTAATAGATTAAATAATCTTATTATCATAGA 600
 Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 Db 601 TATACGAAACATTTGTCACACATACATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
 Qy 221 ThrArgGluTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
 Db 661 ACTCGACATGGCGAAGATTCAATCAGTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
 Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
 Db 721 ATCGTGTGCTCTTTTCCGAACTACGATGTAGAACATATCCAAATTCAAACGTCATCCCAA 780
 Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 Db 781 TTAACAAGGGAATTTATACAAGTTCAAGTAATTGAGGATTCCTCAGTTTCTGCTAATATA 840
 Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
 Db 841 CCTAATGGTTTAAATAGGCGGAATTTGGAGTTAGACGCCCATCTTATGGACTTTATG 900
 Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyClyHisLeu 320
 Db 901 AATCTCTTCTTTGTAAGTGCAGAGACTGTAGAACTCAAACTGTGGGGAGGACACTTA 960
 Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 Db 961 GTATGTTACGAAATACGCGCTGGTAACCGTATATAATTTCCCTAGTTACGGGGCTTCAT 1020
 Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 Db 1021 CCTGGTGGCGCCATTTGGATTGCGAGATGAGATCCACGCTCTTTTATCGGACATTATCA 1080
 Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
 Db 1081 GATCCCTGTTTTGTCGAGGAGGATTGGGAATPCCTCATTTATGTACTGGGGCTTAGGGGA 1140
 Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 Db 1141 GTAGCATTTCAACAAACTGTCAGAACCCACCCGAAACATTTAGAAATAGTGGGACCAT 1200
 Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
 Db 1201 GATTCCTAGATGAAATCCCACTCAGGATATAGTGGGGCACCTTGGAAATGATTATAGT 1260
 Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
 Db 1261 CATGTATTAAATCATGTTACATTTGTACGATGCGCAGGTGAGATTTACGAGGTGATTC 1320
 Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 Db 1321 TGGAGAGCTCCCATGTTCTTTGGACGCGCATGTAGTGAACCCCTACAAATACAAATGAT 1380
 Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
 Db 1381 CCGGAGAGGATTACTCAATACCATTTGGTAAAGCACATACACTTCAGTCAGGTACTACT 1440
 Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
 Db 1441 GTTGTAAAGGGGCGCGGTTTACGGGAGGAGATATTCTTCGACGAAACAAGTGGAGGACCA 1500
 Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
 Db 1501 TTTGCTTATACTATTGTTAATAATGGGCAATTAACCCCAAGGATATCGTGCACAAATA 1560
 Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluAlaPhe 540
 Db 1561 CGTATGCTCTACTACAAATCTAGAAATTTACGTAAACGGTTGCAGGTGACAGGATTTT 1620

QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
DB 1621 GCTGGTCAATTTAAACAAACATGGATACCGGTGACCCATTAACATTCCTCAATTTTAGT 1680
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
DB 1681 TAGCGCAACTATTAAATACAGCTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGGT 1740
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
DB 1741 GCTGTACTTTTAGTTCACGGGAATGAAGTTTATATAGACAGATTTGAAATGATTCCAGTT 1800
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
DB 1801 ACTGCAACATTTGACGACAGAAATGATTTAGAAAGAGACAAAGCGGTGAATGCGCTG 1860
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
DB 1861 TTTACTTCTATAAACCAAAATAGGATATAAACACAGATGTACGGATTATCATATTGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
DB 1921 GTATCCAAATTTAGTGATTTTATCAGATGAATTTGTCTGGATGAAAGCGAGAATTG 1980
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
DB 1981 TCCGAAAGTCAAAACATCGGAAGCGACTCAGTGATGACGGGAATTTACTTCAGATCCA 2040
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700
DB 2041 AACTTCAAGGATCAATAGGAACATAGACCGTGGTGGAGAGGAAGTAGACGATATATACC 2100
QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
DB 2101 ATCCAAAGGAGATGACGTNTTCAAGAAATATGTCACTACACAGTACCTTTGAT 2160
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
DB 2161 GAGTGTATCCAAACGATTTATATCAAAATAAGATAGATGATCGGAATTAACCCATACT 2220
QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
DB 2221 CGTTATCAATTAAGAGGTATATCGAGGATAGTCAAGACTTAGAATCTATTGATCCGC 2280
QY 761 TyrAsnAlaLysHisGlnThrValAsnValLeuGlyThrClySerLeuTrpProLeuSer 780
DB 2281 TATATGCAAAACACGAAACAGTAAATGTGTAGGTACGGGTCTTTATGGCGGCTTTCA 2340
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
DB 2341 GTCCAAAGTCCAATCAGAAGGTGGGAACCGAATCGATGCGCGCACACCTTGAATGG 2400
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
DB 2401 AATCTGTATCTAGATTGTTCTCCGACAGACGGGAAAAATGTGCATCATTCGCATCAT 2460
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
DB 2461 TTCCTCTGGACATTTGATTTGGATGTACAGACTTAAATGAGSACTTAGATGTATGGGTG 2520
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
DB 2521 ATATTCAGATTAAGACGCAAGATGCCATGCAAGACTAGGAATCTAGATTTCTCGAA 2580
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
DB 2581 GAGAAACCATTTAGTCGGGAACACTAGCTCGTGTGAAAGAGCAGAGAAAAATGGAGA 2640
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
DB 2641 GATAACCGTCAAAAAATGGAAATGGAAACAAATATTGTTTATAAAGAGCGAAAAAGATCT 2700

QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
DB 2701 GTAGATGCTTTATTTGTAAACTCTCAATATGATCAATTAACAAGCGGATACGAATATGCC 2760
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
DB 2761 ATGATTCATCGCGCAGATTAACGTGTCATAGAAATTCGGGAAGCGTATCTTCCAGAGTTA 2820
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
DB 2821 TCTGTGATTCGGGTGTAAATGTAGACATTTTCGAAGAATTAAGAGGCGGTATTTTCACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
DB 2881 GCATCTTCTATATATGTCGGAAGATGTCATTAAACCGTGATTTCAATATATGCTTA 2940
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
DB 2941 TCATGCTGGAACGTGAAGGGCATGTAGATGTAGAAGACAAACACACCCGTTCCGGTC 3000
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
DB 3001 CTTGTTGTTCCGGAATCGGAAGCAGAAAGTGTCAAGAAGTTCTGCTCTGTCGGGTCTG 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
DB 3061 GGCTATATCTTCTGCTCAGCGTACAGGAGGGATATGGAGAAGTTGCGTAACCAT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
DB 3121 CATGAGATCGAGAACAATACAGACGAACCTGAAGTTTAGCAACTGCGTAGAAGAGAAGTC 3180
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
DB 3181 TATCCAAACACACGGTAACGTGTATGATTAATGATTAATGCTCAAAATCAAGAAGAATACGGGGT 3240
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
DB 3241 CGGTACACTTCCGTAATCGTGGATATGACGAACCTATGGAAGCAATCTTCTGTACCA 3300
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
DB 3301 GCTGATTATGCTGCTAGCTCTATGAAGAAAAATCGTATACAGATGGAAGAGACAAATCCT 3360
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
DB 3361 TGTGAATCTAACAGAGGATATGGGATTTACACACCACTACCACTGCTATGTGACAAA 3420
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
DB 3421 GAATTAGAGTACTTCCAGAAACCGATAGGTATGGATTGAGATCGAGAACCGAAGGA 3480
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
DB 3481 ACATTCATCGTGCACAGCGTGAATTTACTCTTATGGAGAA 3522
RESULT 4
AA60606
ID AAX60606 standard; DNA; 3522 BP.
XX
AC AAX60606;
XX
DT 27-JUL-1999 (first entry)
XX
DE Wild-type B.t. cryIF toxin gene 811A.
XX
KW Plant-optimised gene; pesticidal toxin; CryIF; CryIaC; CryIc; 158C2c;
KW 31G1a; CryIaB protoxin; insect control; chimeric; ss.
XX
OS Bacillus thuringiensis.
XX
PN W09924581-A2.
XX

PD 20-MAY-1999.
 XX 04-NOV-1998; 98WO-US23457.
 XX 23-OCT-1998; 98US-0178252.
 PR 12-NOV-1997; 97US-0065215.
 PR 02-MAR-1998; 98US-0076445.
 XX (MYCO) MYCOGEN CORP.
 PA Cardineau GA, Narva KE, Stelman SJ;
 PI WPI: 1999-327409/27.
 XX P-PSDB; AAY16792.
 DR Nucleic acids encoding pesticidal proteins, optimized for plant
 XX expression
 PT Disclosure; Page 29-30; 67pp; English.
 PS
 XX The invention relates to nucleic acid sequences, optimised for
 CC expression in plants, that encode: (i) one of the pesticidal toxins
 CC CryIF, CryIAC, CryIAC, 15822c or 31G1a, or (ii) a portion of the CryIab
 CC protoxin. The pesticidal toxins (AAV16790, AAY16792-Y16798) are used for
 CC pest, especially insect control, particularly on plants. The nucleic acid
 CC sequences are used to produce (truncated or chimeric) toxins, and related
 CC fusion genes or proteins, particularly they are used to generate
 CC transgenic plants that show increased resistance to pests. Compared with
 CC wild-type Bacillus thuringiensis sequences, the optimised sequences are
 CC better suited to expression in plants. The present sequence represents a
 CC polynucleotide sequence for a wild-type, full-length B.t toxin gene
 CC designated 81IA.
 XX
 SQ Sequence 3522 BP; 1156 A; 589 C; 782 G; 995 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6244.00 Matches: 1174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-837-961-8 (1-1174) x AAX60606 (1-3522)
 Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrRsoCysLeuAsnProGluVal 20
 Db 1 ATGGAGATATATTCAAATCAATGCGTACCTTACATTTGTTTAAATATCTCTGAAGTA 60
 Qy 21 GlulleuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 Db 61 GAAATATTAATGAAGAAGAGTACTGGCAGATTACCGTAGATATATCTTATCGCTT 120
 Qy 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 Db 121 ACACGTTTCCTTTGAGTGAATTTGTCCAGGTGGGAGTTGGCTTGGATTTATGAT 180
 Qy 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
 Db 181 TTAATATGGGTTTATTAACCTCTCTGATTTGGAGCTATTTCTTTACAGATTGAACAA 240
 Qy 81 LeuIleGluGlnArgIleGluThrLeuCluArgAsnArgAlaIleThrThrLeuArgGly 100
 Db 241 TTGATTTGACAAAGATAGAACAATTTGAAGAAGAACCGGGCAATTTACTACATTTACGAGG 300
 Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 Db 301 TTAGCAGATAGCTATGAAATTTATATTGAACACCTAAGACAGTGGGAAGCAATCCCTAAT 360
 Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
 Db 361 AATGCACAAATTAAGGGAAGATGTGCTATTTCGATTTCGATTATACAGACGAGCTTTAATA 420

QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 DB 421 ACAGCAATAATAATTTTACACTTACAAGTTTGAATCCCTCTTTATCGCTCTATGTT 480
 QY 161 GlnAlaIleAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnClyTrp 180
 DB 481 CAAGCGCGCAATTTACATTTATCACTATTAAAGACGGCTGTATCGTTTGGCGAGGGTGG 540
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
 DB 541 GGACTGGATATAGCTACTGTAAATATCATATATAGATTAAATAATCTTATTCAATAGA 600
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 DB 601 TATACGAAACATTTGTTGGACACATACAAATCAAGGATTAGAAACTTAAGAGGTACTAAT 660
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
 DB 661 ACTCCACATGGCGAAGATTCAATCAGTTAGGACAGATTAAACACTTACTGTATTAGAT 720
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
 DB 721 ATCGTTGCTCTTTTCCGAACTACGATGTAGACATATCCAATTCAAACGCTCATCCAA 780
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 DB 781 TTAACAAGGGAATTTATACAAGTTCAAGTAUTGAGGATCTCCAGTTCTCGCTAATAATA 840
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
 DB 841 CCTAATGGTTTTAATAGGCGGAATTTGGAGTTAGACCGCCCATCTTTATGGACTTAIG 900
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
 DB 901 AATTTCTTTTGTAACTGCAGAGACTCTTAGAAGTCAAACTGTGTGGGAGGACACTTA 960
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 DB 961 GTTAGTTTACGAATAATCGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGCTTCAAT 1020
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 DB 1021 CCTGGTGGCGCATTTGGATTGCAGATGAGATCCACCTCTCTTTTATTCGGACATTATCA 1080
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
 DB 1081 GATCCTGTTTTTGTCCGAGAGGATTTGGGAATCCTCATTTATGTACTGGGCTTAGGGA 1140
 QY 381 ValAlaPheGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 DB 1141 GTAGCATTTTCAACAACTGGTACGAACCCACACCCGAGCATTTAGAAATAGTGGGACCAT 1200
 QY 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyValAlaProTyrAsnAspTyrSer 420
 DB 1201 GATTTCTAGATCAAAATCCCACTCAGGATAATAGTGGGACCTTGGAAATGATTATAGT 1260
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
 DB 1261 CATGTATTAAATCATGTTTACATTTGTACGATGGCCAGGTGAGATTTCAGGAAGTGATTCA 1320
 QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 DB 1321 TGGAGAGCTCCCAATGTTTTCTTGGACGCGGCTAGTGCACCCCTTACAAATACAAATGAT 1380
 QY 461 ProGluArgIleThrGlnIleProLeuValIysAlaHisThrLeuGlnSerGlyThrThr 480
 DB 1381 CCGGAGAGGATTTACTCAATACCATTTGTAAAGACACATACACTTCAGTCAGGTACTACT 1440
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgThrSerGlyGlyPro 500
 DB 1441 GTTGTAAAGAGGCGCGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGACCA 1500
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520

Db 1501 TTTGCTTATACCTATTGTTAATAAATGGCAATACCCAAAGGTATCGTCAAGAATA 1560
 Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
 Db 1561 CGCTATGCCCTCTACTACAACTCTAGAAATTCAGTAAACGGTTGCAAGGTGATTTT 1620
 Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
 Db 1621 GCTGGTCAATTTAACAAAAAATAGGATACCGGTGACCCCAATTAACATTCATCTTTAGT 1680
 Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
 Db 1681 TACGGCAACTATTAAATACAGCTTTTACATTCCTCCCAATGAGCAGAGTAGTTTCACAGTAGT 1740
 Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
 Db 1741 GCTGATACCTTTAGTTACAGGAATGAAGTTTATATAGACAGATTTGAATTGATCCAGTT 1800
 Qy 601 ThrAlaThrPheGluAlaGlnTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
 Db 1801 ACTGCCAACATTTGAACAGCAATATGATTTAGAAAGACACAAAGCGGTGAATCGCGTG 1860
 Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
 Db 1861 TTTACTTCTATRAACCAATAGGATAAACAACAGATGTCAAGGATTTATCATATTGATCAA 1920
 Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGlnLysArgGluLeu 660
 Db 1921 GTATCCAAATTTAGTGATTTGTTTATCAGATGAATTTTGTCTGGATGAAAGCGAATG 1980
 Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680
 Db 1981 TCCGAAAGTCAACATCGGAAGCACTCAGTGATCAGCGGAATTTACTTCAAGATCCA 2040
 Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
 Db 2041 AACTTCAAGGCATCAATAGGCAACTAGACCGTGGTGGAGGAAGTAGTACGGATATTACC 2100
 Qy 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
 Db 2101 ATCCAAGAGGAGATCAGCTATTCAAGAAATTTATGTCACTACCACTACCGTACCTTTGAT 2160
 Qy 721 GluCystyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
 Db 2161 GAGTGTATCCACGATTTTATCAAAATAATAGATGAGTCGGAATTAACACCTATACT 2220
 Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
 Db 2221 CGTTATCAATTAAGAGGGTATATCGAGGATAGTCAAGACTTTAGAAATCTATTGTATCCGC 2280
 Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
 Db 2281 TATATGCCAAACACGNAACAGTAATGTGCTAGGTACGGGTCTTATGGCGGCTTCA 2340
 Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
 Db 2341 GTCCAAAGTCCCAATCAAGAAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTGAATG 2400
 Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
 Db 2401 AATCCTGATCTAGATTGTTCTCGAGAGCGGGAAATGTGCATCATATTTCGATCAT 2460
 Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
 Db 2461 TTTCTCTGGACATGATGTGGTGTACAGACTTAATAGGACTTAGATGTATGGGTG 2520
 Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGluAsnLeuGluPheLeuGlu 860
 Db 2521 ATATTCAAGATTAAAGCGCAAGATGGCCATGCAAGACTAGGAATCTAGAGTTTCTCGAA 2580
 Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysTrpArg 880

Db 2581 GAGAAACCATTAGTCGGGGAAGCACACAGCTAGCTCGTGTGAAAAGACGAGAAAAATGCAGA 2640
 Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
 Db 2641 GATAAAGCTGAATAATGGAATTTGAAACAAATATTTCTTTATAAAGAGGCAAAAGATCT 2700
 Qy 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
 Db 2701 GTAGATGCTTTATTGTAAACTCTCAATATGATCAATTAACAGCGGATACGAATATTGCC 2760
 Qy 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
 Db 2761 ATGATTTCATCGCGCAGATAAAGCTGTTCATAGATTCGCGAGCGTATCTCCAGAGTTA 2820
 Qy 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
 Db 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAAGAATTAAGGGCGGTATTTCACT 2880
 Qy 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
 Db 2881 GCATTCCTCTATATGATGCGAGAAATGTCTATPAAAAACGGTGATTTCAATATGGCTTA 2940
 Qy 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000
 Db 2941 TCATGCTGGAACGTGAAGGCGATGTAGATGTAGAGAACAACAAACACCCGTCCGGTC 3000
 Qy 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
 Db 3001 CTTGTGTTCGGGAATGGGAAGAGAGTGTCACAAGAAGTTCTGTCTGCCGGTCTG 3060
 Qy 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
 Db 3061 GSCATATATCTCTGTCACAGCTACAAAGGAGGATATGGAGAAGTTGCGTAACCAAT 3120
 Qy 1041 HisGluIleGluAsnAsnThrAspCyluLeuLysPheSerAsnCysValGluGluVal 1060
 Db 3121 CATGAGATTCGAGAAACATACAGACCACTGAAGTTTAGCAACTCGGTAGAGAGAGATC 3180
 Qy 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluTyrGlyGly 1080
 Db 3181 TATCCAAACACACGGTAACGTGTAAATGATTAATCTCAATCAAGAGAATACGGGGT 3240
 Qy 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
 Db 3241 CGGTACACTTCCCGTAATCGTGGATATCAGCAAACTATGGAACCAATCTCTGTACCA 3300
 Qy 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
 Db 3301 GCTGATTATGGTCACTCTATGAAGAAAAATCGTATACAGATGGACGAGAGACAACTCT 3360
 Qy 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
 Db 3361 TGTGAATTAACAGAGGATATGGGATTTACACACACTACACAGCTGGCTATGTGACAAA 3420
 Qy 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
 Db 3421 GAATTAGAGTACTTCCCAACCCGATAGGTATGGATGGATGGAGATCGGAGAAACGAAAGGA 3480
 Qy 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174

RESULT 5

AAS00565

ID AAS00565 standard; DNA; 3522 BP.

XX AAS00565;

XX AAS00565;

DT 14-MAY-2001 (first entry)

DE B. thuringiensis toxin gene 81IA (cryIa).

KW Toxin gene 81IA; cryIa; cutworm; pesticide; corn; soybean; canola;

KW Agrotis ipsilon; Agrotis malefida; Porasagrotis gypaetiana; sunflower;
 KW Xylomyges curialis; Tribe Agrotini; Feltia jaculifera; Euxoa sp.; ds;
 KW cotton.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3522
 FT /*tag= a
 FT /product= "B. thuringiensis toxin 81A (CryIa)"
 XX
 PN WO200113731-A1.
 XX
 XX 01-MAR-2001.
 XX
 XX 23-AUG-2000; 2000WO-US23156.
 XX
 XX 23-AUG-1999; 99US-0150319.
 XX
 XX (MYCO) MYCOGEN CORP.
 XX
 XX Stockhoff BA, Conlan C;
 XX
 XX WPI: 2001-211270/21.
 XX P-PSDB; AAU00533.
 XX
 XX Controlling cutworm pests especially black cutworm comprises contacting
 PT the pest with crystal protein CryIF toxin -
 XX
 XX Example 5; Page 42-43; 52pp; English.
 XX
 XX The sequence represents the native polynucleotide of the wild-type, full
 CC length sacillus thuringiensis toxin gene 81A (CryIa). Full-length,
 CC truncated and chimeric CryIF genes and proteins can be used for
 CC controlling cutworm pests, by contacting the pest with a Bacillus
 CC thuringiensis toxin comprising a pesticidal portion of a CryIF toxin.
 CC These genes and proteins are useful for controlling cutworm pests such as
 CC Agrotis ipsilon, Agrotis malefida, Porasagrotis gypaetiana, Xylomyges
 CC curialis, members of the Tribe Agrotini, Feltia jaculifera, Euxoa
 CC messoria, Euxoa scandens, Euxoa auxiliaris, Euxoa detersa, Euxoa
 CC tessellata, Euxoa ochragaster and Peridroma saucia in plants such as
 CC corn, sunflower, soybean, canola and cotton. The plants are transformed
 CC with a polynucleotide encoding a Cry IF protein such that the transformed
 CC plant cells express pesticidal proteins in tissues consumed by the target
 CC pests.
 XX
 XX Sequence 3522 BP; 1156 A; 589 C; 782 G; 995 T; 0 other;

Alignment Scores:

Prod. No.:	0	Length:	3522
Score:	6244.00	Matches:	1174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-837-961-8 (1-1174) x AAS00565 (1-3522)

QY	1	MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal	20
Db	1	ATGGAGAAATATATTCNAATCAATCGGTACCTTCAATGTTTAAATATCTCGAAGTA	60
QY	21	GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu	40
Db	61	GAATATTAATGAAGAAGAAGTACTGGCAGATTACCGGTACATATATCTTATCGCTT	120
QY	41	ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp	60
Db	121	ACAGGTTTCCTTTTGTAGTGAATTTGTCCAGGTCTGGAGTTTCGGTTTGATTTGAT	180
QY	61	LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln	80
Db	181	TTATATGGGGTTTTATTAACCTCTCTGATGGAGCTTATCTTTTACAGATGACAA	240

QY	81	LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly	100
Db	241	TTGATTGAGCAACAATAGAAACATTGGAAGGAACCGGCAATTACTACATTACGAGG	300
QY	101	LeuAlaSpSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn	120
Db	301	TTAGCAGATAGCTATGAAATTTATATTGAAGCAGCTAAGAGAGTGGGAAGCAATTC	360
QY	121	AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle	140
Db	361	AATGCACAATTAAGGAAGATGTCGTATTTCGATTTCCTAATACAGACGACGCTTAA	420
QY	141	ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal	160
Db	421	ACAGCAATAATAATTTTACACTTACAAAGTTTGAATTCCTCTTTATCGGCTATGTT	480
QY	161	GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr	180
Db	481	CAAGCGGCAATTTACATTTATCACTATTAGAGACCTGTATCTGTTGGGAGGTTGG	540
QY	181	GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg	200
Db	541	GGACTGGATATAGCTACTGTTAATAATCAATATAATAGATTATAAATCTTATTATCA	600
QY	201	TyrThrIysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn	220
Db	601	TATACGAACATTTTGGACACATCAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT	660
QY	221	ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp	240
Db	661	ACTCGACATGGGCAAGATTCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT	720
QY	241	IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln	260
Db	721	ATCGTTGCTCTTTTCCGAACTAGCATGTTAGAACAATATCCAAATTCGAACGTCATCC	780
QY	261	LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle	280
Db	781	TTACAGAGGAATTTATACAGTTTCAGATTTCAGGATTCCTCCAGTTTCTGCTAATA	840
QY	281	ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet	300
Db	841	CCTAATGTTTAAATAGSGCGGAATTTGGAGTTTAGACCGCCCATCTTATGGACTTTATG	900
QY	301	AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu	320
Db	901	AATCTTTTGTAACTGCAGAGACTGTTAGAAGTCAAACTGTGCGGAGGACACTTA	960
QY	321	ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn	340
Db	961	GTTAGTTCACGAAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGCTTCAAT	1020
QY	341	ProGlyGlyAlaIleThrPheAlaAspGluAspProArgProPheTyrArgThrLeuSer	360
Db	1021	CCTGTGGCGCCATTTGGATTGCAGATCCAGATCCAGCTCTTTTATTCGACACATTATCA	1080
QY	361	AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly	380
Db	1081	GATCCTGTTTGTCCGAGAGAGATTGGGAATCCTCATTTATGTACTGGGGCTTAGGGGA	1140
QY	381	ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle	400
Db	1141	GTAGCATTTCAACAACTGGTACGAACACACACCCGAACTTTAGAAATAGTGGACCAT	1200
QY	401	AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer	420
Db	1201	GATTCCTAGATGAATCCACCTCAGATAAATAGTGGGACACCTTGGATGATTATAGT	1260
QY	421	HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer	440
Db	1261	CATGTTAATCATGTTACATTTGTACGATGGCCAGGTGAGNTTTCAGGAAGTGATTCA	1320

QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
 Db 1321 TGGAGAGCTCCAATGTTTCTTGAGCGCACCGTAGTGCAACCCCTACAAATCAATGTAT 1380
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
 Db 1381 CCGGAGAGGATTACTCAATACCATGTGTAAAGGACACATACACTTCAGTCAGGTACTACT 1440
 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
 Db 1441 GTGTAAAGAGGCCCGGTTTACGGGAGGAGATATCTTCGACGACACAGTGGAGGACCA 1500
 QY 501 PheAlaTyThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyArgAlaArgIle 520
 Db 1501 TTTGCTTACTATTGTTAATAATAATGGCAATTTACCCCAAGGTATCGTGCAAGAAATA 1560
 QY 521 ArgTyAlaSerThrThrAsnLeuArgIleTyValThrValAlaGlyGluArgIlePhe 540
 Db 1561 CGCTATGCTCTACTACAAATCTAAGAAATTTACGTAAACGGTTGCGAGTGAACGGATTTT 1620
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
 Db 1621 GCTGCTCAATTTACAAACAAATGATACCGGTGACCAATTAACATTCCAATCTTTTAT 1680
 QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
 Db 1681 TACGCAACATTAATACAGCTTTTACATTCCTCCCAATGAGCAGAGTAGTTTCACAGTAGT 1740
 QY 581 AlaAspThrPheSerSerGlyAsnGluValTyIleAspArgPheGluLeuIleProVal 500
 Db 1741 GCTGATCTTTTAGTTACAGGAATGAGTTTATATAGACAGATTTGAAATGATTCACGTT 1800
 QY 601 ThrAlaThrPheGluAlaGluTyAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
 Db 1801 ACTGCAACATTTGAAGCAGATATCATTTAGAAAGGACACAAAGCGGTGATCGCGTG 1860
 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyHisIleAspGln 640
 Db 1861 TTTTACTTCTATAAACCAATAGGGATAAAACAGATGTGACGGATATCATATTGATCAA 1920
 QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 560
 Db 1921 GTATCCAAITTAGTGGAATGTTTATCAGATGAATTTGTCTGGATGAAAGCGGAATG 1980
 QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
 Db 1981 TCCGAGAAAGTCAACATCGCAAGCGCTCAGTGATGAGCGGAATTTACTTCAAGATCCA 2040
 QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyTrpArgLysSerThrAspIleThr 700
 Db 2041 AACTTCAAGGCATCAATAGGCACTAGACCGTGTGAGAGGAAGTACGGATATTACC 2100
 QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyValThrLeuProGlyThrPheAsp 720
 Db 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAATTAATGTCACACTACCGAGTACCTTTGAT 2160
 QY 721 GluCystTyProThrTyLeuTyGlnLysIleAspGluSerLysLeuLysProTyThr 740
 Db 2161 GAGTGTCTATCAACGATTTATATCAAAAAATAGATGATGATGAGTAAATTAACCCCTACT 2220
 QY 741 ArgTyGlnLeuArgGlyTyIleGluAspSerGlnAspLeuGluIleTyLeuIleArg 760
 Db 2221 CGTTATCAATTAAGAGGTATATCGAGGATATGCAAGACTTAGAAATCTATTGATCCGC 2280
 QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTyrrProLeuSer 780
 Db 2281 TATATGCAAAACAGAAACAGTAAATGTGTAGTACGGGTTCTTTATGCGCGCTTTCA 2340
 QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
 Db 2341 GTCCAAAGTCCAAATCAGAAAGTGGAGAACCGAATCATCGCGGCCACACTTGAATGG 2400
 QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820

Db 2401 AATCTGTGATGTAGATTGTTCTCGACAGACGGGAAAAATGTGCATCATTCGCAATCAT 2460
 QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
 Db 2461 TTTCTCTTGACATGTATGTTGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2520
 QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
 Db 2521 ATATTCAAGATTAAACGCAAGATGCCATGCAAGACTTAGGAAATCTAGAGTTTCTCGAA 2580
 QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
 Db 2581 GAGAAACCATTAGTCGGGAGCACACTAGTCTCGTGTGAAAGAGCAGAGAAAAATGGACA 2640
 QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyLysGluAlaLysGluSer 900
 Db 2641 GATAAACGTTGAAAAATTTGGAATTTGAAAAAATAATTTGTTATAAAGAGCAAAAGAACT 2700
 QY 901 ValAspAlaLeuPheValAsnSerGlnTyAspGlnLeuGlnAlaAspThrAsnIleAla 920
 Db 2701 GTAGATGCTTTTATTGTAACCTCTCAATATGATCAATTAACAAGCGGATACGAAATATTGCC 2760
 QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyLeuProGluLeu 940
 Db 2761 ATGATTCAATGCGCAGATAAACGTTCTCATACAAITCGGSAAGCGTATCTTCCAGATTA 2820
 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
 Db 2821 TCTGTGATTCGGGTGTTAAATGTAGACATTTTCGAAGAAATTAAGAAGCGGTATTTTCACT 2880
 QY 961 AlaPhePheLeuTyAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
 Db 2881 GCATTTCTTATATGATGCGGAAATGTCAATTAATAACGGTGATTTCAATATGGCTTA 2940
 QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000
 Db 2941 TCATGCTGCAAGCTGAAAGGCGCATGTAGATGTAGAAGAACAAACACCCGTTCCGGTC 3000
 QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
 Db 3001 CTTGTGTGTCGGAATGGGAAGCAGAAAGTGTCAAGAAGATTCGTCTCTCGGTCGT 3060
 QY 1021 GlyTyIleLeuArgValThrAlaTyLysGluGlyTyTrpGlyGluGlyCysValThrIle 1040
 Db 3061 GGTATATCTTCTGTCACACGTCACAGGAGGAGATGAGAGAGGTTTGGTAACCAT 3120
 QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
 Db 3121 CATGAGATCGAGAACATACAGACGAAGTGAAGTTTACCACTGCGTAGAGAGGAAGTC 3180
 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyThrAlaAsnGlnGluGluTyTrpGly 1080
 Db 3181 TATCCAAACACACGTAACGTGTAATGATATACGAAATCTGCAAAATCAAGAAGAAATCGGGGT 3240
 QY 1081 AlaTyThrSerArgAsnArgGlyTyTrpAspGluTrpTyTrpGlySerAsnSerValPro 1100
 Db 3241 CGGTACACTTCCGTAAATCGTGGATATGACGAAACTTTTGAAGCAATTTCTTCTATCCA 3300
 QY 1101 AlaAspTyAlaSerValTyGluLysSerTyThrAspGlyArgArgAspAsnPro 1120
 Db 3301 GCTGATTATGCTGCTATGAGAAAAATCGTATATACAGATGGACGAGAGACAACTCT 3360
 QY 1121 CysGluSerAsnArgGlyTyTrpGlyAspTyThrProLeuProAlaGlyTyTrpValThrLys 1140
 Db 3361 TGTGAATCTAACAGAGGATATGGGATTAACACACACTACCGAGTGGTGTATGTGACAAAA 3420
 QY 1141 GluLeuGluTyTrpPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
 Db 3421 GAATTAGAGTACTTCCCAAGAACCGATTAAGGTATGGATTGATGCGAGAAACCGAAGGA 3480
 QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174

Db 3481 ACATTCATCGTGACAGCGTGAATTAACCTCTATGAGGAA 3522

RESULT 6

AAQ14648

ID AAQ14648 standard; DNA; 4020 BP.

XX AC

XX AAQ14648;

XX DT

31-JAN-1992 (first entry)

XX DE

XX cryIF gene.

XX KW

Insecticide; Lepidoptera control; ss.

XX OS

XX Bacillus thuringiensis.

XX FH

Key Location/Qualifiers

XX CDS

478..4002

XX FT

/*tag= a

XX RBS

467..471

XX FT

/*tag= b

XX PN

WO9116434-A.

XX PD

31-OCT-1991.

XX XX

15-APR-1991; 91WO-US02560.

XX PR

16-APR-1990; 90US-0510327.

XX PA

(ECOG-) ECOGEN INC.

XX PI

Gawron-Burke CM, Chambers JA, Gonzalez JM;

XX DR

WPI; 1991-339822/46.

XX DR

P-PSDB; AAR14856.

XX XX

Purifying and isolating CRY-I type genes - from novel *Bacillus*

XX PT

thuringiensis strain as insecticides

XX PS

Claim 1; Fig 1A-E; 100pp; English.

XX CC

The sequence is that of the cryIF gene which was isolated from

XX CC

Bacillus thuringiensis strains EG6345 and EG6346 obtd. from a maize

XX CC

grain dust sample. The toxin produced by the cryIF gene can be used

XX CC

in insecticide compns. to control lepidoptera, esp. *Ostrinia*

XX CC

nubilalis, *Spodoptera exigua*, and *Plutella xylostella*. See also

XX CC

AAQ14649.

XX SQ

Sequence 4020 BP; 1349 A; 636 C; 870 G; 1165 T; 0 other;

Alignment Scores:

Pred. No.: 0

Length: 4020

Score: 6244.00

Matches: 1174

Percent Similarity: 100.00%

Conservative: 0

Best Local Similarity: 100.00%

Mismatches: 0

Query Match: 100.00%

Indels: 0

DB: 12

Gaps: 0

US-09-837-961-8 (1-1174) x AAQ14648 (1-4020)

Qy 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20

|||||

478 ATGAGGAATAATTCAAAATCAATGCGTACCTTACAAATGTTTAAATAATCCTGAAGTA 537

|||||

Qy 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40

|||||

538 GAAATATTAATGAAGAAGAAGTACTGGCAGATTACCGTTAGATATATCCTTATCGCTT 597

|||||

Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60

|||||

598 ACACGTTCCCTTTGAGTGAATTTGTTCCAGGTGGGAGTTGCGTTTGATTTTGTAT 657

|||||

Qy 61 LeuIleTyrGlyPheIleThrProSerAspTyrPsrLeuPheLeuLeuGlnIleGln 80
|||||
Db 658 TTAATATGGGTTTATAACCTCTTCATGGAGCTTATTTCTTTACAGATTGAACAA 717
Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
|||||
Db 718 TTGATTGACRAAAGAAATAGAAACATTGGAAGGAAACCGGCAATTACTACATTACGAGG 777
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrGluAlaAsnProAsn 120
|||||
Db 778 TTAGCAGATAGCTATGCAATTTATATTGAACACTTAAGAGAGTGGGAAGCAAACTCTAAT 837
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
|||||
Db 838 AATGCACAATTAAGGGAAGATGTCGATTTCGATTTCGTAATACAGACACGCGCTTTAATA 897
Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
|||||
Db 898 ACAGCAATAAATAATTTTACACTTACAAGTTTTTGAATCCCTCTTTATCGGCTATGTT 957
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180
|||||
Db 958 CAAGCGGGAATTTACATTTATCACTATTAGAGAGCGCTGATCGTTTGGCAGGTTGG 1017
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
|||||
Db 1018 GGACTGGATATAGCTACTGTTAATAATCATTAATATAGATTAAATAATCTTTATTCTAGA 1077
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
|||||
Db 1078 TATACGAACATTTGTCACACATACAAATCAAGGATTAGAAACTTAAGAGGTACTAAT 1137
Qy 221 ThrArgGlnTyrAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
|||||
Db 1138 ACTCGACAATGGCAAGATTCAATCAGTTTAGAGAGAGATTTAAACACTTACTGTATTAGAT 1197
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
|||||
Db 1198 ATCGTTGCTCTTTTCCGAACCTACCATGTTAGAACATATCCAAATTCAAACGTCATCCCAA 1257
Qy 261 LeuThrArgGluIleTyrThrSerValIleGluAspSerProValSerAlaAsnIle 280
|||||
Db 1258 TTAACAAGGGAATTTATACAGTTTCAGTAATGAGGATTCCTCCAGTTCTTCTAATAATA 1317
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
|||||
Db 1318 CCTAATGTTTAAATAGGCGGAATTTGGAGTAGACCGCCCATCTTATGGACTTTATG 1377
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTyrGlyGlyHisLeu 320
|||||
Db 1378 AATCTTTGTTGTAACCTGCAGAGACTGTTAGAACTCAAACTGTGGGGAGGACACTTA 1437
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
|||||
Db 1438 GTTAGTTACGAATAACGCTGTAACCGTATAAAATTTCCCTAGTAGGGGCTTCTCAAT 1497
Qy 341 ProGlyGlyValIleTyrIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
|||||
Db 1498 CTTGGTGGCGCCATTTGGATTGCAGATGAGGATCCACGCTCTTTTATCGGACATTATCA 1557
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
|||||
Db 1558 GATCTGTTTTTGTCCGAGGAGGATTTGGGAATCTCATATTATGTACTGGGCTTAGGSGA 1617
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
|||||
Db 1618 GTAGCATTTCAACAACACTGGTACGAACCCACACCCCAACATTTAGAAATAGTGGGACATA 1677
Qy 401 AspSerLeuAspGluIleProProGlnAsnSerGlyValaProTyrAsnAspTyrSer 420
|||||
Db 1678 GATTCTCTAGATGAATCCCACTCAGGATTAATAGTGGGACCTTGGATGATATAGT 1737
Qy 421 HisValLeuAsnHisValThrPheValArgTyrProGlyGluIleSerGlySerAspSer 440

Db 1738 CATGATTAATAATCATGTTACATTTGTACGATGCCAGCTGAGATTTTCAGAACTGATCA 1797
 QY 441 TTPArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 450
 Db 1798 TGGAGACTCCAAATGTTTCTTGGACGACCGTAGTSCAACCCCTACAANATCAATGAT 1857
 QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
 Db 1858 CCGAGAGAGATTACTCAAAATACCAATCGTAAAGACACATACATCTCAGTCAGGTACTACT 1917
 QY 481 ValValArgGlyProGlyPheThrGlyAspIleLeuArgGlyThrSerGlyGlyPro 500
 Db 1918 GTTGTAGAGGCCCGGGTTTCGGGAGAGATATCTTCGACGACACAGTGGAGGACCA 1977
 QY 501 PheAlaThrIleValAlaHisIleAsnGlyGlnLeuProGlnArgThrArgAlaArgIle 520
 Db 1978 TTTGCTTATACATATGTTATATATAATAGGCAATTAACCCCAAGGTATCGTGCAGAATA 2037
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleThrValThrValAlaGlyGluArgIlePhe 540
 Db 2038 CGCTATGCCCTACTACAAATCTAAGAAATTTACGTACGGTTGCAGGTGACCGGATTTT 2097
 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
 Db 2098 GCTGCTCAATTTAAACAAACAATAGGATACCGGTGACCCATTAACTTCCAAATCTTTAGT 2157
 QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
 Db 2158 TACCGCACTATTATACAGCTTTTACATTCCTCAATGAGCAGAGTAGTTTTCACAGTAGT 2217
 QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
 Db 2218 GCTGATACCTTTAGTTCAGGGAATGAAGTTTATATACACAGATTTTGAATTTGATTCAGTT 2277
 QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
 Db 2278 ACTGCAACATTTGAGCAGAAATAGTTTAGAAGAGACAAAGGCGTGAATGCCGCTG 2337
 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
 Db 2338 TTCTACTTATACCAAAATAGGATAAACACAGATGTACGGATTTATCATATGTATCAA 2397
 QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
 Db 2398 GTATCCCAATTTAGTGGATTTGTTATCATGATGAATTTGCTGGATGAAACGCGAGAATTG 2457
 QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
 Db 2458 TCCGAGAACTCAACATCGACGCGACTCAGTGTATGAGCGGAAATTTACTTCAAGATCCA 2517
 QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
 Db 2518 AACTTCAAGGATCAATAGTCAACTAGACCGTGGTGGAGGGAAGTACGGATATATACC 2577
 QY 701 IleGlnArgGlyAspAspValPheLysGluAsnThrValThrLeuProGlyThrPheAsp 720
 Db 2578 ATCCAAAGAGAGATGAGTATTCAAGAAATATATGTCACACTACCGAGGTACCTTTGAT 2637
 QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
 Db 2638 GAGTGTATCCCAACGATTTTATATCAAAAATAGATGAGTCAAGTAAATTAACACCTATACT 2697
 QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
 Db 2698 CGTTATCAATTAAGAGGGTATATCGAGGATAGTCAAGACTTAGAAATCTATTGATCCGC 2757
 QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlnGlyThrGlySerLeuTrpProLeuSer 780
 Db 2758 TATATGCAAAACACGAAACAGTAAATGCTAGGTACGGTTCTTTATGCGCCCTTCA 2817
 QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800

Db 2818 GTCCAAAGTCCCAATCAGAAAGTGTGGAGAACCAATCGATCGCGCCACACCTTGAATGG 2877
 QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
 Db 2878 AATCTGATCTAGATTGTCTTCAGAGACGGGAAAAAATGTGCACATCAATTCGCATCAT 2937
 QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
 Db 2938 TTTCTCTTGGACATTTGATTTGGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2997
 QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
 Db 2998 ATATTCAAGATTAAAGACCAAGATGCCATGCAACACTAGGAAATCTAGAGTTTCTCGAA 3057
 QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysTrpArg 880
 Db 3058 GAGAAACCAATTAGTTCGGGAGACACTAGCTCGTGTGAAAAGACGAGAAAAAATGGAGA 3117
 QY 881 AspLysArgGluLysLeuGluLeuThrAsnIleValTyrLysGluAlaLysGluSer 900
 Db 3118 GATAAACCTGAAAATTCGAATTTGGAACAATATTGTTTATAAGAGACCAAAATCT 3177
 QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
 Db 3178 GTAGATGCTTTTATTTGTAACCTCTCAATGATCAATTACAGCGGATACGAATATTGCC 3237
 QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
 Db 3238 ATGATTTCATCGCGCAGATAAACGTTTCATAGAATTCGGAGACGATATCTTCCAGAGTTA 3297
 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
 Db 3298 TCTGTGATTCGGGTGTTAAATGTAGACATTTTCGAAGAATTTAAAGGGCGTATTTCCTACT 3357
 QY 961 AlaPheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
 Db 3358 GCATCTTCTCTATGATCGGAGAAATGTCATTAACACGGTGATTTCAATATGGCTTA 3417
 QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
 Db 3418 TCATGCTGGAACGTGAAGGCGATGTAGATGTAGAAGAACAAACACACCGTTCGGTC 3477
 QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
 Db 3478 CTGTGTTTCCGGAATGGGAGACAGAGTGTCAAGAAAGTTTCGTGTCTGTCGGGTCTGT 3537
 QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
 Db 3538 GCGTATATCTTCGTGTACACCGTACAGGAGGAGATATGAGAGAGTTGCGTAACCAT 3597
 QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
 Db 3598 CATGAGATCGAGAACAAATACAGCAACTGAAGTTTAGCACTGCGTAGAAGAGAGTCT 3657
 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
 Db 3658 TATCCAAACACACCGGTAAACGTTAATGATATATACUGCAAAATCAAGAAATACCGGGGT 3717
 QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluTyrThrTyrGlySerAsnSerSerValPro 1100
 Db 3718 GCGTACACTTCCCGTAATCGTGGATATGCAAACTATGGAAGCAATTTCTTCTGTACCA 3777
 QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
 Db 3778 GCTGATTTATCGCTCAGTCTATGAAGAAAAATCGTATACAGATGGCAGAGACAAATCCT 3837
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
 Db 3838 TGTGAATCTAACAGAGGATATGGGATTTACACACCACTACCACTGGCTGTGTGTGACAAA 3897
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
 Db 3898 GAATTAGAGTACTTCCAGAAACCGATAGGTATGGATTGAGATCGGAGAAACGGAAGA 3957

QY 1161 ThrPheLeValAspSerValGluLeuLeuLeuMetGluGlu 1174
 Db 3958 ACATTTCATGCTGGACGCTGGAATTACTCTTATGGAGGAA 3999

RESULT 7

AA05270
 ID AAT05270 standard; DNA; 3522 BP.

AC AAT05270;
 DT 23-JUN-1996 (first entry)

XX
 DE CryIF toxin with limited codon rework coding sequence.

XX Delta endotoxin; crystal protein; chimeric toxin; codon rework;
 KW insecticide; pesticide; Pseudomonas fluorescens;
 KW biological control agent; transgenic plant; insect resistance;
 KW disease resistance; crop improvement; protein engineering; ss.
 XX Bacillus thuringiensis.

XX Key Location/Qualifiers
 FH 1..3522
 FT mat_peptide /tag= a
 FT /product= cryIF_sequence_with_codon_rework
 FT /note= "plasmid pMYC243 sequence"

PN W09530753-A1.

PD 16-NOV-1995.

PF 05-MAY-1995; 95WO-US05431.

PR 06-MAY-1994; 94US-0239476.

XX (MYCO) MYCOGEN CORP.

PI Schwab GE, Thompson M;

XX WPI; 1995-404120/51.

DR P-ESDB; NAR84735.

XX Nucleic acid encoding chimeric Bacillus thuringiensis
 PT delta-endotoxin - providing increased expression in Pseudomonas,
 PT esp. for control of lepidoptera pests.

XX Example 5; Page 45-47; 91pp; English.

XX The sequence represents the cryIF toxin sequence with codon rework,
 CC engineered using oligonucleotide primers H, I, J and K (see
 CC AAT05262-T05265), and present in plasmid pMYC2523. This codon
 CC reworked sequence can be used in the construction of chimeric
 CC toxins, which are expressed in Pseudomonas fluorescens better than
 CC native delta endotoxins. Host cells expressing the chimeric gene
 CC and producing chimeric toxin may be used in insecticide
 CC compositions. Where the host cells are plant cells, the gene confers
 CC insect resistance to the transformed plant.

XX Sequence 3522 BP; 1149 A; 600 C; 788 G; 985 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 3522
 Score: 6238.00 Matches: 1173
 Percent Similarity: 99.91% Conservative: 0
 Best Local Similarity: 99.91% Mismatches: 1
 Query Match: 99.90% Indels: 0
 DB: 16 Gaps: 0

US-09-837-961-8 (1-1174) x AAT05270 (1-3522)

QY 1 MetGluAsnAlaGluAsnGlyCysValProTyrAsnCysLeuAsnProGluVal 20
 Db

Db 1 ATGGAATAAATATTCAAATCAATGCGTACCTTCAATTTGTTTAAATAATCTCCTGAAGTA 60
 QY 21 GluLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspLeuSerLeuSerLeu 40
 Db 61 GAAATACGACGAAGACGACGACGCGCGCTGGACATCAGCCTGAGCCTT 120
 QY 41 ThrArgPheLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheasp 60
 Db 121 ACACGTTTCCCTTTGAGTGAATTTGTTCCAGGTGTGGAGTTGCGTTTGGATTATTGAT 180
 QY 61 LeuLeuTrpGlyPheLeuThrProSerAspTrpSerLeuPheLeuGluGluGlu 80
 Db 181 TTAATATGGGGTTTATAACTCTTCGATGGAGCTTATTTCTTTTACAGATTGAACA 240
 QY 81 LeuLeuGluArgGluGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
 Db 241 TTGATTGACAAAGAATAAACAATTGGAAGGAACCGGGCAATTACTACATTACGAGGG 300
 QY 101 LeuAlaAspSerTyrGluLeuLeuGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 Db 301 TTAGCAGATAGCTATGAAATTTATTTGAAGCACTAAGAGAGTGGGAAGCAATCTAAT 360
 QY 121 AsnAlaGluLeuArgGluAspValArgGluPheAlaAsnThrAspAlaLeuIle 140
 Db 361 AATGCACAAATTAAGGGAAGATGCGTATTCGATTTGCTAATACAGACGACGCTTAATA 420
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 Db 421 ACAGCAATAAATAATTTTACACTTACAGTTTGAATTTTGAATCCCTCTTTATCGTCTATGTT 480
 QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 Db 481 CAAGCGCGAATTTACATTTATCACTATTAAAGAGCGCTGATCGTTTGGCGAGGTTGG 540
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuLeuAsnLeuIleHisArg 200
 Db 541 GGACTGGATATAGCTACTCTTAAATATCATTAATAGATTAAATAATCTTATTATACAGA 600
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 Db 601 TATACGAAACATTTGTTGGACATACATAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
 Db 661 ACTCGACAATGGCAAGATTCATCACTAGTTAGAGAGATTAACTTACTTACTTATAGAT 720
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerGln 260
 Db 721 ATCGTTGCTCTTTTCCGAACACGATGTAGAACATATCCCAATCAAAACGTCATCCCAA 780
 QY 261 LeuThrArgGluLeuThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 Db 781 TTRACAGGGGAATTTATACAGTTCAAGTANTGAGGATTCCTCCAGTTCTCCTAATAATA 840
 QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetaspPheMet 300
 Db 841 CCTAATAGGTTTAAATAGGCGGAATTTGGAGTTAGACCCGCCCTCTTATGAGCAATTATG 900
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
 Db 901 AATTCCTTTGTTGTAACGACAGAGCTGTAGAACTCAACGTCGTTGGGAGGACACTTA 960
 QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 Db 961 GTTAGTTTACGAAATACGCGTGTAAACCGTATAAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 Db 1021 CCTGGTGGCGCCATTTGGATTGCAGATGAGATCCACGCTCTCTTTTATCGGGACATTATCA 1080
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
 Db 1081 GATCCCTGTTTGTCCGAGGAGATTGGGAATCTCATATTGTTACTGGGGCTTTAGGGGA 1140

QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
DB 1141 GTAGCATTTTCAACAACTGTTACGAACACACACCGAACATTTAGAAATAGTGGACCAT 1200
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
DB 1201 GATTCCTCTAGATGAATCCACCTCAGGATAATAGTGGGCACCTTGGAAATGATTAGT 1260
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
DB 1261 CATGTATTAAATCATGTTACATTTGTACGATGGCCAGGTGAGATTTTCAGGAAGTGATTC 1320
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
DB 1321 TGGAGAGCTCCCAATGTTTCTTGGAGCACCTAGGATAATAGTGGGCACCTTGGAAATGAT 1380
QY 461 ProGluArgIlePheGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
DB 1381 CCGGAGAGATTACTCAATACCATTTGGTAAAGACATACATTCAGTCAGTACTACT 1440
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
DB 1441 GTTGTAAAGAGGCCCGGTTTACGGGAGGAGATATCTTCGACGACACAGTGGGAGCCA 1500
QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
DB 1501 TTTGCTTATACATTTGTTAATAATAATGGCAATTACCCCAAAAGGTATCGTGCAGAATA 1560
QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
DB 1561 CGCTATGCTCTACFACAAATCTAAGAATTTAGCTACGGTTGCAGGTGAACGGATTTT 1620
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
DB 1621 GCTGTGCAATTTAAACAAACAATGGATACCGGTGACCCATTCACATTCCTTTAGT 1680
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
DB 1681 TAGCGAACTATTAAATACAGCTTTTACATTCCTCAATCGCCAGCAGTAGTTTCACAGTAGT 1740
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
DB 1741 GCTGATACATTTTAGTTCAGGAGATGAGTTTATATAGACAGATTTGAAATGATTCAGTT 1800
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
DB 1801 ACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGAGCACAAAGCGCTGAATGCGCTG 1860
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
DB 1861 TTTACTTCTTATAAACCAATAGGGATAAAAGGGATGTGACGAGTATCATATTGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
DB 1921 GATCCAAATTTAGTGATTTGTATTCAGATGAAATTTGTCTGGATGAAAGCGAGAAATG 1980
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680
DB 1981 TCCGAGAAAGTCAAAACATCGGAGGACATCAGTGATGACCGGAATTTACTTCAAGATCCA 2040
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
DB 2041 AACTTCAAGAGGATCAATAGGCACTAGACCGTGGTGGAGAGGAAGTACCGGATATTACC 2100
QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
DB 2101 ATCCAAAGAGGAGATGACGTATTCAAGAAAAATATGTTCACACTACCGAGTACCTTTGAT 2160
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
DB 2161 GAGTGCTATCCAACTATTATATCAAAAAATAGATGAGTCGAAATTTAAACCCCTATACT 2220

QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
DB 2221 CGTTATCAATTAAGAGGATATATCGAGGATAGTCAAGACTTAGAAATCTATTGATCCGC 2280
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
DB 2281 TATAATGCAAAACACGAAACAGATAATGTCTAGGTACGGTCTCTTTATGCCGCTTCA 2340
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
DB 2341 GTCCAAAGTCCAAATCAGAAAGTGTGGAGAACCGAATCGATCGCGCCACACCTTGAATGG 2400
QY 801 AspProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
DB 2401 AATCCYGAICTAGATTGTTCTCTCAGAGACGGGAAAAAATGTGCACATCATTCGCATCAT 2460
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
DB 2461 TTTCTCTTGGACATTTGATGTGGATGTACAGACTTAAATCAGGACTTAGATGTATGGGTG 2520
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
DB 2521 ATATTCAAGATTAAAGACGCAAGATGCCATGCAAGACTTAGGAAATCTAGAGTTTCTCGAA 2580
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880
DB 2581 GAGAAACCATTTAGTCGGGAGGACACTAGCTCGTGTGAAAGACGACAGAAAAATGGAGA 2640
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
DB 2641 GATAAACGTTGAAAAATTTGGAATTTGAAACAAATATTGTTTATAAGAGGCAAAAGATCT 2700
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
DB 2701 GTAGATGCTTTATTGTTAACTCTCAATATGATCAATTAACAAGCGGATAGAAATTTGCC 2760
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
DB 2761 ATGATTTCATCGGCAGATAAACGTTTCATAGATTTCCGGAACGCTATCTTCCAGAGTTA 2820
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
DB 2821 TCTGTGATTTCCGGGTATAATGTAGACATTTTCGAAAGATTAAGAGGCGCTATTTTCACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
DB 2881 GCATTTCTTCTATGATGCGAGAAATGTCATTAACACGGTATTTCAATAATGCTTA 2940
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000
DB 2941 TCATGCTGCAACGTTGAAAGGCGCATGTAGATGTAGAAGACAAACACACCGTTCCGGTC 3000
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
DB 3001 CTGTGTGTTTCCGGAATGGGAAGCAGAGTGTCAAGAAAGTTCTGTCTGTCCGGTCTGT 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGlyGlyTyrGlyGluGlyCysValThrIle 1040
DB 3061 GCGTATATCTTCTGTTGTCACGCTACAGGAGGATATGGAGAGGTTTGCCTTAACCAT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
DB 3121 CATGATCGAGAACAAATACACGCACTGAACTTAGCACTGGTGAAGAGGAAGTTC 3180
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyGly 1080
DB 3181 TATCCAAACAAACACGTAACGTTAATGATTATCTGCAAAATCAAGAAATACGGGGT 3240
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100
DB 3241 GCGTACACTTCCGTAATCGTGATATGCAAACTTATGGAAGCAATTTCTTCTGTACCA 3300
QY 1101 AlaAspTyrAlaSerValTyrGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120

Db	3301	GCTGATTATGCGTCAGTCTATGAGAAAAATCGTATACAGATGGACGAGACAAATCCT	3360
Qy	1121	CysGluSerAsnArgGlyTVrGlyVAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
Db	3361	TGTGAATCTTACAGAGAGATATGGGGATTACACACCACTACCACTGGCTATGTGACAAA	3420
Qy	1141	GluLeuGluTyrPheProGluThrAspLysValTrrPileGluIleGlyGluThrGluGly	1160
Db	3421	GAATTACAGTACTTCCAGAAACCGATAGGTATGGATTGAGATCGGNAACCGAAGGA	3480
Qy	1161	ThrPheIleValaspSerValGluLeuLeuLeuMetGluGlu	1174
Db	3481	ACATTCATCGTGGACACGCGTGAATTACTCCTTATGGAGAA	3522
RESULT 8			
AA	18722		
ID	AA18722	standard; DNA; 3522 BP.	
XX			
AC	AA18722;		
XX			
DT	18-AUG-1996	(first entry)	
XX			
DE		Codon-reworked CryIF toxin gene from pMYC2243.	
XX			
KW		CryIF; crystal protein; chimeric toxin; protoxin; pMYC2243;	
KW		delta-endotoxin; codon usage; splice overlap extension;	
KW		mutagenesis; chimeric gene; fusion protein; Pseudomonas fluorescens;	
KW		KryIA(b); KryIA(c); synergy; Lepidoptera; insect;	
KW		biological control agent; transgenic plant; insect resistance;	
KW		crop improvement; ss.	
XX			
OS		Bacillus thuringiensis.	
XX			
PN		U55508264-A.	
XX			
PD		16-APR-1996.	
XX			
PF		06-DEC-1994; 94US-0349867.	
XX			
PR		06-DEC-1994; 94US-0349867.	
XX			
PA		(MYCO) MYCOGEN CORP.	
XX			
PI		Bradfish GA, Schwab GE, Thompson M;	
XX			
WPI		WPI: 1996-208745/21.	
DR		P-PSDB; AAR94914.	
DR			
PT		Compan. for controlling lepidopteran pests - comprises CryIF and	
PT		CryIA(c) chimeric core toxin-contg. proteins.	
XX			
PS		Example 5; Column 53-56; 59pp; English.	
XX			
CC		This sequence encodes a Bacillus thuringiensis CryIF delta-	
CC		endotoxin. A gene from pMYC2047 has been subjected to splice	
CC		overlap extension to alter codons in a limited region in the cryIF	
CC		fragment to favor G or C in the wobble position, to improve	
CC		expression in Pseudomonas spp. Correct clones are identified by	
CC		PCR using primers P and Q (AAR18717-18), and the resulting clone is	
CC		pMYC2243. The cryIF fragment may be fused with cryIA(b) and/or	
CC		cryIA(c) fragments to give fusion proteins by recombinant DNA	
CC		methods. The resulting chimeric genes may be cloned in a	
CC		Pseudomonas fluorescens lactose-inducible strain to produce	
CC		chimeric toxins. The toxins, when combined in synergy, have	
CC		unexpectedly enhanced toxicity to lepidopteran pests. P.	
CC		fluorescens or B. thuringiensis cells expressing the genes may be	
CC		used as insect biological control agents, or transgenic plants	
CC		expressing the genes may become resistant to insect attack.	
XX			
SQ		Sequence 3522 BP; 1150 A; 602 C; 785 G; 985 T; 0 other;	
Alignment Scores:			

Pred. No. :	0	Length:	3522
Score:	6237.00	Matches:	1173
Percent Similarity:	99.91%	Conservative:	0
Best Local Similarity:	99.91%	Mismatches:	1
Query Match:	99.89%	Indels:	0
DB:	17	Gaps:	0
US-09-837-961-8 (1-1174) x AAT18722 (1-3522)			
Qy	1	MetGluAsnAsnIleGlnAsnGlnCysValProGlyrAsnCysLeuAsnAsnProGluVal	20
Db	1	ATGGAATATATATTCAAATCAATGCGTACCTTACAAATGTTTAAATATCTCTGAAGTA	60
Qy	21	GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu	40
Db	61	GAATACTGAACGAAGAACGACGACCGCGCGCTCGCGCTGCACATCAGCCTGAGCCTT	120
Qy	41	ThrArgPheLeuLeuSerGluPheValProGlyValGlyValalalpheGlyLeuPheAsp	60
Db	121	ACCGTTTCCTTTTGAGTGAATTTGTTCACAGGTGCGAGTTTCGGATTTTCGATTTATTTGAT	180
Qy	61	LeuIleTyrGlyPheIleThrProSerAspTyrSerLeuPheLeuLeuGlnIleGluGln	80
Db	181	TTRATATGGGTTTATACTCCTCTGATTTGGAGCTTATTTCTTTTACAGATTGAACAA	240
Qy	81	LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly	100
Db	241	TTGATTGAGCAAGAATAGAAACATTTGAAAGGAACGGGCAATTACTACATTACGAGGG	300
Qy	101	LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrPgluAlaAsnProAsn	120
Db	301	TTAGCAGATAGCTATGAAATTTATATTGAAGCACTTAAGAGGTGGGAACAAATCCTAAT	360
Qy	121	AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle	140
Db	361	AATGCACAATTAAGGAAGATGCGTATTCGATTTGCTAATACAGACGACGCTTTAATA	420
Qy	141	ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal	160
Db	421	ACAGCAATAATAATTTACATTACATTCACAGTTTGAATCCCTCTTTATCGGCTCATGTT	480
Qy	161	GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr	180
Db	481	CAGCGCGGAATTTACATTTATCCTATTAGAGAGCGCTGTATCGTTTGGCAGGGTGG	540
Qy	181	GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg	200
Db	541	GGACTCGATATAGCTACTGTGTAATAATCATTTATAATAGATTAAATAAATCTTATTTCATAGA	600
Qy	201	TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn	220
Db	601	TATACGAACATTTGTTGGACATACAAATCAAGGATTAGAAACATTAAGAGGTTACTAAT	660
Qy	221	ThrArgGlnTyrAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp	240
Db	661	ACTCGCAATGGGCAAGATTCAATCAGTTTAGSAGAGATTAAACACTTACTGTATTAGAT	720
Qy	241	IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln	260
Db	721	ATCGTTGCTCTTTTCCGAACACAGATGTTAGAACATATCCAAATTCAAACGTCATCCCAA	780
Qy	261	LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle	280
Db	781	TTAACAAGGGAATTTATACAGTTTCAGTAATTGAGGATTTCCAGTTTCTGCTAATATA	840
Qy	281	ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet	300
Db	841	CCTAATPGTGTTTAATAGGCGGAAATTTGGAGTTAGACCGCCCATCTTATGAGCTTTATG	900
Qy	301	AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTyrPglYgIyHisLeu	320
Db	901	AATCTCTCTTTGTAACTGCAGAGACTGTAGAAGTCAAACTGTGTGGGAGGACACTTA	960

Alignment Scores:

QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
DB 961 GTTAGTTCAGAAATACGGCTGTAACCGTATAAAATTCCTAGTTACGGGTCITCAAT 1020
QY 341 ProGlyGlyAlaIleThrPheAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
DB 1021 CCTGGTGGCGCCATTTGGATTCAGATGAGGATCCACGCTCTTTTATCGGACATTATCA 1080
QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
DB 1081 GATCCTGTTTTCTCGAGAGAGATTGGGAATCCATATGCTAGTGGGCTTAGGGGA 1140
QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
DB 1141 GTAGCATTTCAACAACTGGTACGACACACACCCGAACATTTAGAAATAGTGGACCAATA 1200
QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
DB 1201 GATTCCTAGATGAATCCCACTCAGGATAATAGTGGGGCACCTTGGGAATGATTATAGT 1260
QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
DB 1261 CATGTATTAAATCATGTTACATTGTCAGTGGCAGGTGACATTTTCAGAAAGTGATTCA 1320
QY 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
DB 1321 TGGAGAGCTCCAATGTTTTCTTGGACGCCCTAGTGCACCCCTACAAATACAATTGAT 1380
QY 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrPro 500
DB 1381 CCGGAGAGATTACAAATACCATTTGGTAAAGACACATACACTTCAGTCAGGTACTACT 1440
QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
DB 1441 GTTGTAAAGAGGCCCGGGTTTACGGGAGAGATATTCCTCGACGACACAGTGGAGGACA 1500
QY 501 PheAlaThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
DB 1501 TTTGCTTTACTATTGTTAAATAAATGGCAATTTACCCCAAGGTATCGTGCAAGAAATA 1560
QY 521 ArgTyrAlaSerThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
DB 1561 CGCTATGCTCTACACAAATCTAGAAATTTACGTAAACGGTTGCGAGGTGAACGGATTTT 1620
QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
DB 1621 GCTGTGCAATTTAACAACAATATGATACCGGTGACCCATTAACATTCCTCAATTTTAGT 1680
QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
DB 1681 TACGCAACTATTAAATACAGCTTTTACATTCCTCAATGAGCCAGATAGTTTCACAGTAGT 1740
QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
DB 1741 GCTGATATTTTAGTTCAGGAATGAGTTTATATAGACAGATTTGAAATGATTCCAGTT 1800
QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
DB 1801 ACTGCAACATTTGAAGCAGATATGATTTAGAAAGAGCACAAAAGCGGTGATCGCGTG 1860
QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
DB 1861 TTTACTCTTAATAACCAATAGGATAAACAACAGATGTGACGGATTTATCAVATTGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
DB 1921 GTATCCAAATTTAGTGGATGTTTATCAGATGAATTTTCTCGGATGAAAGCGGAAATG 1980
QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
DB 1981 TCCGAGAAAGTCAACATGCGAGGACTCAGTGTATGAGCGGAATTTACTTCAAGATCCA 2040
QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700

DB 2041 AACTTCAAGGCATCATAGGCACTAGACCGTGGTGGAGAGAAGTACGGATATATACC 2100
QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
DB 2101 ATCCAAGAGGAGATCAGCTATTCAAGAAAAATTATGTACACACTACCGGTACTTTTGTAT 2160
QY 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLysLeuLysProTyrThr 740
DB 2161 GAGTGTATCCCAACGATTATATCAAAAAATAGATGAGTCGAAATATAAACCCCTACT 2220
QY 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
DB 2221 CGTTATCATTTAAGAGGGTATATCGAGGATAGTCAACACTTAGAAATCTATTTGATCCGC 2280
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
DB 2281 TATAATGCAAAACACGAAACAGTAATGTCTAGGTACGGTCTTTATATGGCGGCTTCA 2340
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
DB 2341 GTCCAAAGTCCCAATCAGAAAGTGTGGAAACCGAATCGATGGCGCCACACTTGAATGG 2400
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
DB 2401 AATCCTGATCTAGATTGTTCTCGAGAGCGGGAATAATGTGCACATCATTCGCATCAT 2460
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
DB 2461 TTCTCCTTGACATGATGTTGGATGTACAGACTTAAATGAGGACTTAGATGTATGGGTG 2520
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
DB 2521 ATATTCAAGATTAAACGCAAGATGGCCATGCAAGACTAGGAATCTAGAGTTTCTCGAA 2580
QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
DB 2581 GAGAAACCATTAGTCGGGGAACCACTAGCTCGTGTGAAAGAGCAGAGAAAAATGAGCA 2640
QY 881 AspLysArgGluLysLeuGluLeuThrAsnIleValTyrLysGluAlaLysGluSer 900
DB 2641 GATAACCGTGAATAATTTGGAATTTGGAACAAATATTGTTATAAGAGGCCAAAGAATCT 2700
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
DB 2701 GTAGATGCTTTTATTGTTAACTCTCAATATGATCAATTAACAAGCGATACGAAATATGCC 2760
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
DB 2761 ATGATTCATCGGCACATAAACGCTGTTTCATAGAAATTCGGAAGCGTATCTTCCAGTTA 2820
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
DB 2821 TCTGTGATTCGGGTGTAATGTAGACATTTTCGAGAAATTTAAAAGGCGTATTTTCACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
DB 2881 CCAATCTCTTATATGATCGCGAATAATGTCAATTAACGCGGTGATTTCATTAATGGCTTA 2940
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnAsnHisArgSerVal 1000
DB 2941 TCATGCTGAACGCTGAAGGCGCATGTAGATGTAGAAAGCAACAAACACCCGTTCCGGTC 3000
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
DB 3001 CTTGTGTTCCGGAATGGAAAGCAGAGTGTACAAAGAGTTCGTTCTGTCTGTCGGGTCT 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
DB 3061 GGCATATATCCTTCGTGTGCACAGCGTACAGGAGGATATGAGAGAGGTTCGGTAACCAT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluGluVal 1060

Db 3121 CATGAGATCGAGACAAATACAGACGAAGTGAAGTTTACCAACTCGCTAGAGAGGAGATC 3180
 QY 1061 TyrProAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
 Db 3181 TATCCAAACACACGGTACGCTGTATGATATATCTGCAATCAAGAGATACGGGGT 3240
 QY 1081 AlaTyrThrSerArgAsnAsglyTyrAspGluThrTyrGlySerAsnSerValPro 1100
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 QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
 Db 3301 GCTGATTATCGGTCAGTCTATGAGAAAATCGTATACAGATGAGAGAGACAATCCT 3360
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
 Db 3361 TGTGAATCAACAGAGGATATGGGATACACCACTACAGCTGGCTATGTGCAAAA 3420
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
 Db 3421 GAATTAGAGTACTTCCAGAACCGATAGAGTATGAGATGAGATCGGAGAAACGGAAGA 3480
 QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
 Db 3481 ACATTCATCGTGGACACGGTGAATTAATCTCTTATGGAGGAA 3522
 RESULT 9
 AAT05250
 ID AAT05250 standard; DNA; 3522 BP.
 XX AC AAT05250;
 XX DT 27-MAY-1996 (first entry)
 DE CryIF/436 chimeric toxin coding sequence.
 KW Delta endotoxin; crystal protein; chimeric toxin; insecticide;
 KW pesticide; pseudomonas fluorescens; biological control agent;
 KW transgenic plant; insect resistance; disease resistance;
 KW crop improvement; protein engineering; ss.
 XX OS Bacillus thuringiensis.
 XX FH Key Location/Qualifiers
 FT mat_peptide 1..3522
 FT /tag= a
 FT /product= cryIF/436_chimeric_toxin
 FT /note= "plasmid pMYC2254 sequence"
 XX W09530753-A1.
 XX 16-NOV-1995.
 XX 05-MAY-1995; 95WC-US05431.
 XX 06-MAY-1994; 94US-0239476.
 XX (MYCO) MYCOGEN CORP.
 XX PI Schwab GE, Thompson M;
 XX WPI; 1995-404120/51.
 DR P-PSDB; AAR84732.
 XX Nucleic acid encoding chimeric Bacillus thuringiensis
 PT delta-endotoxin - providing increased expression in Pseudomonas,
 PT esp. for control of lepidoptera pests.
 XX Claim 10; Page 56-57; 91pp: English.
 XX The sequence represents the cryIF/436 chimeric toxin
 CC coding sequence of plasmid pMYC2254. The chimeric toxin is
 CC expressed in Pseudomonas fluorescens better than native

CC delta endotoxins. Host cells expressing the chimeric gene and
 CC producing chimeric toxin may be used in insecticide compositions.
 CC Where the host cells are plant cells, the gene confers insect
 CC resistance to the transformed plant.
 XX Sequence 3522 BP; 1140 A; 606 C; 795 G; 981 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 3522
 Score: 6049.00 Matches: 1143
 Percent Similarity: 97.79% Conservative: 5
 Best Local Similarity: 97.36% Mismatches: 26
 Query Match: 96.88% Indels: 0
 DB: 16 Gaps: 0
 US-09-837-961-8 (1-1174) x AAT05250 (1-3522)
 QY 1 MetGluAsnAspIleGluAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
 Db 1 ATGGAAATATATTCARAAATCAATCGTACCTTACAATGTTTAAATATCTCGAATA 60
 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 Db 61 GAAATACTGACGAAAGAACGACGACCGCGCTGGACATCAGCCTGAGCCT 120
 QY 41 ThrArgPheLeuLeuSerCiuPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 Db 121 ACACGTTTCCTTTTGGTGAATTTGTCAGGTGGGAGTGGCTTTGGATATTATGAT 180
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGluIleGluGln 80
 Db 181 TTAATATGGGGTTTATAACTCTTCTGATGGAGCTTATTTCTTACAGATTGAACA 240
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
 Db 241 TTGATTGACAAAGAAATAGAAACATTGGAAGAAACCGGCAATTAATACAGAGCGCTTAA 300
 QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120
 Db 301 TTACAGATAGCTATGAATTTATTTATGAGACACTAAGAGAGTGGAGCAATCTAAT 360
 QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
 Db 361 AATGCACAATTAAGGAGAGATGCGGTATTCGATTGCTAATACAGAGCGCTTAAATA 420
 QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
 Db 421 ACAGCAATAAATAATTTTACACTTACAAGTTTGAATCCCTCTTTATCGGCTATGTT 480
 QY 161 GlnAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
 Db 481 CAAGCGCGCAATTTACATTTATCACTATTAGAGAGCGCTGTATCGTTTGGCAGGTTGG 540
 QY 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuHisArg 200
 Db 541 GGACTGGATATAGCTACTCTTTAATATCAATTAATAGATTAATAAATCTTATTCATAGA 600
 QY 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
 Db 601 TATACGAAACATTGTTTGGACACATACATCAAGGATTAGAAAACCTTAGAGGTACTAAT 660
 QY 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
 Db 661 ACTCGACAATGGCAAGATTCAATCAGTTTAGAGAGATTTAACACTTACTGTATTAGAT 720
 QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
 Db 721 ATCGTTGCTCTTTTCCGAACTACCATGTTAGAACAATATCCCAATTCACACGTCATCCAA 780
 QY 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
 Db 781 TTAACAAGGAAATTTATACAAAGTTCAGTAAATGAGGATCTCCAGTTCCTGCTAATAATA 840

QY 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
 DB 841 CCTAATGGTTTAAATAGCGCGGAAATTGGAGTTAGCCGCCCATCTTATGGACATTATG 900
 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320
 DB 901 AATTCCTTTGTTGTAACTGCGAGAGACTGTTAGAAGTAAACTGCTGGGGAGGACACTTA 960
 QY 321 ValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
 DB 961 GTTAGCTTCAGCAATACCGGTGTACCGTATACCGTATAAATTTCCCTAGTTACGGGGCTTCAAT 1020
 QY 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
 DB 1021 CCTGGTGGCGCATTTGGATTGCAGATGAGGATCCAGTCCTTTTATCGGACATTATCA 1080
 QY 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
 DB 1081 GATCCTGTTTTGTCGAGGAGGATTTGGGAATCCATCTATATGTACTGGGGCTTAGGGGA 1140
 QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
 DB 1141 GTAGCATTTTCACAACTGTGTACAGACACACACCCGAAACATTTAGAAATAGTGGGACCATTA 1200
 QY 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
 DB 1201 GATTCCTCTAGATGAATCCCACTCAGGATAATAGTGGGACACCTTGGAAATGATTATAGT 1260
 QY 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
 DB 1261 CATGTATTAAATCATGTGTACATTTGTACGATGGCCAGGTGAGATTCAGGAAGTGATTCATCA 1320
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 QY 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
 DB 1441 GTTGTAAAGGCGCGGGTTTACGGGGAGAGATATTCGACGAGCAACAAGTGGAGGACCA 1500
 QY 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
 DB 1501 TTTGCTTATATTGTTAAATAAATGGCAATTTACCCCAAGGTATCGTCCAAAGATA 1560
 QY 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyLeuArgIlePhe 540
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 QY 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
 DB 1621 GCTGGTCAATTTACAAACCAATGGATACCGGTACCGCATTAACATTCATCTTTTATG 1680
 QY 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
 DB 1681 TACGCAACTATTATACAGCTTTTACATTCCTCAATGACCCAGAGTAGTTTCACAGTAGT 1740
 QY 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
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 QY 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
 DB 1801 ACTGCACATTTGAGCAGAGATATGATTTAGAAAGAGACACAAAAGCGCGGTGAATCGCGTG 1860
 QY 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
 DB 1861 TTTACTTCTATAACCAATAGGATTAACACAGATGTGACGGATTATCATATCCATCGA 1920
 QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660

DB 1921 GFGTCCCAATTTAGTTACGTATTTATTCGGATGATTTTGTCTCGATCAAAAGCGAGNATG 1980
 QY 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
 DB 1981 TCCGAGAAAGTCAACACATCGGAAGGAGCTCAGTGATGACGCAATTTACTCCAAGATTCA 2040
 QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
 DB 2041 AATTTCAAGACATTAAATAGGCACCAACGCTGGGTGGGGCGGAAGTACAGGGATTAC 2100
 QY 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
 DB 2101 ATCCAAGGAGGGAGTACGTATTTAAGAAATTAAGTACGTACACACTATCAGGTACCTTTGAT 2160
 QY 721 GluCysTyrProThrTyrIleLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
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 QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
 DB 2401 AATCCTGACTTAGATTGTTCGTAGGAGTGGAGAAAAGTGTGCCCATCATTCGGCATCAT 2460
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 QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
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 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
 DB 2821 TCTGTGATTCGGGTGTCAATCGCGCTATTTTGAAGAATTAGAAGGCGGTATTTTCACT 2880
 QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
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 QY 981 SerCysTrpAsnValLysGlyPheValAspValGluGluGlnAsnAsnHisArgSerVal 1000
 DB 2941 TCCGCTGGAACGTAAGAGGCGATGTAGATGAGAAGCAACAAACACCCGCTCGGTC 3000
 QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020


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Db 3001 CTTGTTTCCGGAATGGGAGCAGAGTGTCTACAGAGTTCGTCTCTCGGTCCG 3060
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DB 3061 GGCATATCTCTGCTCACAGCGTACAGGAGGGATATGGAGAGGTTCGGTAACCAT 3120
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
DB 3121 CATGAGATCGAGAACATAACAGACGAACCTGAAGTTTAGCAACTGTCTAGAAGAGGA 3180
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyGly 1080
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DB 3481 ACATTCATCTGTGGACAGCGTGAATTAATCTCTCTATGGAGAA 3522
RESULT 10
AAT18702
ID AAT18702 standard; DNA; 3522 BP.
XX
AC AAT18702;
XX
DT 18-AUG-1996 (first entry)
XX
DE CryIF/436 chimeric toxin gene from pMYC2254.
XX
KW CryIF; CryIA(c); CryIA(b); crystal protein; chimeric toxin;
KW protoxin; pMYC2254; delta-endotoxin; chimeric gene; fusion protein;
KW Pseudomonas fluorescens; synergy; Lepidoptera; insect;
KW biological control agent; transgenic plant; insect resistance;
KW crop improvement; ss.
XX
OS Bacillus thuringiensis.
XX
FH key Location/Qualifiers
FT mat_peptide 1..1803
FT /tag= a
FT /note= "CryIF toxin gene fragment"
FT 1804..3444
FT /tag= b
FT /note= "CryIA(c)/CryIA(b) 436 protoxin gene fragment"
XX
US508264-A.
XX
PN 16-APR-1996.
XX
PD 06-DEC-1994; 94US-0349867.
XX
PR 06-DEC-1994; 94US-0349867.
XX
PA (MYCO ) MYCOGEN CORP.
XX
PI Bradfish GA, Schwab GE, Thompson M;
XX
DR WPI; 1996-208745/21.

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DR P-PSDB; AAR94908.
XX
Compn. for controlling lepidopteran pests - comprises CryIF and
CryIA(c) chimeric core toxin-contg. proteins.
XX
Claim 7; Column 71-74; 59pp; English.
XX
This sequence encodes a Bacillus thuringiensis chimeric CryIF/436
delta-endotoxin. The toxin contains a full toxin portion of cryIF
and a heterologous protoxin segment derived from cryIA(c)-cryIA(b)
toxin 436. The sequence is constructed by substitution of 436
protoxin module for the cryIA(b) protoxin fragment in pMYC2523
(AAT18723). The 436 protoxin sequence (AAR94911) consists of cryIA(c)
sequence except at the very C-terminus. Protoxin DNA is amplified
by PCR with primers F (AAT18708) and M (AAT18719), using plasmid
pMYC467 as a template. A 3-piece ligation is set up with SpeI-PvuII
toxin DNA and SpeI-BstEII vector DNA from pMYC2523 and PvuII-BstEII
PCR protoxin module DNA. Correct plasmids are identified by PCR
using primers F and G (AAT18709). The resulting chimeric gene may be
cloned in a Pseudomonas fluorescens lactose-inducible strain to
produce a chimeric toxin. The toxin, when combined with another
chimeric toxin in synergy, has unexpectedly enhanced toxicity to
Lepidopteran pests. P. fluorescens or B. thuringiensis cells
expressing the gene may be used as an insect biological control
agent, or a transgenic plant expressing the gene may become resistant
to insect attack.
XX
SQ Sequence 3522 BP; 1140 A; 606 C; 795 G; 981 T; 0 other;
Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6049.00 Matches: 1143
Percent Similarity: 97.79% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 26
Query Match: 96.88% Indels: 0
DB: 17 Gaps: 0
US-09-837-961-8 (1-1174) x AAT18702 (1-3522)
QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
DB 1 ATGGAAATAATATTCAAAATCAATGCGTACCTTCAATGTTTAAATTAATCCTGAAGTA 60
QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
DB 61 GAAATACTGACGAAGAAGACGACGACCGCCGCTGCGCTGACATCAGCCTGAGCCTT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
DB 121 ACACGTTTCCITTTGAGTGAATTTCTCCAGGTGTGGAGTTCGTTGGATTATTGAT 180
QY 61 LeuIleTyrGlyPheIleThrProSerAspTyrSerLeuPheLeuGluIleGluGln 80
DB 181 TTAATATGGGGTTTATAACTCCTTCTGATTGGAGCTTATTTCTTTACAGATTGAACA 240
QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrLeuArgGly 100
DB 241 TTGATTGACCAAGAAAGTAACATTTGGAAGGAAACCGGCAATTACTACATTAGAGGG 300
QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTyrGluAlaAsnProAsn 120
DB 301 TTAGCAGATAGCTATGAAATTTATATTCAAGCACTAAGAGAGTGGGAAGCAATCCTAAT 360
QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
DB 361 AATGCACAAATTAAGGGAGATGTCGATTTCGATTTCGTAATACAGACGACGCTTTAATA 420
QY 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
DB 421 ACAGCAATAATAATTTTACACTTACAAAGTTTGAATFCCCTCTTTATCCGCTATGTT 480
QY 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTyr 180

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Db 481 CRAAGCGCGAATTACATTTATACATTAATTAAGACAGCGCTGTATCGTTGGCGAGGTTGG 540
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GCAGTGGATATAGCTACTGTTAATAATCATATTAATAGATTAATAAATCTTATTCATAGA 600
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TATACGAAACATGTTTGGACACATACATCAAGTCAAGGATTAGAAACCTTAAGAGGTACTAAT 660
Qy 221 ThrArgGluTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
Db 661 ACTCGAATAGGGCAAGATTCATACAGTTAGGAGAGATTTACACACTTACTGTATTAGAT 720
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
Db 721 ATCGTTGCTCTTTTCCGAACTACGATGTTAGAACATATCCAAATTCACACGTCATCCCAA 780
Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
Db 781 TTAACAAGGGAATTTATACAAAGTTCAGTAATAGGATTCCTCAGTTCTGCTAATATA 840
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProPheHisLeuMetAspPheMet 300
Db 841 CTTAATGGTTTTAATAGGCGGAATTTGGAGTAGACCGCCCACTTATGAGACTTTATG 900
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
Db 901 AATTCITTTGTTGTAATCGACAGACTGTTAGAGTCAAACTGTGTGGGAGGACACTTA 960
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
Db 961 GTTAGTTCACGAATACGGCTGTACCGTATACCGTATAAAATTCCTAGTTACGGGCTTCAT 1020
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheTyrArgThrLeuSer 360
Db 1021 CTTGTTGGCGCCCACTTGGATTCAGATGAGGATCCACGTCCTTTTATCGGACATTATCA 1080
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
Db 1081 GATCTGTTTTTGTCCGAGGAGATTGGGAATCCTCATATGTAAGTGGGCTTAGGGGA 1140
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
Db 1141 GTAGCATTTCAACAACCTGGTACGACACACACCGCAACATTTAGAAATAGTGGGACATA 1200
Qy 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyValaProchProAsnAspTyrSer 420
Db 1201 GATTCCTAGATGAATCCCACTCAGGATATATAGTGGGCACTTGGATGATTATAGT 1260
Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGlyIleSerGlySerAspSer 440
Db 1261 CATGTATTAAATCATGTTTACATTTGTACCATGGCCAGGTGAGATTTTCAGGAAGTGATCA 1320
Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
Db 1321 TGGAGAGTCCAAATGTTTCTTGGACGCCCTAGTAGTGCACCCCTACAAATACAAATGAT 1380
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCGGAGAGATTACTCAATATACATTTGGTAAAGACATACACTTCAGTCAGGTACTACT 1440
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
Db 1441 GTTGTAAAGAGGCCCGGGTTTACGGGAGAGATATTTCTTCGACGACAAAGTGGAGACCA 1500
Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGluArgTyrArgAlaArgIle 520
Db 1501 TTTGCTTATACATTGTTTAAATAATGGGCAATTTACCCCAAGGTATCTGTCAGAATA 1560
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 CCTATGCCCTCTACTACAATCTAAGAAATTTACGTAAACGGTTGCAGGTGAACGGATTTT 1620

Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAATTTTAAACAAAACATGGATACCGGTGACCATTAACATTCCTCAATCTTTAGT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TAGGCAACTATTAAATACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTTCACAGTAGGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACCTTTAGTTTACGGGAATGAAGTTTATATAGACAGATTGAAATTCATTCCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAACAGAAATATGATTTAGAAAGACACAAAGCGGTGAATGGCGTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTATRAACCAATAGGGATAAANAACAGATGTGACGGATTATCATATCGATCGA 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTGTCCAAATTTAGTTTACGTATTATCGGATGAATTTTGTCTGGATGAAAGCGAGAATTG 1980
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
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Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700
Db 2041 AATTTCAAAGACATTAATAGGCAACCAACGCTGGTGGGCGGGAAGTACAGGATTAAC 2100
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
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Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
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Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
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Db 2401 AATCTCTGACTTAGATTGTTCTGTAGGATGGAGAAAGTGTGCCCATCATTCGCATCAT 2460
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
Db 2461 TTCTCTTATAGACATTGATGTAGATGTACAGACTTAAATGAGGACCTAGGTGTATGGTG 2520
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
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Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
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Db 481 CAAAGCGGGAATTTACATTTATCATATTAAAGAGACGCTGTATPCGTTTGGGCGAGGTTGG 540
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Db 541 GGACTGGATATACCTACTGTTAATAATCATTAATAAGATTAAATAATCTTATTCATAGA 600
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TATACGAACATTTGTTGGACACATACATCAAGGATTAGAAAACCTTAGAGGTACTAAT 660
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrValLeuAsp 240
Db 661 ACTCGACATGGCGAGATTCATCAATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
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Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProTrpAsnAspTyrSer 420
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Qy 441 TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
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Db 1441 GTTGTAAAGAGGCGCGGTTTACGGAGAGAGATATTCTTCGAGGAACAAGTGGAGGACCA 1500
Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
Db 1501 TTTGCTTATCTATTCTTAAATAATGGCAATTTACCCCAAGGATCGTGCAGAAATA 1560
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAAAGGTTTCAGGTGAAACGGATTTT 1620

Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGGTCAATTTAAACAAACATGGATACCGGACCCCAATTAACATTCCAATCTTTTAGT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TAGCGAACATTAATATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTACAGTAGGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATACTTTTAGTTTCAGGAATGAAGTTTATATATACAGAGATTTGAATGATTCAGT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAACAGAAATGATTTAGAAAGACACAAAGGGGTGAATGCGCTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
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Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTCTCCATTTAGTTACGTATTTATCGGATGAATTTTGTCTGGATGAAAGCGAGAATTG 1980
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro 680
Db 1981 TCGGAAAGATCAACATCGAAGCAGCTCAGTGATGAACGCAATTTACCCAGAGTCA 2040
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
Db 2041 AATTTCAAAGACATTAATAGGCAACAGACGTGGTGGGCGGAAGTACAGGATTAAC 2100
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAGGAGGGATCACGTATTTAAGAAATATAGTCACTACATCAGGTACTTTGAT 2160
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTGTATCCCAACATATTTGTATCAAAAATATCGATGAATCAAAATTAAGACGCTTACC 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTATCAATTAAGAGGTTATATCGAAGATAGTCAAGACTTAGAATCTATTTAATTCGC 2280
Qy 761 TyrAsnAlaLysHisGlnThrValAsnValLeuGlyThrClySerLeuTrpProLeuSer 780
Db 2281 TACAATGCAAAACATGAAACAGTAAATGTGCCAGGTACGGGTTCCCTATGCGCGCTTCA 2340
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAspArgCysAlaProHisLeuGluTrp 800
Db 2341 GCCCAAGTCCCAATCGAAGAGTGGAGAGCCGAATCGATGCCGCCACACCTTGAATGG 2400
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGlyLysCysAlaHisHisSerHisHis 820
Db 2401 AATCCTGACTTAGATTGTCGTAGGATGGAGAAAGTGTGCCCATCATTCGCATCAT 2460
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
Db 2461 TTTCTCTTAGACATTTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Qy 841 IlePheLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2521 ATCTTTAAGATTAAAGCAGCAAGATGGCAGCAAGACTAGGGAATCTAGAGTTTCTCGAA 2580
Qy 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTrpArg 880
Db 2581 GAGAAACCATTAGTAGAGAGCGCTAGCTCGTGTGAAAGAGCGGAGAGAAATGGAGA 2640
Qy 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2641 GACAAACGTAAGAAATTTGGAATGGGAAACAAATATCTGTTTATAAGAGGCAAAAGAACT 2700

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QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
DB 2701 GTAGATGCTTATTGTAACTCTCAATATGATCAATTAACGGGATAGAATATGCC 2760
QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
DB 2761 ATGATTCAATCGGCAGATAAATCGTTTCATAGCATTCGAGAGCTTATCTGCGTGCAGCTG 2820
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
DB 2821 TCTGTGATTCGGGGTGCAATGCGGTATTTTGAAGAATTAAGAAGCGGTATTTCACT 2880
QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
DB 2881 GCATTCTCCTATATGATCGAGAAATGTCATTAAATGCTGATTTTAAATAGGCTTA 2940
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
DB 2941 TCTGTGTAAGCTGAAGGCGATGTAGATGTAGAAGAACAAACACACCGCTTCGGTC 3000
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
DB 3001 CTTGTGTTCCGAATGGAGCAGAGGTGTCACAGAAGTTCTGTCTCGCGGTCTG 3060
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyCysValThrIle 1040
DB 3061 GCGTATATCTTCGTGCACAGCTACAGGAGGATATGGAGAAGTTCGTTAACCAT 3120
QY 1041 HisGluIleGluAsnThrAspGluLeuLysPheSerAsnGlyValGluGluVal 1060
DB 3121 CATGAGATCGAACAATAACAGCAACTGAAGTTTAGCAACTGTGTAGAAGAGGAAGTA 3180
QY 1061 TyrProAspAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGlyGly 1080
DB 3181 TATCCAAACACACGCTACGTGTAATGATTATCTACGCACTCAAGAAGAAATATGAGGT 3240
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
DB 3241 ACCTACACTTCCTCGTAATCGAGATATGACGGAGCTATGAAGCAATTCCTCTGACCA 3300
QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgAspAsnPro 1120
DB 3301 GCTGATTATGATCATCGCTATGAGCAAAAGCATATACAGATGCGACCAAGACAATCCT 3360
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
DB 3361 TGTGAATCTAACAGAGATATGGGATACACACCTACCGCTGCTGCTATGTGACAAA 3420
QY 1141 GluLeuGlyTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
DB 3421 GAATTAGAGTACTTCCAGAAACCGATAAGGTATGATTGAGATCGGAGAACGGAAGA 3480
QY 1161 ThrPheIleValAspSerValGluLeuLeuMetGluGlu 1174
DB 3481 ACATTATCGTGGACAGCGTGAATTAATCTCTATGGAGAA 3522
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RESULT 12

AAAT05249

ID AAAT05249 standard; DNA; 3444 BP.

XX

AC AAAT05249;

XX

DT 26-MAY-1996 (first entry)

DE

DE CryIF/cryIA(b) chimeric toxin coding sequence.

XX

KW Delta endotoxin; crystal protein; chimeric toxin; insecticide;

KW pesticide; Pseudomonas fluorescens; biological control agent;

KW transgenic plant; insect resistance; disease resistance;

KW crop improvement; protein engineering; ss.

XX

OS Bacillus thuringiensis.

XX

```
Key Location/Qualifiers
mat_peptide 1..3444
tag= a
product= cryIF/cryIA(b) chimeric toxin
note= "plasmid pMYC2244 sequence"
```

W09530753-Al.

XX 16-NOV-1995.

XX 05-MAY-1995; 95WO-US05431.

XX 06-MAY-1994; 94US-0239476.

XX (MYCO) MYCOGEN CORP.

XX Schwab GE, Thompson M;

XX WPI: 1995-404120/51.

XX P-PSDB; AAR84731.

XX Nucleic acid encoding chimeric Bacillus thuringiensis

XX delta-endotoxin - providing increased expression in Pseudomonas,

XX esp. for control of lepidoptera pests.

XX Claim 7; Page 40-42; 9pp; English.

XX The sequence represents the cryIF/cryIA(b) chimeric toxin

XX coding sequence of plasmid pMYC2244. The chimeric toxin is

XX expressed in Pseudomonas fluorescens better than native

XX delta endotoxins. Host cells expressing the chimeric gene and

XX producing chimeric toxin may be used in insecticide compositions.

XX Where the host cells are plant cells, the gene confers insect

XX resistance to the transformed plant.

XX

SQ Sequence 3444 BP; 1125 A; 580 C; 765 G; 974 T; 0 other;

Alignment Scores:

Pred. NO.: 0 Length: 3444

Score: 5902.00 Matches: 1121

Percent Similarity: 96.08% Conservative: 7

Best Local Similarity: 95.49% Mismatches: 20

Query Match: 94.52% Indels: 26

DB: 16 Gaps: 1

US-09-837-961-8 (1-1174) x AAAT05249 (1-3444)

QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnGlyAsnAsnProGluVal 20

DB 1 ATGGAGATAATTAATCAAAATCAATGCGTACCTTACAAITGTTTAAATATCTGAAGTA 60

QY 21 GluIleLeuAsnGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40

DB 61 GAAATATTAAATGAAGAAAGAGTACTGSCAGATTACCGTTAGATATATCCTTATCGCTT 120

QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60

DB 121 ACACGTTTCTTTCAGTGAATTTGTTCCAGGTGTGGAGTTGCGTTGATTTATTTGAT 180

QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80

DB 181 TTAATATGGGTTTATTAACCTCTGATGAGCTTATTTCTTTTACAGATTGAACAA 240

QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100

DB 241 TTGATTGAGCAAGAAATAGAAACATTGGAAGGAACCGGGCAATTACTACATTAGAGGG 300

QY 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpGluAlaAsnProAsn 120

DB 301 TTACAGATAGCTATGAAATTTATATTGAAGCAGTAAAGAGAGTGGGAAGCAATCCTAAT 360

QY 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeu 140

XX

Db 361 AATGCACAAATTAAGGAGATGTCGATTCGATTGCTAATACAGACGACGCTTTAATA 420
Qy 141 ThrAlaIleAsnAspPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAAATAATTTACACTTACAGTTTGAAGTTTGAATCCCTCTTTTTCGCGTCTATGTT 480
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp 180
Db 481 CAAGCGCGCAATTTACATTTATCATTATAGAGACGCTGTATCGCTTTGGCGAGGTTGG 540
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GCACTGGATATAGCTACTGTTAATAATCATTAATAATAGATTAATAAATCTTATTCATAGA 600
Qy 201 TyrThrLysHisCysLeuAspPheThrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TATACGAACAATGTTTGGACACATCAACAATCAAGGATTAGAAAACCTTAAGAGGTACTAAT 660
Qy 221 ThrArgGlnTrpAlaArgPheAsnGlnPheArgArgAspLeuThrLeuThrValLeuAsp 240
Db 661 ACTCGACATGGCAGGATTCATCAGTTTAGGAGAGATTTAACACTTACTGTATTAGAT 720
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
Db 721 ATCGTGTGCTCTTTTCCGAACCTACGATGTTAGAACATATCCCAATTCAAACGTCATCCCAA 780
Qy 261 LeuThrArgGluIleThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
Db 781 TTAACAAGGGAATTTATACAAGTTTCAAGTAATGAGGATCTCCAGTTTCTGCTAATATA 840
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
Db 841 CCTAATGTTTAAATAGGCGGAATTTGGAGTTAGACCCGCCCATCTTATGACITTATG 900
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
Db 901 AATCTCTTGTGTTAACTGCAGAGACTGTTAGAACTCAAACTGTGTGGGAGGACACTTA 960
Qy 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
Db 961 GTTAGTTTCAGAAATACGGCTGGTAACCGTATAAATTTCCCTAGTTACGGGGTCTTCAAT 1020
Qy 341 ProGlyGlyAlaIleTrpIleAlaAspGluAspProArgProPheThrArgThrLeuSer 360
Db 1021 CCTGTTGGCGCCATTTGGATTCAGATGAGATCCACGTCCTTTTATCGACATTATCA 1080
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
Db 1081 GATCCTGTTTTTTCGAGAGGAGATTGGGAATCCCTCATTATGTACTGGGGCTTAGGGGA 1140
Qy 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
Db 1141 GTAGCATTTCAACAACCTGGTACGAACACACCCGAACATTTAGAATAATAGTGGACCATA 1200
Qy 401 AspSerLeuAspGluIleProProGlnAspAsnSerGlyAlaProtrpAsnAspTyrSer 420
Db 1201 GATTCTCTAGATGAATCCACCTCAGGATATAGTGGGACCTTTGGAATGATTATAGT 1260
Qy 421 HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer 440
Db 1261 CATGTATTAATCATGTTTACGATGGCCAGGTGAGATTTTCAGGAAGTGATTCA 1320
Qy 441 TrpArgAlaProMetPheSerTrpHisArgSerAlaThrProThrAsnThrIleAsp 460
Db 1321 TGGAGAGCTCCCAATGTTTCTTGGACGCGGAGTAGGCAACCCCTACAATACAAATGAT 1380
Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCGGAGAGGATTTACTCAATATACATTTGGTAAAGCACATACACTTCAGTCAGGTACTACT 1440
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
Db 1441 GTTGTAAAGGGGCCGGGTTTACGGGAGGAGATATTCTTCGAGGAACAAGTGGAGGACCA 1500

Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle 520
Db 1501 TTTGCTTATACTATTGTTAATAAATGGCAATTTACCCAAAGGTATCGTCCAGAATA 1560
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 CGCTATGCTCTACTACAAATCTAAGAATTTACGTAAACGGTTGCAGGTGAACGGATTTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGTCAATTTAAACAAACAAATGGATACCGGTGACCCCAATTAACATTCCTTTTACT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TACGCACTATTAAATACAGCTTTTACATTTCCCAATGAGCCAGAGTAGTTTCACAGTAGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATCTTTTAGTTTCAGGGAATGAAGTTTATATAGACAGATTTGAATGTATCCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGluTyrAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAAGCAGATATGATTTAGAAAGAGCACAAAGCGGTGAATGCGCTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTyrHisIleAspGln 640
Db 1861 TTTACTTCTATAACCAATAGGGATAAAACAGATGTCACGGATTTATCATATCGATCGA 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAAATTTAGTTGAGTGTATTCTGATGAATTTGTCTGATGAAAAAAGAATTG 1980
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
Db 1981 TCCGAAAGAGTCAACATCGAAGGACCTTAGTAGTAGCGGAATTTACTTCAAGATCCA 2040
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
Db 2041 ACTTTTAGAGGATCAATAGACAACTAGACCGTGGTGGAGAGAGTAGTACGGATATACC 2100
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAGGAGCGGATGACGTATTCAAGAGAGATTTACGTTACGCTATTTGGGTACCTTTGAT 2160
Qy 721 GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
Db 2161 GAGTGTATCCCAACGTTATTATCAAAAAATAGATGAGTCGAAATTAAGAGCCTATACC 2220
Qy 741 ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
Db 2221 CGTTACCAATTAAGAGGTATATCGAAGATAGTCAAGACTTAGAATCTATTAAATCCG 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrpProLeuSer 780
Db 2281 TACAATGCCAAACACAAAACAGTAAATGTCCAGGTACGGGTTCCTTATGCGCGCTTCA 2340
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
Db 2341 GCCCCAAGTCCCAATC----- 2355
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
Db 2356 -----GGAAATGTCCCATCATTTCCCATCAT 2382
Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
Db 2383 TTCTCCTTGGACATTGATGTTGATGTACAGACTTAAATAGGAGACTTAGGTGTATGGGTG 2442
Qy 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
Db 2443 AWATTCAAGATTAAAGCAAGATGCCATGCAAGACTAGAAATCTAGAAATTTCTCGAA 2502

QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTyrArg 880
 DB 2503 GAGAAACCATATAGAGAGAGCACTACCTCGTGTGAAAGAGCGGAGAAAATGGAGA 2562
 QY 881 AspLysArgGluLysLeuGluLysLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
 DB 2563 GACAAACGTGAAAAATGGAAATGGAAACAAATATCTTTATAGAGGCGAAAGATCT 2622
 QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
 DB 2623 GTAGATGCTTATTTGTAACCTCTCAATATGATAGATTACAAGCGGATACCAACATCGCG 2682
 QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
 DB 2683 ATGATTCATCGCGCAGATRAACGGTTCATAGCATTCGAGAAGCTTATCTGCGCTGAGCTG 2742
 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
 DB 2743 TCTGTGATTCGCGGTGTCAATGCGGCTATTTTGAAGAATTAGAAGGCGGTATTTCACT 2802
 QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
 DB 2803 GCATTCCTCCTATGATCGGAGAAATGTCATTAAAAATGATGATTTAATAATGCTTA 2862
 QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluGlnAsnHisArgSerVal 1000
 DB 2863 TCTGCTGGAACGTGAAGGCAATGATGATGATAGAGACAAACACACACCTTCGGTC 2922
 QY 1001 LeuValValProGluTrpGluAlaGluValSerGluGluValArgValCysProGlyArg 1020
 DB 2923 CTGTGTTCGCGAATGGGAAGCAGAAAGTGTCAAGAAGTTCGTCTCTCCGCGGTCT 2982
 QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrClyGluGlyCysValThrIle 1040
 DB 2983 GCGTATATCTCTGTCACAGCGTACAGAGGGGATATGGAGAAGGTTCGCTAACCAT 3042
 QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
 DB 3043 CATGAGATCGAAGCAATACAGAGCACTGAAGTTAGCAACTGTGTAGAGAGGAGTA 3102
 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGly 1080
 DB 3103 TATCCAAACCAACACGGTACGTATATGATTTACTGCGACTCAAGAAGAAATATGAGGT 3162
 QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100
 DB 3163 ACGTACACTTCCTGTAATCGAGATATGACGGAGCTATGAAGCAATCTCTCTGTACCA 3222
 QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgAspAsnPro 1120
 DB 3223 GCTGATTATGATCAGCCTATGAAGAAAGCAATATACAGATGGAGAGACATCTCT 3282
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
 DB 3283 TGTGAATCTAACAGAGATATGGGATATACACACCACTACCAGCTGGCTATGTGACAAA 3342
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160
 DB 3343 GAATTAGAGTACTTCCGAGAACCGATAGAGTATGAGATGAGATCGGAGAAACGGA 3402
 QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
 DB 3403 ACATTCATCGTGACAGCGTGAATTTACTTCTATGAGGAA 3444
 RESULT 13
 AAT05251
 ID AAT05251 standard; DNA; 3444 BP.
 AC
 XX
 XX
 XX
 DT 27-MAY-1996 (first entry)
 XX
 DE CryIF/cryIA(b) chimeric toxin coding sequence.

XX
 KW Delta endotoxin; crystal protein; chimeric toxin; insecticide;
 KW pesticide; Pseudomonas fluorescens; biological control agent;
 KW transgenic plant; insect resistance; disease resistance;
 KW crop improvement; protein engineering; ss.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..3444
 FT /tag= a
 FT /product= cryIF/cryIA(b) chimeric toxin
 FT /note= "plasmid pMYC2523 sequence"
 XX
 XX W09530753-A1.
 XX
 PD 16-NOV-1995.
 XX
 PF 05-MAY-1995; 95WO-US05431.
 XX
 PR 06-MAY-1994; 94US-0239476.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Schwab GE, Thompson M;
 XX
 XX WPI; 1995-404120/51.
 DR P-PSDB; AAR84733.
 XX
 PT Nucleic acid encoding chimeric Bacillus thuringiensis
 PT delta-endotoxin - providing increased expression in Pseudomonas,
 PT esp. for control of lepidoptera pests.
 XX
 PS Claim 13; Page 50-52; 9ipp; English.
 XX
 CC The sequence represents the cryIF/cryIA(b) chimeric toxin (with
 CC codon rework) coding sequence of plasmid pMYC2523. The chimeric
 CC toxin is expressed in Pseudomonas fluorescens better than native
 CC delta endotoxins. Host cells expressing the chimeric gene and
 CC producing chimeric toxin may be used in insecticide compositions.
 CC Where the host cells are plant cells, the gene confers insect
 CC resistance to the transformed plant.
 XX
 SQ Sequence 3444 BP; 1119 A; 592 C; 769 G; 964 T; 0 other;

Alignment Scores:
 Pred. No.: 0 Length: 3444
 Score: 5902.00 Matches: 1121
 Percent Similarity: 96.08% Conservative: 7
 Best Local Similarity: 95.49% Mismatches: 20
 Query Match: 94.52% Indels: 26
 DB: 16 Gaps: 1
 US-09-837-961-8 (1-1174) x AAT05251 (1-3444)
 QY 1 MetGluAsnAsnIleGlnAsnGlnCysValProTyrAsnCysLeuAsnAsnProGluVal 20
 DB 1 ATGGAATAAATAATTCAAATAATCATGCTACCTTACATTTGTTAAATAATCCTGAAGTA 60
 QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
 DB 61 GAATACTGAACAGACAGACGACCGCCGCTGGACATGACCTGAGCCTT 120
 QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
 DB 121 ACACGTTCCCTTTTGTGAGTGAATTTGTTCCAGGTGTGGAGTTGCGTTGGATATTGAT 180
 QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
 DB 181 TTAATATGGGTTTATAACTCTCTGATTCGAGCTTATTCTTTTACAGATTGAACAA 240
 QY 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100

Db 241 TTGATTGACCAAGAATAAGAACATTTGGAAAGAACCGGGCAATTAACATTACGAGGG 300
Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrrpGluAlaAsnProAsn 120
Db 301 TTAGCAGATAGCTATGAATTTATATTGAGCAGCTAAGAGAGTGGGAACAATCCTAAT 360
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
Db 361 AATGCACAATTAAGGAAGATGCGTATTCGATTGCTTAATACAGACGACGCTTTAATA 420
Qy 141 ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
Db 421 ACAGCAATAAATAATTTACATTTCAAGTTTCAAGTTTGAATCCCTTTTATCGGCTCATGTT 480
Qy 161 GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrrp 180
Db 481 CAAGCGCGAATTTACATTTACATTTAAGACGCGCTGTATCGGTTTGGCAGGGTTGG 540
Qy 181 GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg 200
Db 541 GGACTGGATATAGCTACTGTTAATATCATTTAATATAGATTAAATCTTATTCATAGA 600
Qy 201 TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn 220
Db 601 TATACCAACATTTGTCGACACATACATCAATCAAGGATTAGAAACTTAAGAGGTACTAAT 560
Qy 221 ThrArgGlnTrrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp 240
Db 661 ACTCGACAAATGGCAAGATTCATCAGTTTAGGAGAGATTAAACACTTACTGTATTAGAT 720
Qy 241 IleValAlaLeuPheProAsnTyrAspValArgThrTrrpIleGlnThrSerSerGln 260
Db 721 ATCGTTGTCTCTTTCCGAACATPACGATGTTAGAACATATCCCAATTCACACGTCATCCCAA 780
Qy 261 LeuThrArgGluIleTrrpThrSerValIleGluAspSerProValSerAlaAsnIle 280
Db 781 TTAACAGGGAATTTATACAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCA 840
Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
Db 841 CCTAATGGTTTAAATAGCGCGAATTTGAGTTAGAGTTAGAGTTAGAGTTAGAGTTAG 900
Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrrpGlyGlyHisLeu 320
Db 901 AATTCCTTTGTTTAACTGACAGAGACTGTAGAACTCAAACTGTGTGGGGAGGACACTTA 960
Qy 321 ValSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
Db 961 GTTAGCTCACGAAATACGGCTGGTACCGTATTAATTTCCCTAGTTACGGGCTTTCAT 1020
Qy 341 ProGlyGlyAlaIleTrrpIleAlaAspGluAspProArgProPheTrrpArgThrLeuSer 360
Db 1021 CCTGTGGCGCCATTTGGATTGCAGATGAGGATCCAGTCCCTTTTATCGGACATTATCA 1080
Qy 361 AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly 380
Db 1081 GATCCTGTTTGTCCGAGGAGGATTGGGAATCCCTCATTTATGCTAGTGGGCTTAGGGGA 1140
Qy 381 ValAlaPheGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
Db 1141 GTAGCATTTCAACAACATGGTACGAACACACCCCGAAACATTTAGAAATAGTGGGACCATTA 1200
Qy 401 AspSerLeuAspGluIleProGlnAspAsnSerGlyAlaProTrrpAsnAspTrrpSer 420
Db 1201 GATTCCTAGATGAATCCCACTCAGGATATAGTGGGACCTTGGATGATTATAGT 1260
Qy 421 HisValLeuAsnHisValThrPheValArgTrrpProGlyGluIleSerGlySerAspSer 440
Db 1261 CATGTATTAAATCATGTTTACATTTTACGATGGCCAGGTTGAGATTTCAGGAAGTGATTCA 1320
Qy 441 TrrpArgAlaProMetPheSerTrrpThrHisArgSerAlaThrProThrAsnThrIleAsp 460
Db 1321 TGGAGGCTCCCAATGTTTCTTGGAGCGCACCGTAGTGCAACCCCTACAAATACAATTGAT 1380

Qy 461 ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr 480
Db 1381 CCGGAGAGATTACTCAAAATACCATTTGGTAAAGCACAATACACTTCAGTCAGTACTACT 1440
Qy 481 ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro 500
Db 1441 GTTGTAAAGAGGCCCGGTTTACGGGAGGAGATATTCTTCGACGAACAAGTGGAGGCCA 1500
Qy 501 PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTrrpArgAlaArgIle 520
Db 1501 TTTGCTTTACTATTGTTAATATAATGGCAATTAACCCAAAGGTATCGTGAAGAATA 1560
Qy 521 ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe 540
Db 1561 CGCTATGCTCTACTACAAATCTAAGAAATTTACGTAAACGGTTGCAAGTGAACGGATTTT 1620
Qy 541 AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer 560
Db 1621 GCTGTCAATTTAACAACAACATGGATACCGGTGACCATTAACATTCCAATCTTTTAGT 1680
Qy 561 TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly 580
Db 1681 TAGGCAACTATTAAATACAGCTTTTACATTCCTCAATGAGCCAGAGTAGTTTCACAGTAGT 1740
Qy 581 AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal 600
Db 1741 GCTGATCTTTTAGTTCAGGGAATGAAGTTTATATAGACAGATTTGAATGTGATTCAGTT 1800
Qy 601 ThrAlaThrPheGluAlaGluTrrpAspLeuGluArgAlaGlnLysAlaValAsnAlaLeu 620
Db 1801 ACTGCAACATTTGAAGCAGAAATATGATTTAGAAAGACACAAAGCGGTGAATGGCTG 1860
Qy 621 PheThrSerIleAsnGlnIleGlyIleLysThrAspValThrAspTrrpHisIleAspGln 640
Db 1861 TTTACTTCTATAAACCAATAGGATATAAAACAGATGTGACGATTTATCATATCGATCGA 1920
Qy 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
Db 1921 GTATCCAATTTAGTTGAGTGTATCTGAAGAATTTGTCTGGATGAAAAAAGAATTG 1980
Qy 661 SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
Db 1981 TCCGAGAAAGTCAACATCGGAAGCGACTTAGTGATGACGGAATTTACTTCAAGATCCA 2040
Qy 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrrpArgGlySerThrAspIleThr 700
Db 2041 AACTTTAGAGGATCAATAGACAACACTAGACCGTGGCTGGAGAGGAAGTACGATATTACC 2100
Qy 701 IleGlnArgGlyAspAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
Db 2101 ATCCAAGGAGCGGATGACGTATTCAAGAGAAATACGTTACGCTATGGGTACCTTGTAT 2160
Qy 721 GluCysTyrProThrTrrpLeuTyrGlnLysIleAspGluSerLysLeuLysProTrrpThr 740
Db 2161 GAGTGTATCCCAACGTATTATATCAAAAAATAGATGAGTCGAAATTAAGACCTATACC 2220
Qy 741 ArgTyrGlnLeuArgGlyTrrpIleGluAspSerGlnAspLeuGluIleTrrpLeuIleArg 760
Db 2221 CGTTACCAATTAAGAGGATATATCGAAGATAGTCAAGACTTAGAAATCTATTAAATCCG 2280
Qy 761 TyrAsnAlaLysHisGluThrValAsnValLeuGlyThrGlySerLeuTrrpProLeuSer 780
Db 2281 TACATGCCAACACCAACACAGTAATGTGCCAGGTACGGGTTCTTATGGCCGCTTTCA 2340
Qy 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrrp 800
Db 2341 GCCCAAGTCCCAATC----- 2355
Qy 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
Db 2356 -----GGAAAATGTGCCCATCATTCCTCATCAT 2382

QY 821 pheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTtpVal 840
 Db TTTCTCTTGGACATTGATGTTGGATGTACAGACTTAAATGAGGACCTAGGTGTATGGGTG 2442
 QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu 860
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 QY 861 GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysLysTprArg 880
 Db GAGAAACCATTAAGTGAAGGACGACTAGCTGCTGTAAGAGCGGAGAGAAAATGCGA 2562
 QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
 Db GACAAACGTGAAATTTGATGCGGAAACAAATATGTTTAAAGAGGCAAAAGAAATCT 2622
 QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
 Db GTAGATGCTTTATTTGTAACCTCAATATATAGATTACAAGCGGATACCAACATCGCG 2682
 QY 921 MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu 940
 Db ATGATTCATCGCGCATAAACCGGTTCATAGCATTCGAGAGCTTATCTGCTGAGCTG 2742
 QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
 Db TCTGTGATTCGGGTGCTCAATCGCGCTATTTTGAGAAATTAGAAGCGGCTATTTTCACT 2802
 QY 961 AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
 Db GCATTCCTCCTATATGATCGGAGAAATGTCATTAATAATGGTGATTTTAATAATGCTTA 2862
 QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGluAlaAsnHisArgSerVal 1000
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 QY 1001 LeuValValProGluTyrGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
 Db CTTGTGTTCCGGATGGGAACGAGNAGTGTACAGAAGTTCGTGTCGTCCGGGTCT 2982
 QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
 Db GGCTATATCCTTCGTGTACAGGTACAAAGGAGGATATGGAGAGGTTGCGTAACCAT 3042
 QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
 Db CATGATTCGAGAAATACAGCAACCTGAATTTAGCAACTGTGTAGAGAGGAAGTA 3102
 QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly 1080
 Db TATCCAAACACACGCTACGTTAATGATTTACTGCGACTCAGAAGAATATGAGGT 3162
 QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100
 Db ACCTACACTCTCGTAATCGAGGATATGACGGAGCCTATGAAGCAATCTTCTGTGACCA 3222
 QY 1101 AlaAspTyrAlaSerValTyrGluGluLysSerTyrThrAspGlyArgArgAspAsnPro 1120
 Db GCTGATATGCTACGCTATGAGAAAGAAAGCATATACAGATGGACGAGAGACAATCCT 3282
 QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
 Db TGTGAATCTACAGAGGATATGGGATTTACACACCTACACAGCTGCGCTATGTGACAAA 3342
 QY 1141 GluLeuGluTyrPheProGluThrAspLysValTyrIleGluIleGlyGluThrGluGly 1160
 Db GAATTAGAGTACTTCCGAAACCGATAGGTATGATGATGAGATCGGAGAAACGGAAGA 3402
 QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
 Db ACATTCATCGTGAGACGCTGGAATTTACTTCTTATGGAGGA 3444

RESULT 14

ART18701
 ID AAT18701 standard; DNA; 3444 BP.
 AC AAT18701;
 DT 18-AUG-1996 (first entry)
 DE CryIF/CryIA(b) chimeric toxin gene from pMYC2244.
 KW CryIF; CryIA(b); crystal protein; chimeric toxin; protoxin;
 KW pMYC2244; delta-endotoxin; chimeric gene; fusion protein;
 KW Pseudomonas fluorescens; CryIA(c); synergy; Lepidoptera; insect;
 KW biological control agent; transgenic plant; insect resistance;
 KW crop improvement; ss.
 OS Bacillus thuringiensis.
 FT mat_peptide 1..1803 Location/Qualifiers
 FT mat_peptide /*tag= a
 FT mat_peptide /note= "CryIF toxin gene fragment"
 FT mat_peptide 1804..3444
 FT mat_peptide /*tag= b
 FT mat_peptide /note= "CryIA(b) protoxin gene fragment"
 US5508264-A.
 16-APR-1996.
 06-DEC-1994; 94US-0349867.
 06-DEC-1994; 94US-0349867.
 (MYCO) MYCOGEN CORP.
 Bradfisch GA, Schwab GE, Thompson M;
 WPI: 1996-208745/21.
 P-PSDB; AAR94907.
 Compsn. for controlling lepidopteran pests - comprises CryIF and
 CryIA(c) chimeric core toxin-contg. proteins.
 Claim 6; Column 45-48; 59pp; English.
 This sequence encodes a Bacillus thuringiensis chimeric
 CryIF/CryIA(b) delta-endotoxin. The toxin contains a full toxin
 portion of cryIF and a heterologous protoxin segment derived from
 CryIA(b). The sequence is constructed by substitution of an Apal
 fragment from cryIF clone pMYC2047 with the Apal fragment in
 pMYC2239 (AAT18721, containing cryIA(c) at the N-terminus, cryIF up
 to the toxin-protoxin junction, and a cryIA(b) protoxin segment)
 to give pMYC2244. The product contains cryIF up to the
 toxin-protoxin junction and cryIA(b) to the end of the coding
 region. The resulting chimeric gene may be cloned in a Pseudomonas
 fluorescens lactose-inducible strain to produce a chimeric toxin.
 The toxin, when combined with a cryIA(c) chimeric toxin in synergy,
 has unexpectedly enhanced toxicity to lepidopteran pests. P.
 fluorescens or B. thuringiensis cells expressing the gene may be
 used as an insect biological control agent, or a transgenic plant
 expressing the gene may become resistant to insect attack.
 Sequence 3444 BP; 1125 A; 580 C; 765 G; 974 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 3444
 Score: 5902.00 Matches: 1121
 Percent Similarity: 96.08% Conservative: 7
 Best Local Similarity: 95.49% Mismatches: 20
 Query Match: 94.52% Indels: 26
 DB: 17 Gaps: 1
 US-09-837-961-8 (1-1174) x AAT18701 (1-3444)


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Db 2161 GAGTGTATCCACGATATTTATATCAAAATAGATGAGTCAAAATTAAGCCCTATACC 2220
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Db 2221 CGTTACCAATTAAGAGGTTATATCGAAGATAGTCAAGACTTAGAAATCTATTTAAATCGC 2280
QY 761 TyrAsnAlaLysHisGluThrValAsnValLeuGluThrClySerLeuTrpProLeuSer 780
Db 2281 TACAAATGCCAAACAGAAAGATGAATGTCCAGGTACGGGTTCCCTATATGCGCGCTTCA 2340
QY 781 ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTrp 800
Db 2341 GCCCAAGTCCCAATC----- 2355
QY 801 AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisSerHisHis 820
Db 2356 -----GGAAATGTGCCATCATCCCATCAT 2382
QY 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTTPVal 840
Db 2383 TTCCTCTGGACATTCATGTTGGATGTACAGACTTAATGAGGACTTAGGTGTATGGTG 2442
QY 841 IlePheLysIleLysThrGlnAspGlyHisAlaAargLeuGlyAsnLeuGluPheLeuGlu 860
Db 2443 ATATTCAAGATTAAAGCAAGATGCCATGCAAGACTAGGAATCTAGAAATTCICGAA 2502
QY 861 GluLysProLeuValGlyGluAlaLeuAlaAargValLysAargAlaGluLysLysTrpArg 880
Db 2503 GAGAAACCAATTAGTAGGAAGCACTAGCTGCTGTGAAAGAGCGGAGAAAAAATGGAGA 2562
QY 881 AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer 900
Db 2563 GACAACGCGAARAATGGATGGGAACAATAATTGTTTAAAGAGGCAAAAGAAATCT 2622
QY 901 ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla 920
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QY 921 MetIleHisAlaAlaAspLysArgValHisAargIleAargGluAlaTyrLeuProGluLeu 940
Db 2683 ATGATTTCATCGCGCAGATAAACCGCTTCATAGCATTCGAGAAGCTTATCTGCGTAGCTG 2742
QY 941 SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr 960
Db 2743 TCTGTGATTCGGGTGCTCAATGCGGTATTTTGAAGAATTAGAAGGCGGTATTTTCACT 2802
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Db 2803 GCATTCCTCCTATATCATCGAGAAATGTCATTAAAAATGGTGATTTTAATAATGCTTA 2862
QY 981 SerCysTrpAsnValLysGlyHisValAspValGluGluAsnAsnHisAargSerVal 1000
Db 2863 TCTGCTGGAAGCTGAAGCGGATGTAGATGTAGAAGAACAAACCAACACCGCTTCGGTC 2922
QY 1001 LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg 1020
Db 2923 CTTGTGTTCCGGAATGGAAACAGCAAGCTGTCAAGAACTTCGTGCTCGGTGCTG 2982
QY 1021 GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluCysValThrIle 1040
Db 2983 GCGTATATCCTTCGTGTACAGCGGTACAAGGAGGATATGGAGAAGGTTGCGTAACCAT 3042
QY 1041 HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal 1060
Db 3043 CATGAGATCGAACAATACAGCAAGCTGAAGTTTAGCAACTGTGTAGAAGAGGAAGTA 3102
QY 1061 TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGluGluGluTyrGlyGly 1080
Db 3103 TATCCAAACACACAGGTACGTATGATGATTACTGCGACATCAAGAAATATGAGGT 3162
QY 1081 AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerValPro 1100

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Db 3163 ACGTACACTTCTCGTAAATCCAGGATATGACGGAGCCTATGAAAGCAATTTCTCTGTACCA 3222
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Db 3223 GCTGATTATGATCAGCTATGATGAAGAAAAGCATATACAGATGACGAGAGACAATCCT 3282
QY 1121 CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
Db 3283 TGTGAATCTAACAGAGATATGGGATTACACACCACTACCACTGCTATGTGACAAA 3342
QY 1141 GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
Db 3343 GAATTAGACTACTTCCAGNAACCGATAGGTATGATGAGATCGAGAACGGAAGGA 3402
QY 1161 ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
Db 3403 ACATTCATCGTGACACGCTGGAATTACTTCTTATGGAGAA 3444

RESULT 15
AAT18723
ID AAT18723 standard; DNA; 3444 BP.
XX
AC AAT18723;
XX
DT 18-AUG-1996 (first entry)
XX
DE CryIF/CryIA(b) codon-reworked chimeric toxin gene from pMYC2523.
XX
KW CryIF; CryIA(b); crystal protein; chimeric toxin; protoxin;
KW pMYC2523; delta-endotoxin; codon usage; splice overlap extension;
KW mutagenesis; chimeric gene; fusion protein; Pseudomonas fluorescens;
KW CryIA(c); synergy; Lepidoptera; insect; biological control agent;
KW transgenic plant; insect resistance; crop improvement; ss.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..1803
FT /tag= a
FT /note= "CryIF toxin gene fragment"
FT mat_peptide 1804..3444
FT /tag= b
FT /note= "CryIA(b) protoxin gene fragment"
XX
US5508264-A.
XX
PD 16-APR-1996.
XX
PF 06-DEC-1994; 94US-0349867.
XX
PR 06-DEC-1994; 94US-0349867.
XX
PA (MYCO ) MYCOGEN CORP.
XX
PI Bradfisch GA, Schwab GE, Thompson M;
XX
DR WPI; 1996-208745/21.
XX
DR P-PSDB; AAR94907.
XX
CC Compsn. for controlling lepidopteran pests - comprises CryIF and
CryIA(c) chimeric core toxin-contg. proteins.
XX
PS Example 6; Column 61-66; 59pp; English.
XX
CC This sequence encodes a Bacillus thuringiensis chimeric
CryIF/CryIA(b) delta-endotoxin. The toxin contains a full toxin
portion of cryIF and a heterologous protoxin segment derived from
CryIA(b). A cryIF gene from pMYC2047 has been subjected to splice
overlap extension to alter codons in a limited region in the cryIF
fragment to favor G or C in the wobble position, to improve
expression in Pseudomonas spp., giving pMYC2243 (AAT18722). An ApaI
fragment from this clone is substituted for an ApaI fragment from
pMYC2244 (AAT18701), to give pMYC2523. The product contains cryIF up

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1861 TTTACTTCTATAAAACCAATAGGATATAAAACAGATGTGACGGATTATCATATCGATCGA 1920
QY ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu 660
1921 GTATCCCAATTAGTTAGTGTATATCATGATGAAATTTTGTCTGGATGAAAAAAGAAATG 1980
QY SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuLeuGlnAspPro 680
1981 TCCGAGAAAGTCAACATCGAAGCGACTAGTGTATGATGAGCGGAATTTACITCAAGATCCA 2040
QY AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTrpArgGlySerThrAspIleThr 700
2041 AACTTTAGAGGGATCAATAGACAACTAGACCGTGGCGAGGAGAGTACGGATATATACC 2100
QY IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
2101 ATCCAAGAGCGGATGACGTATTCAAGAGAAATTTACGTACGCTATTGGGTACCTTTGAT 2160
QY GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr 740
2161 GAGTGCCTATCCAAACGCTATTTATCAAAAAATAGATGATCGAATAATTAAGAGCCTATACC 2220
QY ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg 760
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2341 GCCCCAGTCCCAATC----- 2355
QY AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis 820
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2623 GTAGATGCTTTATTTGTAACCTCAATATGATAGATTACAAGCGGATACCAACATCGCG 2682
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QY AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu 980
2803 GCATTCCTCCTATATGATCGGAGAAATGTCATTAATAAATGGTGAATTTAATAATGGCTTA 2862
QY SerCysTrpAsnValLysGlyHisValAspValGluGluAsnAsnHisArgSerVal 1000

```

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2863 TCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAGAAACAAAAACAACACCGTTCTGGTC 2922
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2923 CTTGTGTTCCGGAATGGGAACAGAGTGTACAGAGATTCGTGTCTGTCGGGTGCT 2982
QY GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluGlyCysValThrIle 1040
2983 GCGTATATCTCTCGTGTACAGCTACAGAGGAGGATATGGAGAGGTTCGCTAACCAT 3042
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QY AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro 1100
3163 ACGTACACTTCTCGTAAATCGAGGATATGACGGAGCCTATGAAAGCAATCTTCTGTACCA 3222
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3223 GCTGATATGCTATCAGCCTATGAAAGAAAAAGCATATACAGATGGACGAGAGACAATCT 3282
QY CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys 1140
3283 TGTGAATCTAACAGAGAGATATGGGGATACACACCCACTACCGAGCTGGCTGTGTGACAAA 3342
QY GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly 1160
3343 GAATTAGAGTACTTCCCAAAACCCGATAGGTATGATGAGATCGGAGAAACGGAGGA 3402
QY ThrPheIleValAspSerValGluLeuLeuLeuMetGluGlu 1174
3403 ACATTCATCGTGACACGCGTGAATTAATCTTCTATGGAGGAA 3444

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Search completed: November 27, 2002, 23:36:56

Job time : 700 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 27, 2002, 20:24:30 : Search time 6507 seconds
(without alignments)
5250.760 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNINQCVFYNCLNNEPV.....IGETGTFTIVDSVELLMEE 1174

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plo -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
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-WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6244	100.0	3522	6	AR050193	AR050193 Sequence
2	6244	100.0	3522	6	AR060321	AR060321 Sequence
3	6244	100.0	3522	6	AR105486	AR105486 Sequence
4	6244	100.0	3522	6	AX088274	AX088274 Sequence
5	6244	100.0	3522	6	I19464	I19464 Sequence 24
6	6244	100.0	3522	6	I22418	I22418 Sequence 24
7	6244	100.0	3522	6	I76417	I76417 Sequence 7
8	6244	100.0	3525	1	BACCRXIF	M73254 Bacillus th
9	6244	100.0	5649	1	BACCRIFA	M63897 Bacillus th
10	6049	96.9	3522	6	AR050195	AR050195 Sequence
11	6049	96.9	3522	6	AR060323	AR060323 Sequence
12	6049	96.9	3522	6	I19466	I19466 Sequence 28
13	6049	96.9	3522	6	I22420	I22420 Sequence 28
14	5902	94.5	3444	6	AR050192	AR050192 Sequence
15	5902	94.5	3444	6	AR050194	AR050194 Sequence
16	5902	94.5	3444	6	AR060320	AR060320 Sequence
17	5902	94.5	3444	6	AR060322	AR060322 Sequence
18	5902	94.5	3444	6	I19465	I19465 Sequence 22
19	5902	94.5	3444	6	I19466	I19465 Sequence 26
20	5902	94.5	3444	6	I22417	I22417 Sequence 22
21	5902	94.5	3444	6	I22419	I22419 Sequence 26
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23	5674	90.9	3450	6	AR050191	AR050191 Sequence
24	5674	90.9	3450	6	AR060319	AR060319 Sequence
25	5674	90.9	3450	6	I19462	I19462 Sequence 20
26	5674	90.9	3450	6	I22416	I22416 Sequence 20
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28	5415	86.7	3504	6	AR085763	AR085763 Sequence
29	5415	86.7	3504	6	I73041	I73041 Sequence 3
30	5406	86.6	4120	1	AB012288	AB012288 Bacillus
31	5399.5	86.5	3649	1	BTCPYPRTD	222512 B.thuringie
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33	4815.5	77.1	3531	6	AR107431	AR107431 Sequence
34	4815.5	77.1	3531	6	AR156713	AR156713 Sequence
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ALIGNMENTS

RESULT 1

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LOCUS AR050193 3522 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5827514.
ACCESSION AR050193
VERSION AR050193.1 GI:5972918
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 3522)
Bradfish, G.A., Thompson, M. and Schwab, G.B.
Pesticidal compositions
JOURNAL Patent: US 5827514-A 24 27-OCT-1998;
FEATURES
1. 3522
Location/Qualifiers
Source /organism="unknown"
BASE COUNT 1150 a 601 c 786 g 985 t
ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 3522
Score: 6244.00 Matches: 1174
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-837-961-8 (1-1174) x AR050193 (1-3522)

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Db 61 GRANTACTGACAGAGACACACACCGCGCCCTGCCGCTGGACATCAGCCCTGAGCCCT 120
QY 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
Db 121 ACACGTTTCTCTTTAGTGAATTTGTTCCAGGTGTGGAGTTCGGTGGATTTTAT 180
QY 61 LeuIleTrpGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
Db 181 TTAATATGGGGTTTATAACTCTCTTGATTTGGAGCTTATTTCTTTACAGATTGAACA 240
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 VERSION AR060321.1 GI:5986771
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 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 AUTHORS Thompson, M. and Schwab, G. E.
 TITLE .beta.-Endotoxin expression in pseudomonas fluorescens
 JOURNAL Patent: US 5840554-A 24-NOV-1998;
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 Location/Qualifiers
 source 1. 3522
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BASE COUNT 1150 a 601 c 786 g 985 t
 ORIGIN

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US-09-837-961-8 (1-1174) x AR060321 (1-3522)

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DEFINITION AR105486
ACCESSION AR105486
VERSION AR105486.1 GI:12819083
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3522)
AUTHORS Payne,J. and Sick,A.J.
TITLE Bacillus thuringiensis isolate active against lepidopteran pests,
and genes encoding novel lepidopteran-active toxins
JOURNAL Patent: US 6096708-A 7 01-AUG-2000;
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AX088274

LOCUS

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ACCESSION

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PAT 17-MAR-2001

VERSION AX088274.1 GI:13397177

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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DEFINITION Sequence 24 from patent US 5508264.
ACCESSION I19464
VERSION I19464.1 GI:1599819
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 3522)
Bradfish, G.A., Thompson, M. and Schwab, G.E.
TITLE Pesticidal compositions
JOURNAL Patent: US 5508264-A 24 16-APR-1996;
FEATURES Location/Qualifiers
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BASE COUNT 1150 a 601 c 786 g 985 t
ORIGIN

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QY 21 GluIleLeuAsnGluGluArgSerThrGlyArgLeuProLeuAspIleSerLeuSerLeu 40
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QY 61 LeuIleTyrGlyPheIleThrProSerAspTrpSerLeuPheLeuGlnIleGluGln 80
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VERSION I22418.1 GI:1602772
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ORGANISM Unknown.
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AUTHORS Thompson,M. and Schwab,G.E.
TITLE Delta-endotoxin expression in pseudomonas fluorescens
JOURNAL Patent: US 5527883-A 24 18-JUN-1996;
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I76417
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DEFINITION Sequence 7 from patent US 5691308.
ACCESSION I76417
VERSION I76417.1 GI:3012571
KEYWORDS

SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3522)
 AUTHORS Payne, J. and Sick, A. J.
 TITLE *Bacillus thuringiensis* isolate active against lepidopteran pests
 JOURNAL Patent: US 5691308-A 7 25-NOV-1997;
 FEATURES
 Location/Qualifiers
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BASE COUNT 1156 a 589 c 782 g 995 t
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 Best Local Similarity: 100.00% Mismatches: 0
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US-09-837-961-8 (1-1174) x 176417 (1-3522)

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RESULT 8

BACCRYIF

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

FEATURES

source

gene

CDS

BACCRYIF 3525 bp DNA linear BCT 26-APR-1993
Bacillus thuringiensis (cryIF) gene, complete CDS.

M73254

M73254.1 GI:142755

insecticidal delta-endotoxin.

Bacillus thuringiensis (strain PS81I, sub_species aizawai), DNA.

Bacillus thuringiensis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

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Feitelson, J.S.

Unpublished (1991)

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QY	121	AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAlaLeuIle	140
DB	361	AATGCACAATTAAGGAAGATGCGGTATTGCTATTGCTAAATACAGCACGCTTTAATA	420
QY	141	ThrAlaIleAsnAsnPheThrLeuThrSerPheGluIleProLeuSerValTyrVal	160
DB	421	ACAGCAATAAATAATTTACATTCACATTTGAAATCCCTTTTATTCGGTCTATGTT	480
QY	161	GlnAlaAlaAsnLeuHisLeuSerLeuLeuArgAspAlaValSerPheGlyGlnGlyTrp	180
DB	481	CAAGCGCGCAATTTACATTTATCACTATTAAAGAGACCGCTGTATCGTTTGGCAGGGTGG	540
QY	181	GlyLeuAspIleAlaThrValAsnAsnHisTyrAsnArgLeuIleAsnLeuIleHisArg	200
DB	541	GGACITGGATATAGCTACTGTTAATAATCATTTAATAAGATTAAATAATCTTATCATAG	600
QY	201	TyrThrLysHisCysLeuAspThrTyrAsnGlnGlyLeuGluAsnLeuArgGlyThrAsn	220
DB	601	TATAGAAACATTGTTTGGACACATACAAATCAAGGATTAGAAACTTAAGAGGTACTAAT	660
QY	221	ThrArgGlnTrpAlaArgPheAsnGlnPheArgAspLeuThrLeuThrValLeuAsp	240
DB	661	ACTCCACAATGGCAGAGATTCATCAATCAGTTTACGAGAGATTTACACTTACTGTATTAGAT	720
QY	241	IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln	260
DB	721	ATCGTTGCTCTTTTCCGAACATACGATGTAGACATATCCAATCAAACGTCATCCCAA	780
QY	261	LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle	280
DB	781	TTAAACAAGGGAATTTATACAAGTTTCACTAATGTAGGATTTCCAGATTTCTGCTAATATA	340
QY	281	ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet	300
DB	841	CCTATGTTTAAATAGGGCGGAATTTGGAGTTAGACCCGCCCACTTTATGAGCTTTATG	360
QY	301	AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu	320
DB	901	AATTCCTTTGTTTAACTCAGAGACTGTTAGAAGTCAAACCTGTGTGGGAGGACACTTA	380
QY	321	ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn	340
DB	961	GTTAGTTTACGAAATACGGCTGCTAACCGTATATAAATTTCCCTAGTTTACGGGCTCTTCAAT	400
QY	341	ProGlyGlyAlaIleThrIleAlaAspGluAspProArgProPheTyrArgThrLeuSer	360
DB	1021	CCTGGTGGCGCCATTGGAITGCAGATGAGGATCCACGTCCTTTTATCGGACATTATCA	420
QY	361	AspProValPheValArgGlyGlyPheGlyAsnProHisTyrValLeuGlyLeuArgGly	380
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QY	381	ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle	400
DB	1141	GTAGCATTTTCAACAACTGCTGACGACACACCCGCAACATTTAGAAATATAGTGGACCAT	460
QY	401	AspSerLeuAspGluIleProProGlnAspAsnSerGlyValaProTrpAsnAspTyrSer	480
DB	1201	GATTCCTAGATGAATATCCACCTCAGGATATATAGTGGGCGACCTTGGGAATGATATAGT	540
QY	421	HisValLeuAsnHisValThrPheValArgTrpProGlyGluIleSerGlySerAspSer	500
DB	1261	CATGTATTAATCATGTTACATTTGACGATGSCCAGGTGAGATTTTACAGAGTGAATCA	560
QY	441	TrpArgAlaProMetPheSerTrpThrHisArgSerAlaThrProThrAsnThrIleAsp	600
DB	1321	TGGAGAGCTCCCAATGTTTCTTGGACGACCGTAGTGCACACCCCTACAATACAATGTAT	660
QY	461	ProGluArgIleThrGlnIleProLeuValLysAlaHisThrLeuGlnSerGlyThrThr	720
DB	1381	CCGGAGAGATTTACTCAATATACATTTGGTAAAGACACATACACTTCAGTCAGGTACTACT	780
QY	481	ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro	840
DB	1441	GTTGTAAAGAGGCGCGGTTTACGGGAGGAGATATTTCTTCGAGAAACAAGTGGAGGACCA	900
QY	501	PheAlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle	960
DB	1501	TTTGCTTATCTACTATTGTTAATAATGGCAATATCCCAAGAGTATCTGTCGAAGAATA	1020
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DB	1561	CGCTATGCTCTACTACAAATCTAGAAATTTACGTAAACGGTTCAGGTGACCGATTCTT	1140
QY	541	AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer	1200
DB	1621	GCTGGTCAATTTAACAACAACTGATACCGGTGACCCATTAACATTCACATCTTTTACT	1260
QY	561	TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly	1320
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Db 1861 TTTCCTCTATAAACCAATAGGATGATAAAACAGATGTGACGATTATCATATGATCAA 1920
QY 641 ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluTyrArgGluLeu 660
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QY 681 AsnPheLysGlyIleAsnArgGlnLeuAspArgGlyTyrArgGlySerThrAspIleThr 700
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Db 2041 AACTTCAAGGCATCAATAGGCACACTAGACCGTGGTTGGAGAGGAGTACGGATATTACC 2100
QY 701 IleGlnArgGlyAspValPheLysGluAsnTyrValThrLeuProGlyThrPheAsp 720
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QY 981 SerCysTyrAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal 1000
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LOCUS BACCRVIFA 5649 bp DNA linear BCT 26-APR-1993
DEFINITION Bacillus thuringiensis insecticidal crystal protein (CryIF) gene,
complete cds.
ACCESSION M63897
VERSION 1 GI:142757
KEYWORDS insecticidal crystal protein.
SOURCE Bacillus thuringiensis (strain EG6346, sub-species aizawai) DNA.
ORGANISM Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE 1 (bases 1 to 5649)
AUTHORS Chambers,J.A., Jelen,A., Gilbert,M.P., Jany,C.S., Johnson,T.B. and
Gawron-Burke,C.
TITLE Isolation and characterization of a novel insecticidal crystal
protein gene from Bacillus thuringiensis subsp. aizawai
J. Bacteriol. 173 (13), 3966-3976 (1991)
MEDLINE 91286178
PubMed 2061280
FEATURES
Location/Qualifiers
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/organism="Bacillus thuringiensis"
/strain="EG6346"
/sub_species="aizawai"
/db_xref="taxon:1428"

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Db	1858	CCGGAGAGGATTAATCAATACCATTTGGTAAAGACACATACACTTCAGTCAGGTACTACT	1917
Qy	481	ValValArgGlyProGlyPheThrGlyGlyAspIleLeuArgArgThrSerGlyGlyPro	500
Db	1918	GTTGTAAAGAGGCGCGGTTTACGGGAGGAGATATCTTCGACGAACAAGTGGAGGACCA	1977
Qy	501	PheNlaTyrThrIleValAsnIleAsnGlyGlnLeuProGlnArgTyrArgAlaArgIle	520
Db	1978	TTTGCATTATCTATGTTAATAATAATGGCCAAATTACCCCAAGGATATCGTGCAGAATA	2037
Qy	521	ArgTyrAlaSerThrThrAsnLeuArgIleTyrValThrValAlaGlyGluArgIlePhe	540
Db	2038	CGCTATGCCCTCTACTCAAAATCTAAGAAATTTACGTAAACGGTTGCAGGTGAACGGATTTTT	2097
Qy	541	AlaGlyGlnPheAsnLysThrMetAspThrGlyAspProLeuThrPheGlnSerPheSer	566
Db	2098	GCTGGTCAATTTAAACAAAACATGGATACCGGTGACCCATTAACTATCCATCTTTTAGT	2157
Qy	561	TyrAlaThrIleAsnThrAlaPheThrPheProMetSerGlnSerSerPheThrValGly	580
Db	2158	TACGCAACTATTAAATACAGCTTTTACATTCCCAATGAGCCAGAGTAGTTTCCACAGTAGGT	2217
Qy	581	AlaAspThrPheSerSerGlyAsnGluValTyrIleAspArgPheGluLeuIleProVal	600
Db	2218	GCTGATACTTTTACGTACGGGAATGAAGTTTATATAGACAGATTGCAATTTGATTCACAGTT	2277
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Qy	641	ValSerAsnLeuValAspCysLeuSerAspGluPheCysLeuAspGluLysArgGluLeu	660
Db	2398	GTATCCAAATTTAGTGGATTTTATCAGATGAATTTTGTCTGGATGAAGACGGAAATG	2457
Qy	661	SerGluLysValLysHisAlaLysArgLeuSerAspGluArgAsnLeuGlnAspPro	680
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Db	2578	ATCCAAAGAGGAGATGACCTATTCAAGAAATTTATGTACACTACCGAGGTACCTTTGAT	2637
Qy	721	GluCysTyrProThrTyrLeuTyrGlnLysIleAspGluSerLysLeuLysProTyrThr	740
Db	2638	GAGTGCATCCACAGTATTATATCAAAAAATAGATGAGTCGAAATTTAAACCCCTATACT	2697
Qy	741	ArgTyrGlnLeuArgGlyTyrIleGluAspSerGlnAspLeuGluIleTyrLeuIleArg	760
Db	2698	CGTTATCAATTAAGAGGGTATATCGAGGATAGTCAGACTTAGAATCTATTATTCATCCGC	2757
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Db	2758	TATTAATGCAAAACACGAAACAGTAAATGTCTAGGTACGGGTTCCTTTATGGCCGCTTTCA	2817
Qy	781	ValGlnSerProIleArgLysCysGlyGluProAsnArgCysAlaProHisLeuGluTyrP	800
Db	2818	GTCCAAAGTCCANTCAGAAAGTGTGGAGAACCGAATCGATGGCCGCCACACTTGAATGG	2877
Qy	801	AsnProAspLeuAspCysSerCysArgAspGlyGluLysCysAlaHisHisSerHisHis	820
Db	2878	AATCCTGATCTAGATTGTTCTCTGCAGACAGGGGAAAAATGTGCATCATCTGCATCAT	2937

Qy	821	PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal	840
Db	2938	TTCTCCTTGGACATTGATGTTGGATGTACAGACTTAAATGAGGACTTACATGTATGGGTG	2997
Qy	841	IlePheLysIleLysThrGlnAspGlyHisAlaArgLeuGlyAsnLeuGluPheLeuGlu	860
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Qy	861	GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgGluAlaGluLysLysTrpArg	880
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Qy	881	AspLysArgGluLysLeuGluLeuGluThrAsnIleValTyrLysGluAlaLysGluSer	900
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Db	3178	GTAGATCGTTTATTGTTGAACTCTCAATATGATCAATATTACAAGCGGATACCAAAATTGGCC	3237
Qy	921	MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu	940
Db	3238	ATGATTCAATCGGCAGATAAACGTGTTCATGAATTCGGGAACGCTATCTTCCAGAGTTA	3297
Qy	941	SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgGluPheThr	960
Db	3298	TCTCTGATTCCGGGTGTAAATGTAGACATTTTCGAAGAATTAAGAAGCGGTATTTTCACT	3357
Qy	961	AlaPhePheLeuTyrAspAlaArgAsnValIleLysAsnGlyAspPheAsnAsnGlyLeu	980
Db	3358	GCATTTCTCTATGATGCGGAAAGATGCAATTAAGAAGCGGTATTTCAATAATGGCTTA	3417
Qy	981	SerCysTrpAsnValLysGlyHisValAspValGluGlnAsnAsnHisArgSerVal	1000
Db	3418	TCATGCTGGAACGTGAAAGGCGATGTAGATGTAGAAGACAAACACACCGTTCGGTC	3477
Qy	1001	LeuValValProGluTrpGluAlaGluValSerGlnGluValArgValCysProGlyArg	1020
Db	3478	CTTCTGTTCCGGAATGGGAAGCAGAAAGTGTCCACAGAAGATTCTGTCTGTCCGGGTCGT	3537
Qy	1021	GlyTyrIleLeuArgValThrAlaTyrLysGluGlyTyrGlyGluLysCysValThrIle	1040
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Qy	1041	HisGluIleGluAsnAsnThrAspGluLeuLysPheSerAsnCysValGluGluVal	1060
Db	3598	CATCAGATCGAGAACATAACAGACGAATGAAGTTTAGCACTGCGTAGAAGAGAAATC	3657
Qy	1061	TyrProAsnAsnThrValThrCysAsnAspTyrThrAlaAsnGlnGluGluTyrGlyGly	1080
Db	3658	TATCCAAACACACCGTAAAGTGTATGATGATTACTGCAAAATCAAGAAGATACGGGGGT	3717
Qy	1081	AlaTyrThrSerArgAsnArgGlyTyrAspGluThrTyrGlySerAsnSerSerValPro	1100
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Qy	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
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Qy	1141	GluLeuGluTyrPheProGluThrAspLysValTrpIleGluIleGlyGluThrGluGly	1160
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RESULT 10

AR050195 AR050195 3522 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 28 from patent US 5827514.
ACCESSION AR050195
VERSION AR050195.1 GI:5972920
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
1 (bases 1 to 3522)
AUTHORS Bradfisch,G.A., Thompson,M. and Schwab,G.E.
TITLE Pesticidal compositions
JOURNAL Patent: US 5827514-A 28 27-OCT-1998;
FEATURES Location/Qualifiers

source
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/organism="unknown"

BASE COUNT 1140 a 606 c 795 g 981 t
ORIGIN

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Best Local Similarity: 97.36% Mismatches: 26
Query Match: 96.88% Indels: 0
DB: 6 Gaps: 0

US-09-837-961-8 (1-1174) x AR050195 (1-3522)

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QY 241 IleValAlaLeuPheProAsnTyrAspValArgThrTyrProIleGlnThrSerSerGln 260
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QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTyrpGlyGlyHisLeu 320
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QY 321 ValSerSerArgAsnThrAlaGlyAsnArgIleAsnPheProSerTyrGlyValPheAsn 340
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QY 381 ValAlaPheGlnGlnThrGlyThrAsnHisThrArgThrPheArgAsnSerGlyThrIle 400
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RESULT 11

LOCUS AR060323 3522 bp DNA linear PAT 29-SEP-1999
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 ACCESSION AR060323
 VERSION AR060323.1 GI:5986773
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3522)
 AUTHORS Thompson,M. and Schwab,G.E.
 TITLE .beta.-Endotoxin expression in pseudomonas fluorescens
 JOURNAL Patent: US 5840554-A 28 24-NOV-1998;
 FEATURES Location/Qualifiers
 source 1..3522
 BASE COUNT 1140 a 606 c 795 g 981 t
 ORIGIN

Alignment Scores:

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 Best Local Similarity: 97.36% Mismatches: 26
 Query Match: 96.88% Indels: 0

DB: 6 Gaps: 0
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LOCUS I19466 3522 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 28 from patent US 5508264.
ACCESSION I19466
VERSION I19466.1 GI:1599821
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3522)
AUTHORS Bradfisch,G.A., Thompson,M. and Schwab,G.E.
TITLE Pesticidal compositions
JOURNAL Patent: US 5508264-A 28 16-APR-1996;
FEATURES
Source 1..3522
Location/Qualifiers
BASE COUNT 1140 a 606 c 795 g 981 t
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Alignment Scores:
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Percent Similarity: 97.79% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 26
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DB: 6 Gaps: 0
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Qy 41 ThrArgPheLeuLeuSerGluPheValProGlyValGlyValAlaPheGlyLeuPheAsp 60
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Qy 81 LeuIleGluGlnArgIleGluThrLeuGluArgAsnArgAlaIleThrThrLeuArgGly 100
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Qy 101 LeuAlaAspSerTyrGluIleTyrIleGluAlaLeuArgGluTrpClnAlaAsnProAsn 120
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Db 301 TTACGAGATAGCTATGAATTTATATTGTAAGCACACAAAGAGATGGGAACCAATCTTAAT 360
Qy 121 AsnAlaGlnLeuArgGluAspValArgIleArgPheAlaAsnThrAspAspAlaLeuIle 140
Db 361 AATGCACAAATTAAGGAAGATGGGTATTCGATTGCTTAATACAGACACCGCTTTAATA 420
Qy 141 ThrAlaIleAsnAspPheThrLeuThrSerPheGluIleProLeuLeuSerValTyrVal 160
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Qy 261 LeuThrArgGluIleTyrThrSerSerValIleGluAspSerProValSerAlaAsnIle 280
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Qy 281 ProAsnGlyPheAsnArgAlaGluPheGlyValArgProProHisLeuMetAspPheMet 300
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Qy 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyGlyHisLeu 320
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Qy 821 PheSerLeuAspIleAspValGlyCysThrAspLeuAsnGluAspLeuAspValTrpVal 840
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Qy	861	GluLysProLeuValGlyGluAlaLeuAlaArgValLysArgAlaGluLysIleThrArg	880
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Db	2641	GACAAACGTGAAAAATGGAAATGGGAATGGGAAACAATATCGTTATTAAGAGCGAAAGAAATCT	2700
Qy	901	ValAspAlaLeuPheValAsnSerGlnTyrAspGlnLeuGlnAlaAspThrAsnIleAla	920
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Qy	921	MetIleHisAlaAlaAspLysArgValHisArgIleArgGluAlaTyrLeuProGluLeu	940
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Qy	941	SerValIleProGlyValAsnValAspIlePheGluGluLeuLysGlyArgIlePheThr	960
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Qy	1121	CysGluSerAsnArgGlyTyrGlyAspTyrThrProLeuProAlaGlyTyrValThrLys	1140
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DEFINITION	Sequence 28 from patent US 5527883.	linear	PAT 07-OCT-1
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 QY 301 AsnSerLeuPheValThrAlaGluThrValArgSerGlnThrValTrpGlyHisLeu 320
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RESULT 14
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ACCESSION AR050192
VERSION AR050192.1 GI:5972917
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 3444)
AUTHORS Bradfisch,G.A., Thompson,M. and Schwab,G.E.
TITLE Pesticidal compositions
JOURNAL Patent: US 5827514-A 22 OCT-1998;
FEATURES
Location/Qualifiers
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BASE COUNT 1125 a 580 c 765 g 974 t
ORIGIN

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Best Local Similarity: 95.49% Mismatches: 20
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US-09-837-961-8 (1-1174) x AR050192 (1-3444)

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ACCESSION AR050194
VERSION AR050194.1 GI:5972919
KEYWORDS
SOURCE Unknown.
ORGANISM Uncl.
REFERENCE 1 (bases 1 to 3444)
AUTHORS Braafisch,G.A., Thompson,M. and Schwab,G.B.
TITLE Pesticidal compositions
JOURNAL Patent: US 5827514-A 26 27-OCT-1998;
FEATURES
Location/Qualifiers
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BASE COUNT 1119 a 592 c 769 g 964 t
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Best Local Similarity: 95.49% Mismatches: 20
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Search completed: November 28, 2002, 01:25:30
Job time : 6715 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 18:38:09 ; Search time 74 seconds
(without alignments)
252.635 Million cell updates/sec

Title: US-09-837-961-8
Perfect score: 6244
Sequence: 1 MENNIOQCVPYCNLNPEV.....IGETGTFIVDSVLLIMEE 1174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues
Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5879	94.2	1148	10	US-09-826-660-2
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4	4804.5	76.9	1177	10	US-09-873-873-10
5	4804.5	76.9	1177	10	US-09-873-873-12
6	4804.5	76.9	1177	10	US-09-873-873-14
7	4745.5	76.0	1177	10	US-09-873-873-28
8	4647.5	74.4	1177	10	US-09-873-873-34
9	4313.5	69.1	1193	10	US-09-873-873-30
10	4211.5	67.4	1155	10	US-09-756-643-2
11	4148	66.4	1178	10	US-09-851-194-2
12	4042.5	64.7	1163	10	US-09-826-660-21
13	4039	64.7	1156	10	US-09-826-660-15
14	3629.5	58.1	1186	10	US-09-826-660-23
15	3185	51.0	605	10	US-09-826-660-4
16	2708	43.4	547	10	US-09-826-660-11
17	2077	33.3	1210	12	US-10-032-717-4
18	2020	32.4	1206	12	US-10-032-717-2
19	1713.5	27.4	1163	10	US-09-756-526A-2

20	1597.5	25.6	1109	10	US-09-756-526A-4
21	1001	16.0	673	12	US-10-032-717-18
22	981	15.7	667	12	US-10-032-717-8
23	944	15.1	669	12	US-10-032-717-10
24	944	15.1	669	12	US-10-032-717-16
25	935.5	15.0	643	10	US-09-826-660-25
26	935	15.0	667	12	US-10-032-717-6
27	933	14.9	333	10	US-09-851-194-4
28	933	14.9	673	12	US-10-032-717-12
29	932	14.9	673	12	US-10-032-717-22
30	932	14.9	673	12	US-10-032-717-40
31	925.5	14.8	670	12	US-10-032-717-24
32	925.5	14.8	670	12	US-10-032-717-44
33	923	14.8	616	12	US-10-032-717-20
34	912	14.6	620	12	US-10-032-717-30
35	911	14.6	620	12	US-10-032-717-32
36	911	14.6	620	12	US-10-032-717-42
37	904.5	14.5	617	12	US-10-032-717-34
38	904.5	14.5	617	12	US-10-032-717-46
39	883.5	14.1	644	10	US-09-943-692-2
40	876	14.0	655	10	US-09-826-660-27
41	698	11.2	1257	10	US-09-738-363-6
42	671	10.7	1289	10	US-09-738-363-4
43	606	9.7	1385	10	US-09-738-363-2
44	433	6.9	140	10	US-09-062-104A-2
45	178	2.9	803	10	US-09-738-363-12

ALIGNMENTS

RESULT 1
US-09-826-660-6
; Sequence 6, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1174
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-826-660-6

Query Match	100.0%;	Score	6244;	DB	10;	Length	1174;	
Best Local Similarity	100.0%;	Pred. No.	0;					
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								0;
QY	1	MENNIOQCVPYCNLNPEVILNEERSTGRLPDLSLSTRFLSLRFLSPVPGVGVAFGLFD	60					
Db	1	MENNIOQCVPYCNLNPEVILNEERSTGRLPDLSLSTRFLSLRFLSPVPGVGVAFGLFD	60					
QY	61	LIWGFITPDSWLSFLLOEQIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN	120					
Db	61	LIWGFITPDSWLSFLLOEQIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN	120					
QY	121	NAQLREDVRIRFANTDADALITAINNFILTSFEIPLLSYVVOAANHLISLLRDAYSFGQGW	180					
Db	121	NAQLREDVRIRFANTDADALITAINNFILTSFEIPLLSYVVOAANHLISLLRDAYSFGQGW	180					


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QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLNLRGNTQWARFNQFRRLTLTVLD 240
DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLNLRGNTQWARFNQFRRLTLTVLD 240
QY 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
DB 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
QY 301 NSLFTVTAETVRSQTVGGLHVSRRNAGNRPSPSVGVFNPGGAIWIAEDDPPFYRTLS 360
DB 301 NSLFTVTAETVRSQTVGGLHVSRRNAGNRPSPSVGVFNPGGAIWIAEDDPPFYRTLS 360
QY 361 DPVVRGGGPNHYVGLRGVAFQQTGNTHTFRNSGTIDSLDEIPPODSSGAPNDYS 420
DB 361 DPVVRGGGPNHYVGLRGVAFQQTGNTHTFRNSGTIDSLDEIPPODSSGAPNDYS 420
QY 421 HVLNHTVFRWPGESISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
DB 421 HVLNHTVFRWPGESISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNGLQPRYRARIYASTNLRIVYTVAGERIF 540
DB 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNGLQPRYRARIYASTNLRIVYTVAGERIF 540
QY 541 AGQFNKMTDGTPLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPV 600
DB 541 AGQFNKMTDGTPLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLDFECLDEKREL 660
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLDFECLDEKREL 660
QY 661 SEKVHAKLSDERNLQDPNFKGINRQLDGRWGSTDITIQGDDVFKENVYVLPCTED 720
DB 661 SEKVHAKLSDERNLQDPNFKGINRQLDGRWGSTDITIQGDDVFKENVYVLPCTED 720
QY 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 780
DB 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 780
QY 781 VQSPRKCGEPNRCAPHLWNPDLDCSRRDGEKCAHSHHFLSDIDVCGTDLNEDLDVWV 840
DB 781 VQSPRKCGEPNRCAPHLWNPDLDCSRRDGEKCAHSHHFLSDIDVCGTDLNEDLDVWV 840
QY 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELTNTVYKEAKES 900
DB 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELTNTVYKEAKES 900
QY 901 VDALFVNSOYDQLOADNTAMIHAADKRVHRIREAYLPBLSVPGVNVDFEELKGRIFT 960
DB 901 VDALFVNSOYDQLOADNTAMIHAADKRVHRIREAYLPBLSVPGVNVDFEELKGRIFT 960
QY 961 AFPLDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020
DB 961 AFPLDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020
QY 1021 GYLIRVATYKEGEGCVTIHEIENNTDELKFSNCVEEVEYVNNVTCDNYTANOEYGG 1080
DB 1021 GYLIRVATYKEGEGCVTIHEIENNTDELKFSNCVEEVEYVNNVTCDNYTANOEYGG 1080
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DB 1081 AYTSNRGYDETYGNSVPADYASYIEKSYTDGRRDNPCSNRGYGDYTPLPAGYVTK 1140
QY 1141 ELEYFPETDKVNIETEGTETIVDSVELLME 1174
DB 1141 ELEYFPETDKVNIETEGTETIVDSVELLME 1174

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RESULT 2
 US-09-826-660-2
 ; Sequence 2, Application US/09826660
 ; Patent No. US20010026940A1

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; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
; US-09-826-660-2

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Query Match          94.2%; Score 5879; DB 10; Length 1148;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1117; Conservative 8; Mismatches 23; Indels 26; Gaps 1;

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DB 1 MENNIQCVPCVNCNLPNEVEILNEERSTGRPLDLSLTRELLSEFVPGVGVAFGLFD 60
QY 61 LWGFTTPSDWSLFLQIEQLIEQRIETLERNAITTLRLGLADSYEIIYALREWEANPN 120
DB 61 LWGFTTPSDWSLFLQIEQLIEQRIETLERNAITTLRLGLADSYEIIYALREWEANPN 120
QY 121 NACLREDVRIRANTDDALITAINNETLTSPRIPLLSVVVQANLHLSLLRDAVSQGW 180
DB 121 NACLREDVRIRANTDDALITAINNETLTSPRIPLLSVVVQANLHLSLLRDAVSQGW 180
QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLNLRGNTQWARFNQFRRLTLTVLD 240
DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLNLRGNTQWARFNQFRRLTLTVLD 240
QY 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
DB 241 IVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVRPPHLMDFM 300
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DB 301 NSLFTVTAETVRSQTVGGLHVSRRNAGNRPSPSVGVFNPGGAIWIAEDDPPFYRTLS 360
QY 361 DPVVRGGGPNHYVGLRGVAFQQTGNTHTFRNSGTIDSLDEIPPODSSGAPNDYS 420
DB 361 DPVVRGGGPNHYVGLRGVAFQQTGNTHTFRNSGTIDSLDEIPPODSSGAPNDYS 420
QY 421 HVLNHTVFRWPGESISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
DB 421 HVLNHTVFRWPGESISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNGLQPRYRARIYASTNLRIVYTVAGERIF 540
DB 481 VVRGPGFTGGDILRRTSGGPFAYTIIVNGLQPRYRARIYASTNLRIVYTVAGERIF 540
QY 541 AGQFNKMTDGTPLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPV 600
DB 541 AGQFNKMTDGTPLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSGNEVYIDRFELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLDFECLDEKREL 660
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLDFECLDEKREL 660
QY 661 SEKVHAKLSDERNLQDPNFKGINRQLDGRWGSTDITIQGDDVFKENVYVLPCTED 720

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QY 59 FDLIWTGTFSDWSLFLQIOLBOLIEORIETLERNRAITTLRGLADSEYIYEALREWEAN 118
Db 61 VDIWIGFPGSONDAFLVQIOLBOLINEEFAFNQAISRLGLESLNLYOYAESFREWEAD 120
QY 119 PNAQLREDVIRFANTDDALITAINNFTLSFEIPLLSVYVQAANHLSLRLDRAVSFGQ 178
Db 121 PTNPALREEMRIQNDMNSALTTPILFAVQNYQVPLLSVYVQAANHLSLRLDVSFGQ 180
QY 179 GWGLDIATVNNHYNRLINLHRYTKHCLDYNQGLENLGRNTQWARFNQFRDLTLTV 238
Db 181 RWGFDAAATINSRYNDLTRIGNYTDYAVRWNTGLERWVGPDSDRWVRYNQFRRLTLTV 240
QY 239 LDIVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSNAPNGFNRA---EFGVRPP 294
Db 241 LDIVALFPNDVRYPIRTVSQTLREIYTNVLE-----NFDGSRFGSAOGIERSIRSP 294
QY 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWAIED 351
Db 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWAIED 351
QY 352 PRPFYRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTHRTFRNSGTIDSLDEIP 407
Db 355 GQGVYRTLSTLTYRRPPIRTVSQTLREIYTNVLE-----NFDGSRFGSAOGIERSIRSP 414
QY 408 PQDMSGAPNDYSHVLNVITVFRPGETSGSDSWRAPMFSWTHRSATPTNTIDPERITQI 467
Db 415 PQDMSGAPNDYSHVLNVITVFRPGETSGSDSWRAPMFSWTHRSATPTNTIDPERITQI 474
QY 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYSTN 527
Db 475 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYSTN 534
QY 528 LRIYTVAGERIFAGQFNKMTDGPDLFQSFYSYATINTAFTFPMSSQSFYTGADTFSSG 587
Db 535 LRIYTVAGERIFAGQFNKMTDGPDLFQSFYSYATINTAFTFPMSSQSFYTGADTFSSG 594
QY 588 NEVYIDRELIPVTATFAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQVSNLVD 647
Db 595 NEVYIDRELIPVTATFAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQVSNLVD 654
QY 648 LSDEFCLDEKRELSEKVKHAKLSERNLQDPNFKGNRLQDRGWRGSTDITIQRGDDV 707
Db 655 LSDEFCLDEKRELSEKVKHAKLSERNLQDPNFKGNRLQDRGWRGSTDITIQRGDDV 714
QY 708 FKENTVTLPGTFDECYPTLYQKIDESKLKPYTRLQRYIEDSDLEIYLIRYNAKHET 767
Db 715 FKENTVTLPGTFDECYPTLYQKIDESKLKPYTRLQRYIEDSDLEIYLIRYNAKHET 774
QY 768 VNVLTGSLWPLSVQSPTRKGEPRNRCAPHLBNWPDLDSCDRGDKCAHSHHFLDIDV 827
Db 775 VNVLTGSLWPLSVQSPTRKGEPRNRCAPHLBNWPDLDSCDRGDKCAHSHHFLDIDV 834
QY 828 GCTDLNEDIDVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAKWRDKREKLE 887
Db 835 GCTDLNEDIDVWVIFKIKTQDGHARLGNLEFLEERPLVGEALARYKRAKWRDKREKLE 894
QY 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRYHRIEAYLPELSVIPGVN 947
Db 895 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRYHRIEAYLPELSVIPGVN 954
QY 948 VDIPELGRIFTAPFLDARVINKGDPNGLSCWNKVGHDVBEQNNHRSVLVVPWE 1007
Db 955 AAFIELEGRIETAFSLYDARVINKGDPNGLSCWNKVGHDVBEQNNHRSVLVVPWE 1014
QY 1008 AEVSQEVRCRPGYILRTAYKEGEGCVTHIELENNITDELKTSNCVEEYVNNVTY 1067
Db 1015 AEVSQEVRCRPGYILRTAYKEGEGCVTHIELENNITDELKTSNCVEEYVNNVTY 1074
QY 1068 CNDYTAQOEYGGAYTSRNGYDEYVGSNSVPADYASVYEKSYTDGRDNPCESNRGY 1127

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Db 1075 CNDYTAQOEYGGAYTSRNGYNEA---PSPADYASVYEKSYTDGRRENPCFENRGY 1130
QY 1128 GDTPLPAGYVTKLEYFPETDKVWIEIETEGTFIVDSVELLMEE 1174
Db 1131 RDTPLPAGYVTKLEYFPETDKVWIEIETEGTFIVDSVELLMEE 1177
RESULT 6
US-09-873-873-14
; Sequence 14, Application US/09873873
; Patent NO. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxin
; FILE REFERENCE: MECO-210--2
; CURRENT APPLICATION NUMBER: US 09/873,873
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-14

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Query Match 76.9%; Score 4804.5; DB 10; Length 1177;
Best Local Similarity 78.5%; Pred. No. 0;
Matches 932; Conservative 66; Mismatches 166; Indels 23; Gaps 9;
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Db 1 MDNPNINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSTQFLLSEFVPGAGEVLGL 60
QY 59 FDLIWTGTFSDWSLFLQIOLBOLIEORIETLERNRAITTLRGLADSEYIYEALREWEAN 118
Db 61 VDIWIGFPGSONDAFLVQIOLBOLINEEFAFNQAISRLGLESLNLYOYAESFREWEAD 120
QY 119 PNAQLREDVIRFANTDDALITAINNFTLSFEIPLLSVYVQAANHLSLRLDRAVSFGQ 178
Db 121 PTNPALREEMRIQNDMNSALTTPILFAVQNYQVPLLSVYVQAANHLSLRLDVSFGQ 180
QY 179 GWGLDIATVNNHYNRLINLHRYTKHCLDYNQGLENLGRNTQWARFNQFRDLTLTV 238
Db 181 RWGFDAAATINSRYNDLTRIGNYTDYAVRWNTGLERWVGPDSDRWVRYNQFRRLTLTV 240
QY 239 LDIVALFPNDVRYPIQTSQTLREIYTSVIEDSPVSNAPNGFNRA---EFGVRPP 294
Db 241 LDIVALFPNDVRYPIRTVSQTLREIYTNVLE-----NFDGSRFGSAOGIERSIRSP 294
QY 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWAIED 351
Db 295 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSGVF-NPGGAIWAIED 351
QY 352 PRPFYRTLSDPVFVRG---GFGNPHY-VLGLRGVAFQQTGTHRTFRNSGTIDSLDEIP 407
Db 355 GQGVYRTLSTLTYRRPPIRTVSQTLREIYTNVLE-----NFDGSRFGSAOGIERSIRSP 414
QY 408 PQDMSGAPNDYSHVLNVITVFRPGETSGSDSWRAPMFSWTHRSATPTNTIDPERITQI 467
Db 415 PQDMSGAPNDYSHVLNVITVFRPGETSGSDSWRAPMFSWTHRSATPTNTIDPERITQI 474
QY 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYSTN 527
Db 475 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYSTN 534

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QY	528	LRIVTVAGERIFAGCNKMTDGPDLTFQSPSYATINTATTFPMSSQSFVTGADTFSSG	587
Db	535	LRIVTVAGERIFAGCNKMTDGPDLTFQSPSYATINTATTFPMSSQSFVTGADTFSSG	594
QY	588	NEVYIDRFELIPVTATFEAYELERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVD	647
Db	595	NEVYIDRFELIPVTATFEAYELERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVD	654
QY	648	LSDEFCLDEKRELSEKVKHAKLSDERNLDPNFKGINRQLDRGRGSTDITIQRGDDV	707
Db	655	LSDEFCLDEKRELSEKVKHAKLSDERNLDPNFKGINRQLDRGRGSTDITIQRGDDV	714
QY	708	FKENYVTLPGTFDECPYLYIQIDESKLKPYTRQLRGYTEDSQDLEIYLIRYNAKHET	767
Db	715	FKENYVTLPGTFDECPYLYIQIDESKLKPYTRQLRGYTEDSQDLEIYLIRYNAKHET	774
QY	768	VNYLGTGSLWPLSVQSPKRCCEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDV	827
Db	775	VNYLGTGSLWPLSVQSPKRCCEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDV	834
QY	828	GCTDLNEDLDVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLE	887
Db	835	GCTDLNEDLDVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLE	894
QY	888	LETNIVYKEAKESVDALFVNSQYDOLQADTNIAHAAADKRVHIREAYLPELSVIPGVN	947
Db	895	WETNIVYKEAKESVDALFVNSQYDOLQADTNIAHAAADKRVHIREAYLPELSVIPGVN	954
QY	948	VDIFEELKGRIFTAFLXDARNVKNKGDFNNGLSQWNVKGVHDVVEEQNNHRSVLVVPWE	1007
Db	955	AAIFEELKGRIFTAFLXDARNVKNKGDFNNGLSQWNVKGVHDVVEEQNNHRSVLVVPWE	1014
QY	1008	AEVSQVRVCPGSGYILRVYATKBYGEGCVTHIEHNNTDELKFSNCVBEVYPNNVT	1067
Db	1015	AEVSQVRVCPGSGYILRVYATKBYGEGCVTHIEHNNTDELKFSNCVBEVYPNNVT	1074
QY	1068	CNDYTANQOEYGGATYSRNRGYDetyGNSVPADYASVYEKSYTDGRDNPCESNRGY	1127
Db	1075	CNDYTANQOEYGGATYSRNRGNEA----PSPADYASVYEKSYTDGRDNPCESNRGY	1130
QY	1128	GDYTPLPAGYVVKLEYFPETDKVWIEIGETEGTIFVDSVELLIMEE	1174
Db	1131	RDYTPLPAGYVVKLEYFPETDKVWIEIGETEGTIFVDSVELLIMEE	1177
RESULT 7			
US-09-873-873-28			
; Sequence 28, Application US/09873873			
; Patent No. US20020064865A1			
; GENERAL INFORMATION:			
; APPLICANT: Malvar, Thomas			
; APPLICANT: Gilmer, Amy Jelen			
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum			
; FILE REFERENCE: MECO:210--2			
; CURRENT APPLICATION NUMBER: us/09/873,873			
; CURRENT FILING DATE: 2001-08-20			
; PRIOR APPLICATION NUMBER: US 09/253,341			
; PRIOR FILING DATE: 1999-02-19			
; PRIOR APPLICATION NUMBER: US 08/922,505			
; PRIOR FILING DATE: 1997-09-03			
; PRIOR APPLICATION NUMBER: US 08/754,490			
; PRIOR FILING DATE: 1996-11-20			
; NUMBER OF SEQ ID NOS: 35			
; SOFTWARE: Patent version 3.0			
; SEQ ID NO 28			
; LENGTH: 1177			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Hybrid Delta-Endotoxin			
US-09-873-873-28			

[illegible]

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Db 1015 AEVSEVRVCPGRGYILRYTAYKEGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVT 1074
Qy 1068 CNDYTAQOEYGGATSRNRYGDEYTGNSNVPADYASVYEKSYTDGRDNPCEENRGY 1127
Db 1075 CNDYVNOEYGGATSRNRYGNEA----PSPADYASVYEKSYTDGRRENPCENRGY 1130
Qy 1128 GDTPLPAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLME 1174
Db 1131 RDTPLPVGYYTKLEYFPETDKVWIEIGETGTFIVDSVELLME 1177

RESULT 8
US-09-873-873-34
; Sequence 34, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 1177
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-34

Query Match 74.4%; Score 4647.5; DB 10; Length 1177;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 907; Conservative 72; Mismatches 185; Indels 23; Gaps 9;

Qy 1 MENNIQ-NOCPVNCNANPEVILNEER-STGRPLDLSLSTRLLSEFVPCGVAVFGL 58
Db 1 MWNPNNEICPIYCNLSNEVEVGERETGTPTDLSLTHQFLSEFVPGAGVVLGL 60
Qy 59 FDLINGFITPDSWFLQLEOIRIETLERNRAITTLRLGLADSYEIIYIEALREWEAN 118
Db 61 VDLINGIFGSPQWDAFLVQIEQLINQRIEFAFNQAIISLEGSLNLYQIYAESFREWEAD 120
Qy 119 PNAQLRDVRIREFANTDALLITAINNFTLTSEFIPLLSVYQAAHLHSLRLDAVSFGQ 178
Db 121 PTNPALREMERIQFNDMSALTAIPLFAVQYQVLLSVYQAAHLHSLRLDVSFVGQ 180
Qy 179 GGLDIATVNNHYNRLINLIRHYTHCLDTYNOGLENLRTGNTROWARENOPRDLTLTV 238
Db 181 RRGFPAATINSRYNDLTRILGNVTDYAVRWYNGLEVRWGPDSRWVRYNQFRRLTLTV 240
Qy 239 LDVALFPNDYRTYPIQTSOLLTRIETYSVIEDSPVANIPNGFNRA----EFGVRPP 294
Db 241 LDVALFPNDYRSRYPIRTVSQLTRIETIYNVLE-----NFDGSPFGSAQGIERSIRSP 294
Qy 295 HLMDFWNSLFTVAETVRSQVWCGH--LVSSRTAGNRNIPFSGYVF-NPGGAINTADED 351
Db 295 HLMDLNLSITITDAHRGYYIYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQOORIVAQL 354
Qy 352 PRPEYFTLSDPVEVRG--GFGNPHY-VLGLRGVAFQQTGNTNTRFRNSGTIDSLDEIP 407
Db 355 GQGVYFTLSTLRRFPNTGINNQQLSVLDGTETFAVGTSSNLPFSVYRKSGVDSLDEIP 414
Qy 408 PDNSGAPWNDYSHLVNHVTFVFWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITOI 467
Db 408 PDNSGAPWNDYSHLVNHVTFVFWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITOI 467
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Db 415 PONNVPPRQGFSHRLSHVSMFRSGFSNSSSVIIIRAPKFSWIHRSAEFNIIASDITOI 474
Qy 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPEAYTIVNINGQLPQRYRIRVASTTN 527
Db 475 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPEAYTIVNINGQLPQRYRIRVASTTN 534
Qy 528 LRIYTVVAGERIFAGQFNKMTDGTPLTFQSPSYATINTAFTFPMSSQSFYTGADTFSSG 587
Db 535 LRIYTVVAGERIFAGQFNKMTDGTPLTFQSPSYATINTAFTFPMSSQSFYTGADTFSSG 594
Qy 588 NEVYIDRFELIPVTATPEAYDLERAQKAVNALFTSINOIGIKTVDTHIDQVSNLVD 647
Db 595 NEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNOLGKTNVTDTHIDQVSNLVT 654
Qy 648 LSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNPKGINRQLDRGWRGSTDITIOGGDDV 707
Db 655 LSEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIOGGDDV 714
Qy 708 FKENVYTLPGTFDECYPTYLYOKIDESKLPYTRYQLRGYIEDSODLELYLIRYNAKHET 767
Db 715 FKENVYTLPGTFDECYPTYLYOKIDESKLPYTRYQLRGYIEDSODLELYLIRYNAKHET 774
Qy 768 VNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDV 827
Db 775 VNVLTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDV 834
Qy 828 GCTDLNEDLVVWIFKIKTODGHARLGNLEFLEEKPLVGEALARKVRAKKWRDKREKLE 887
Db 835 GCTDLNEDLVVWIFKIKTODGHARLGNLEFLEEKPLVGEALARKVRAKKWRDKREKLE 894
Qy 888 LETNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRYHRIRIERYLPELSVIPGVN 947
Db 895 WETNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRYHRIRIERYLPELSVIPGVN 954
Qy 948 VDIFEELKGRIFTAFFLYDARNYKNGDPNGLSCWNVKGVHDVDEQNHRSVLVVPEWE 1007
Db 955 AAIFELEGRIFTAFSLYDARNYKNGDPNGLSCWNVKGVHDVDEQNHRSVLVVPEWE 1014
Qy 1008 AEVSEVRVCPGRGYILRYTAYKEGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVT 1067
Db 1015 AEVSEVRVCPGRGYILRYTAYKEGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVT 1074
Qy 1068 CNDYTAQOEYGGATSRNRYGDEYTGNSNVPADYASVYEKSYTDGRDNPCEENRGY 1127
Db 1075 CNDYVNOEYGGATSRNRYGNEA----PSPADYASVYEKSYTDGRRENPCENRGY 1130
Qy 1128 GDTPLPAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLME 1174
Db 1131 RDTPLPVGYYTKLEYFPETDKVWIEIGETGTFIVDSVELLME 1177

RESULT 9
US-09-873-873-30
; Sequence 30, Application US/09873873
; Patent No. US20020064865A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Gilmer, Amy Jelen
; TITLE OF INVENTION: Polynucleotide Compositions Encoding Broad-Spectrum S-Endotoxins
; FILE REFERENCE: MECO:210--2
; CURRENT APPLICATION NUMBER: US/09/873,873
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/253,341
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 08/922,505
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: US 08/754,490
; PRIOR FILING DATE: 1996-11-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1193
; TYPE: PR
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hybrid Delta-Endotoxin
US-09-873-873-30

Query Match 69.1%; Score 4313.5; DB 10; Length 1193;
Best Local Similarity 70.3%; Pred. No. 0;
Matches 844; Conservative 97; Mismatches 226; Indels 33; Gaps 12;

QY 1 MNNNQ-NCVPCYNCLNPEVEILNEER-STGRPLDLSLTRFLSEFVPGVAGFL 58
DB 1 MDNNPNINEICPNCLSNPEVEVLGGRIETGYTIDISLSTQFLLSEFVPGAGFVLG 60
QY 59 FDLINGFITPDSWSLFLQIOLEIQRITLERNRAITTLRGLADSEYIYIALREWEAN 118
DB 61 VDIWIGIFGSPQWDAPFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWEAD 120
QY 119 PNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYQAAANLHLSLLRDVSPGQ 178
DB 121 PTNPALREEMRIQFNDMNSALTATPLFAVQNVQVPLLSVYQAAANLHLSVLDRDVSFQ 180
QY 179 GGLDIATVNNHYNRLINLHRYTKCLDYYNOGLENLRGNTROWARNQFRDLTLV 238
DB 181 RWGFAAATINSYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDWRYNQFRRELTIV 240
QY 239 LDIVALFPNDYRTYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
DB 241 LDIVALFPNDYRTYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
QY 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPYSYGVF-NPGGAIWIADED 351
DB 295 HLMDFMNSLFTVAETVRSOTVWGGH--LVSSRNTAGNRINFPYSYGVF-NPGGAIWIADED 351
QY 352 PRPFTLSDPVRG---GFGNPHY-VLGLRGVAFQOQTGTHTRFRNSGTIDSLDEIP 407
DB 355 GCGVTRTSLTYRRPFGNIGINQQSLVLDGTFFAYGTSSNLPFSAVYRKSGTVDSLEIP 414
QY 408 PDNSGAPNDYSHVNLNHYTVFVRWPCIEISGDSWRAPMFSSWTHRSATPTNTDPERITOI 467
DB 415 PNNNVPPQGFHRLSHVMSFSGFSNSVSIIRAPMFSSWTHRSATPTNTDPERINOI 474
QY 468 PLVKAHTLOSCTVVRGPGFTGGDILRRSTGGPFAYTIYVINGQLPQRYRARIKASTTN 527
DB 475 PLVKGFRVWGGTSVITGPGFTGGDILRRSTGGPFAYTIYVINGQLPQRYRARIKASTTN 527
QY 528 LRIYV-TVAGERIFAGQ-----FNKMTDGTPLFQSFYATINTATFPMSQSFTV- 579
DB 535 ARVIVLTGAASTGVGGQVSVNMPLOKTMIEIGENLTSRTFRYTDFSNPTFRANPDITIGIS 594
QY 580 -----GADTFSSGNEVYIDREELIPVATFEAYDLERAKAVNALFTSINOIGIKTDVT 634
DB 595 EQPLFGAGSISG-ELYIDKILILADATFEASDLERAKAVNALFTSINOIGIKTDVT 653
QY 635 DYHDOVSNLVCLEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWR 694
DB 654 DYHDOVSNLVCLEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWR 713
QY 695 GSTDITIORGDVFNKYVTLPGTDECYPTLYOKIDESKLPKYTRYLGRYIEDSQDL 754
DB 714 GSTDITIORGDVFNKYVTLPGTDECYPTLYOKIDESKLPKYTRYLGRYIEDSQDL 773
QY 755 EYILIRYNAKHETVNVGLTSLVQSPVIRKCCPEPNCAPHLEWNPDLDCSCEGK 814
DB 774 EYILIRYNAKHETVNVGLTSLVQSPVIRKCCPEPNCAPHLEWNPDLDCSCEGK 833
QY 815 AHHSHFSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKR 874
DB 834 AHHSHFSLDIDVGCTDLNEDLDVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKR 893
QY 875 ABKKWRDKREKLEETNIVYKAKESVDALFVNSQYDQLOADNTNAMIHAADKRVHIRE 934
DB 894 ABKKWRDKREKLEETNIVYKAKESVDALFVNSQYDQLOADNTNAMIHAADKRVHIRE 953

QY 935 AYLPESLVIPGVNVDIFEELKGRIFTAFPLYDARNVKNKGDENNGLSCWNVKGVHDVEEQ 994
DB 954 AYLPESLVIPGVNAAIFEELEGRIFTAYSLYDARNVKNKGDENNGLCWNVKGVHDVEEQ 1013
QY 995 NNHRSVLVPEWEAEVSRQVRCVPCRGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSN 1054
DB 1014 NNHRSVLVPEWEAEVSRQVRCVPCRGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSN 1073
QY 1055 CVVEEYVPNTVTCNDYTANQEEYGGAYTSRNGYDETYGSSNSVPADYASVYEKSYTD 1114
DB 1074 CVVEEYVPNTVTCNNYTGTEYEGYTSRNGYDETYGSSNSVPADYASVYEKSYTD 1133
QY 1115 GRSDNCPESNRCYGYDTPLPAGYVTKELYFPETDKWLEIGETEGTFFVDSVELLME 1174
DB 1134 GRSDNCPESNRCYGYDTPLPAGYVTKELYFPETDKWLEIGETEGTFFVDSVELLME 1193

RESULT 10
US-09-756-643-2
; Sequence 2, Application US/09756643
; Patent No. US20010026939A1
; GENERAL INFORMATION:
; APPLICANT: Rice, Douglas
; APPLICANT: Carozzi, Nadine
; APPLICANT: Anderson, David
; APPLICANT: Rajasekaran, Kanniah
; APPLICANT: Rangan, Thirumale
; APPLICANT: Yehofsky, Richard
; APPLICANT: Lotstein, Richard
; APPLICANT: De Framond, Annick
; TITLE OF INVENTION: Insecticidal Cotton Plant Cells
; FILE REFERENCE: S-16768E
; CURRENT APPLICATION NUMBER: US/09/756,643
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 08/218,697
; PRIOR FILING DATE: 1994-03-28
; PRIOR APPLICATION NUMBER: 07/759,969
; PRIOR FILING DATE: 1991-09-16
; PRIOR APPLICATION NUMBER: 07/274,452
; PRIOR FILING DATE: 1988-11-18
; PRIOR APPLICATION NUMBER: 07/122,109
; PRIOR FILING DATE: 1987-11-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-09-756-643-2

Query Match 67.4%; Score 4211.5; DB 10; Length 1155;
Best Local Similarity 70.0%; Pred. No. 0;
Matches 831; Conservative 83; Mismatches 228; Indels 45; Gaps 9;

QY 1 MNNNQ-NCVPCYNCLNPEVEILNEER-STGRPLDLSLTRFLSEFVPGVAGFL 58
DB 1 MDNNPNINEICPNCLSNPEVEVLGGRIETGYTIDISLSTQFLLSEFVPGAGFVLG 60
QY 59 FDLINGFITPDSWSLFLQIOLEIQRITLERNRAITTLRGLADSEYIYIALREWEAN 118
DB 61 VDIWIGIFGSPQWDAPFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWEAD 120
QY 119 PNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYQAAANLHLSLLRDVSPGQ 178
DB 121 PTNPALREEMRIQFNDMNSALTATPLFAVQNVQVPLLSVYQAAANLHLSVLDRDVSFQ 180
QY 179 GGLDIATVNNHYNRLINLHRYTKCLDYYNOGLENLRGNTROWARNQFRDLTLV 238
DB 181 RWGFAAATINSYNDLTRLIGNYTDYAVRWYNTGLERWGPDSRDWRYNQFRRELTIV 240
QY 239 LDIVALFPNDYRTYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294
DB 241 LDIVALFPNDYRTYPIOTSSOLTREIYTSVIEDSPVSANIPNGFNRA---EFGVRPP 294


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Qy 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRTAGNRINPSPYGVF-NPGGAIWIADED 351
Db 295 HLMDLINSITITDAHGEYTWGSHQINASVFGSGPETFPLYGTMGNAAPQORIVAQL 354
Qy 352 PRPFYRTLSDFVVRG---GFGNPHY-VLGLRGVAFQQTGNHRTFRNSGTIDSLDEIP 407
Db 355 GQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAFGTSSNLPYSAVYKSGTVDSLDEIP 414
Qy 408 PQDMSGAPWNDYSHVLNHWTVFVRWPEGEISGSDSWRAPMFWTHRSATPTNTIDPERITQI 467
Db 415 PQNNVPPRQGFQSHLSHVSMFRSGFSNVSIIIRAPMFWTHRSAEFNIIIPSSQITQI 474
Qy 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSQGPAYTIVNNGQLPQRYRIRYASTTN 527
Db 475 PLTASTNLGSGTSVKGPGFTGGDILRRTSQGIQLTSLVNITAPLSQIRYRIRYASTTN 534
Qy 528 LRIYTVVAGERIFAQGNKMTDGTPLTFQSFYATINTAFTFPMSSQSFIVGADTFSSG 587
Db 535 LQFHTSIDGRFINOGNFSATNSGSLNLSQSGSFRVTGFTTFPNSGSSVFTLSAHVFNPG 594
Qy 588 NEVVIDRELIPVTATPEAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 647
Db 595 NEVVIDRELIPVTATPEAEYDLERAQKAVNELFTSSNQIGLKTDTYHIDQVSNLVEC 654
Qy 648 LSDEFCLDEKELSEKVKHAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDV 707
Db 655 LSDEFCLDEKELSEKVKHAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIOGGDDV 714
Qy 708 FKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSDLEIYLRYNKAKHET 767
Db 715 FKENYVTLPGTFDECYPTLYQKIDESKLKAYTRYQLRGYIEDSDLEIYLRYNKAKHET 774
Qy 768 VNVLTGSLWPLSVQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHPSLIDIV 827
Db 775 VNVPGTGLWPLSLAPSPI-----GKCAHSHHPSLIDIV 808
Qy 828 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLPEEKPLVGEALARYKRAEKWKDRKREKLE 887
Db 809 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLPEEKPLVGEALARYKRAEKWKDRKREKLE 868
Qy 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIREAYLPELSVPGVN 947
Db 869 WETNIVYKEAKESVDALFVNSQYDRLQADNTIAMIHAADKRVHRIREAYLPELSVPGVN 928
Qy 948 VDIEELKGRIFTAFPLDYDARNVKNQGFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 1007
Db 929 AAIFEELEGRIFTAFSLDYDARNVKNQGFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 988
Qy 1008 AEVSOEVRVCPGRGYILRVYAKGEGYGCVTIHEIENNTDELKFSNCVEEVEVPYNTVT 1067
Db 989 AEVSOEVRVCPGRGYILRVYAKGEGYGCVTIHEIENNTDELKFSNCVEEVEVPYNTVT 1048
Qy 1068 CNDYTANDEEYGGAYTSNRNGYDVTYGNSSVPADYASVYEKSYTDGRDNPCCSNRGY 1127
Db 1049 CNDYTATQEEVEGTYTSNRNGYDGTAYESNNSVPADYASVYEKSYTDGRDNPCCSNRGY 1108
Qy 1128 GDTPLPAGYVTKLEYFPETDKVWIEIETEGTGFIVDSVELLIMEE 1174
Db 1109 GDTPLPAGYVTKLEYFPETDKVWIEIETEGTGFIVDSVELLIMEE 1155

RESULT 11
US-09-851-194-2
; Sequence 2, Application US/09851194
; Patent No. US20020048799A1
; GENERAL INFORMATION:
; APPLICANT: Adang, Michael J
; TITLE OF INVENTION: Insecticidal Protein Fragments
; FILE REFERENCE: Mps17-8304
; CURRENT APPLICATION NUMBER: US/09/851,194
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 06/617,321

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; PRIOR FILING DATE: 1984-06-04
; PRIOR APPLICATION NUMBER: US 08/477,973
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/687,017
; PRIOR FILING DATE: 1996-07-16
; PRIOR APPLICATION NUMBER: US 08/682,169
; PRIOR FILING DATE: 1996-07-16
; PRIOR APPLICATION NUMBER: US 09/422,833
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 09/612,811
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1178
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; US-09-851-194-2

Query Match 66.4%; Score 4148; DB 10; Length 1178;
Best Local Similarity 69.18; Pred. No. 0;
Matches 828; Conservative 85; Mismatches 241; Indels 44; Gaps 14;

Qy 1 MENNIO-NQCPYPYCNLNPEVEILNEER-STGRCLPLDISLSTRELLSEFVGVGVAFGL 58
Db 1 MDNPNINECIPYCNLSNPEVEVLGERIETGYTPIDISLSTQELLSEFVGVGAGFVLGL 60
Qy 59 FDLIWFPTPSDWSFLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLI 118
Db 61 VDIWIGFPGSDWFLVLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLIQLI 120
Qy 119 PNAQLREDVIRFANTDQALITAINNETLTATFEPLLSVYVQAAANLHLSLRDAVSFQ 178
Db 121 PTNPALREEMKIQFNDMNSALTATPLFAVQNYQVPLLSVYVQAAANLHLSLRDVSFQ 180
Qy 179 GWGLDIATVNNHYNBLINLHRYTKHCLDLYNQGLNENLGTNTROWARFNQFRDLTLTV 238
Db 181 RWGFDAAATINSRYNDLTRIGNYTDYAVRWYNTGLERWVGPDSDRWVRYNQFRDLTLTV 240
Qy 239 LDIVALFNYDVRTYPIQTSQLTREIYTSVIEDSPSVANIPNGFNRA---EFGVRPP 294
Db 241 LDIVALFNYDSRRYPIRTVSQLTREIYTNPVLE-----NFDGFRGSAQGIERSIRP 294
Qy 295 HLMDFMNSLFVTAETVRSQTVMGH--LVSSRTAGNRINPSPYGVF-NPGGAIWIADED 351
Db 295 HLMDLINSITITDAHGEYTWGSHQINASVFGSGPETFPLYGTMGNAAPQORIVAQL 354
Qy 352 PRPFYRTLSDFVVRG---GFGNPHY-VLGLRGVAFQQTGNHRTFRNSGTIDSLDEIP 407
Db 355 GQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAFGTSSNLPYSAVYKSGTVDSLDEIP 414
Qy 408 PQDMSGAPWNDYSHVLNHWTVFVRWPEGEISGSDSWRAPMFWTHRSATPTNTIDPERITQI 467
Db 415 PQNNVPPRQGFQSHLSHVSMFRSGFSNVSIIIRAPMFWTHRSAEFNIIIPSSQITQI 474
Qy 468 PLVKAHTLQSGTTVVRGPGFTGGDILRRTSQGPAYTIVNNGQLPQRYRIRYASTTN 527
Db 475 PLTASTNLGSGTSVKGPGFTGGDILRRTSQGIQLTSLVNITAPLSQIRYRIRYASTTN 534
Qy 528 LRIYTVVAGERIFAQGNKMTDGTPLTFQSFYATINTAFTFPMSSQSFIVGADTFSSG 587
Db 535 LQFHTSIDGRFINOGNFSATNSGSLNLSQSGSFRVTGFTTFPNSGSSVFTLSAHVFNPG 594
Qy 588 NEVVIDRELIPVTATPEAEYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVD 647
Db 595 NEVVIDRELIPVTATPEAEYDLERAQKAVNELFTSSNQIGLKTDTYHIDQVSNLVEC 654
Qy 648 LSDEFCLDEKELSEKVKHAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDV 707
Db 655 LSDEFCLDEKELSEKVKHAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIOGGDDV 714
Qy 708 FKENYVTLPGTFDECYPTLYQKIDESKLKPYTRYQLRGYIEDSDLEIYLRYNKAKHET 767
Db 715 FKENYVTLPGTFDECYPTLYQKIDESKLKAYTRYQLRGYIEDSDLEIYLRYNKAKHET 774
Qy 768 VNVLTGSLWPLSVQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHPSLIDIV 827
Db 775 VNVPGTGLWPLSLAPSPI-----GKCAHSHHPSLIDIV 808
Qy 828 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLPEEKPLVGEALARYKRAEKWKDRKREKLE 887
Db 809 GCTDLNEDLVWVIFKIKTQGHARLGNLEFLPEEKPLVGEALARYKRAEKWKDRKREKLE 868
Qy 888 LETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHRIREAYLPELSVPGVN 947
Db 869 WETNIVYKEAKESVDALFVNSQYDRLQADNTIAMIHAADKRVHRIREAYLPELSVPGVN 928
Qy 948 VDIEELKGRIFTAFPLDYDARNVKNQGFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 1007
Db 929 AAIFEELEGRIFTAFSLDYDARNVKNQGFNGLSCWNVKGVHDVDEEQNNHRSVLVVPWE 988
Qy 1008 AEVSOEVRVCPGRGYILRVYAKGEGYGCVTIHEIENNTDELKFSNCVEEVEVPYNTVT 1067
Db 989 AEVSOEVRVCPGRGYILRVYAKGEGYGCVTIHEIENNTDELKFSNCVEEVEVPYNTVT 1048
Qy 1068 CNDYTANDEEYGGAYTSNRNGYDVTYGNSSVPADYASVYEKSYTDGRDNPCCSNRGY 1127
Db 1049 CNDYTATQEEVEGTYTSNRNGYDGTAYESNNSVPADYASVYEKSYTDGRDNPCCSNRGY 1108
Qy 1128 GDTPLPAGYVTKLEYFPETDKVWIEIETEGTGFIVDSVELLIMEE 1174
Db 1109 GDTPLPAGYVTKLEYFPETDKVWIEIETEGTGFIVDSVELLIMEE 1155

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Db 705 TGITIQGGDDVFKENYVTLGTFDFCEPTYLYQKIDESKLKAFTRYQLRGYIEDSQDLEI 764
Qy 757 YLIIRYNAKHETVNNVLGTSGLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGEKCAH 816
Db 765 YLIIRYNAKHETVNNVPGTGLWPLSLAQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGEKCAH 824
Qy 817 HSHIFSLLDVGCTDLNEDLWVIFKIKTDQGHARLGNLEFLEBKPLVGEALARKVRAE 876
Db 825 HSHFSLLDVGCTDLNEDLWVIFKIKTDQGHARLGNLEFLEBKPLVGEALARKVRAE 884
Qy 877 KKWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHRIREAY 936
Db 885 KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAY 944
Qy 937 LPELSVIRGVNVDIFEEELKGRIFTAFFLYDARNVKNKGDFNGLSCWNVKGVHVDVEBONN 996
Db 945 LPELSVIRGVNVAIFEELEGRIFTAFSLYDARNVKNKGDFNGLSCWNVKGVHVDVEEONN 1004
Qy 997 HRSVLVPEWEAEYSQEVRCVPCGRGYILRVTAIYKEGYGEGCVTHIEIENNTDELKFSNCV 1056
Db 1005 QRSVLVPEWEAEYSQEVRCVPCGRGYILRVTAIYKEGYGEGCVTHIEIENNTDELKFSNCV 1064
Qy 1057 BEEVYPNNTVTCNDYTANOEEYGGAYTSRNRGYDITYGSNSVSPADYASVYEEKSYTDGR 1116
Db 1065 BEEIYPNNTVTCNDYTANOEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGR 1120
Qy 1117 RDNCESTRGYDTPPLPAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLLMEE 1174
Db 1121 RENCPEFRNGRYDTPPLPAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLLMEE 1178

RESULT 12
US-09-826-660-21
; Sequence 21, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826.660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-21

Query Match 64.7%; Score 4042.5; DB 10; Length 1163;
Best Local Similarity 67.3%; Pred. No. 4.8e-314;
Matches 814; Conservative 87; Mismatches 226; Indels 83; Gaps 18;

Qy 1 MENNTQOCVPYNCNLNNEVEILNEER-STGRPLDLSLSTRFLLSEFVPGVGVAGLFL 59
Db 1 MEENNQICPYNCNLNNEVEILNEER-STGRPLDLSLSTRFLLSEFVPGVGVAGLFL 60
Qy 60 DLWGFITPDSWLSPLLOLQIEQRIETLENRAITTLRGLADSYEYIIEALREWEANP 119
Db 61 DFVWGVGPSQWDAFLVQIEQLINERIAEFAARNAIALEGNNFNFIYEAKEWESDP 120
Qy 120 NNAQLRDVIRFANTDDALITAINNFTLTSFEIPLLSVYQAAHLHLRLRDVAFSGQ 179
Db 120 NNAQLRDVIRFANTDDALITAINNFTLTSFEIPLLSVYQAAHLHLRLRDVAFSGQ 179
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Db 121 NNPAIRTRVIDRFRIDGLLDERDIPSFRIISGFVEYPLLVSVAQAANLHLAILRDSVIFGER 180
Qy 180 WGLDIATVNNHYNRLINLIHRYTKHCLDITYNOGUENLGTNTROWARENQFRDUTLVL 239
Db 181 WGLTATVNNHYNRLIRHIDEYADHCANTYNGRLNLPKSYQDWITYNRLRLTLLVL 240
Qy 240 DIVALFPNDVRYTPLOTSSOLTRIEYTSVIEDSP---VSANIPNGENRAE-FGVRRPH 295
Db 241 DIAAFFPNYDNRKPIQPVQQLTREYVTDLPNFPNQLSQSAQLPT-FNVMESSAIRPH 299
Qy 296 LMDFMNSLFTAE--TVRSQTWVGHLVSSRNTAGNRINFPISYGVFNPGGAIWIADEP- 352
Db 300 LFDILNLTITDFWFSVCGNFYWGCHRYISSLLGGNITSPIYG-----REANQBP 351
Qy 353 -----RPFYTLSDPV--FVRGGFNGPHYVL-GLRGVAFQOTGTHHTRTFRNSTIDSL 403
Db 352 RSFTFMGPFVFTLNPTRLQLQCPWAPPPNLRGVGEVFP-STPTN-SFTYRGRCQVDSL 409
Qy 404 DEIPQDNMGAPWNDYSHVLNHTVFRWPEIGELSGSDSNRAP-----MFSMTHRSATPTN 457
Db 410 TELPPEDNVPPREGYSHRLCHAFVQRSG-----TFPLTTGVVFSWTHRSATPTN 460
Qy 458 TIDPERITQIPLVKAHTLQSGTTVVRGPGFTGGDILRFTSGGPFAYTIVNINGQLPQRYR 517
Db 461 TIDPERINQIPLVKGFRVWGTSVITGFTGGDILRNTFTGDFVSLQVNLNSPITQRYR 520
Qy 518 ARIYASTNLRIVY-TVAGERIFAGQ-----FNKMTDGTGDLPTQFSFVATINTATFF 570
Db 521 LRFYASSRDARVITLTGAASTGVGGQSVNMPQLKTKMEIGENLTSRTFRYTFDSNPFSF 580
Qy 571 PMSQSSFTV-----GADTFSSGNEVYIDRELIPVTATFEAEYDLERAQKAVNALFTSI 624
Db 581 RANPDIIIGISQPLFGAGSISSG-ELYIDKIEILADATLEAESDLERAQKAVNALFTSS 639
Qy 625 NQIGIKTDVTDYHIDQVSNLVDCLSDDEFCLDEKRELSKVKHAKLSDERILLQDPNFKG 684
Db 640 NQIGLKTVDVTDYHIDRVSNLVECLSDDEFCLDEKRELSKVKHAKLSDBERNLQDPNFRG 699
Qy 685 INQLDRGWRGSTDITIQGGDDVFKENYVTLPGTFDECYPPYLYQKIDESKLKAYTRYQL 744
Db 700 INQLDRGWRGSTDITIQGGDDVFKENYVTLPGTFDECYPPYLYQKIDESKLKAYTRYQL 759
Qy 745 RGYIEDSQDLEIYLIRYNAKHETVNNVLGTSGLWPLSVQSPIRKCGEPNRCAPHLEWNPDL 804
Db 760 RGYIEDSQDLEIYLIRYNAKHETVNNVLGTSGLWPLSVQSPIRKCGEPNRCAPHLEWNPDL 800
Qy 805 DCSRDGKCAHSHSHFSLLDIDVGCTDLNEDLWVIFKIKTDQGHARLGNLEFLEERPL 864
Db 801 -----GKCAHSHSHFSLLDIDVGCTDLNEDLWVIFKIKTDQGHARLGNLEFLEERPL 853
Qy 865 VGEALARKVRAEKKWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMTHA 924
Db 854 VGEALARKVRAEKKWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMTHA 913
Qy 925 ADKRVHRIREAYLPELSIVPGVNVVDIFEEELKGRIFTAFFLYDARNVKNKGDFNGLSCW 984
Db 914 ADKRVHSIREAYLPELSIVPGVNVVAIFEELEGRIFTAFSLYDARNVKNKGDFNGLSCW 973
Qy 985 VKGHYDVEEQNNHRSVLVPEWEAEYSQEVRCVPCGRGYILRVTAIYKEGYGEGCVTHIEI 1044
Db 974 VKGHYDVEEQNNHRSVLVPEWEAEYSQEVRCVPCGRGYILRVTAIYKEGYGEGCVTHIEI 1033
Qy 1045 NNTDELKFSNCVBEVYPPNNTVTCNDYTANOEEYGGAYTSRNRGYDITYGSNSVSPADYA 1104
Db 1034 NNTDELKFSNCVBEVYPPNNTVTCNDYTANOEEYGGAYTSRNRGYDITYGSNSVSPADYA 1093
Qy 1105 SVYEEKSYTDGRRONPCESNRGYDGYTLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1164
Db 1094 SAYEIKAYTDGRRONPCESNRGYDGYTLPAGYVTKLEYFPETDKVWIEIGETGTFIV 1153
Qy 1165 DSVELLMLLEE 1174
Db 1154 DSVELLMLLEE 1163
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QY	49	VPGVGVAFLDILWGFIYP---SDWSLFLQIEOLIEQRIETIELERNPAITTLRGLADSY	105
Db	72	VPAGQIASFYSLFVGLWPGRDPEWIFLEHVEQOLIRQOVTENTROTALARLQAGNSF	131
QY	106	EIYIEALRWEANPNAQUREDVIRFANTDQALLITANNFTLSFLEPILLSVVVQAANL	165
Db	132	RATQOOSLEDWLENRRDARTSVLYTQYTALEDLDFINAMPLFAIRNOEVPFLMWYQAANL	191
QY	166	HLSLLRDAVSFGQWGLDIATVNNHYNRLNIHRYTHKHCLDTYNOGLNLRGTNTROWA	225
Db	192	HLLLLRDASLFGSEFGLTSOEIQRYVYREVQEKTRYSDYCARWYNTGLNLRGTNAESWL	251
QY	226	RPNQPRDLTLVLDIVALFPYDVRTPIQTSSOLTREIYVTSVIEDSPVS-ANIENGF	284
Db	252	KYNQFRDRTLGLVDLVALFPPSYDRVYPMNTSAQLTREIYT-----DPJGRINAPSGF	305
QY	285	-----NRAEEG-----VPPHLMDFMNSLFVTA-----ETVRSOTVWGGLHVSRRN	325
Db	306	ASTNWFNNAPSFESAEEAVIRPPLLDPBQLTIPSVLSRWSNTQYNNYVWGRLEST	365
QY	326	TAGNRINFPYSYVFNPGGAIWIADEDPREFYRT-----LSDPV----FVARGGFNP	372
Db	366	IRGS-LSTSTHGNTNSINPVLQFTSRDVRVYTESFAGINILLTTPYNGVPEWARENRNP	424
QY	373	-----HYVGLGRVAFQQTGTHNTRFRNSGTIDSLDEIPQDNSGAPWNDYSHVLN	424
Db	425	LNSLRGSLYITGYTVGQY-----LFDSETELPETTERPNYESYSHRLS	470
QY	425	HVTFVWPVGEISGDSWRAPMFSWTHRSATPNTIDPERITOPLVKAHTLOSQTTVVVG	484
Db	471	NIRL-----ISG-NLIRAPVSWTHRSADRNTISSDSITQIPLVKSFNLSGTSVVS	523
QY	485	PQGTGGDIIRTSGGFPATVIVNINGQLPQRYRABIRVASTNIRIYTVVAGERIFAQGF	544
Db	524	PQGTGGDIIRTNVNGSVLWGLNFNNTSLQRYRVRVRYAAQSOTMVLRTVVGSTTFDQGF	583
QY	545	NKWDGTCDPLTFOFSYATINTAFIPKASQ-----STVGADITFSSGNEYVIDRPELIP	599
Db	584	PTMSANESLTSOSFRFAEPVGVISAGSQTAGISISNNAQRQTF-----HFDKIEFIP	637
QY	600	VTATFAEYDLERAQKAVNALFTSNIGIKGTVDYDIDQVSNLIVDCLSDFCLEDKRE	659
Db	638	ITATLEAESDLERAQKAVNALFTSSNQIGLKTVDYDHYDRVSNLVECLSDFCLEDKKE	697
QY	660	LSEKVKHAKLSDERNLLODPNFKGINROLDRGWGSTIDITIQRGDDVFKENYVTLPGTF	719
Db	698	LSEKVKHAKLSDERNLLODPNFRGINQLDRGWGSTIDITIOGGDDVFKENYVTLGTF	757
QY	720	DECYPYLYQIDESLKLXYTYQLRGYLEDSDOLEIYLIRYNAKHVNVVLGWSLWPL	779
Db	758	DECYPYLYQIDESLKLKAYTRYQLEGYLEDSDOLEIYLIRYNAKHVNVVPGTGSWLPL	817
QY	780	SVQSPYTKKGEPNRCAPHLEWNPDDLDCSROGGEKCAHSHHFSLDIDVGCOTDLNEDLVW	839
Db	818	SAPSPI-----GKCAHSHHFSLDIDVGCOTDLNEDLVW	851
QY	840	VIEKIKTQDGHARLGNLEFLBEPKLVGEALARKAEKKRQKREKLELENIYVYKAKE	899
Db	852	VIEKIKTQDGHARLGNLEBEPKLVGEALARKAEKKRQKREKLEWETNIYVYKAKE	911
QY	900	SVDALFVNSQYDOLQADTNIAHIAADKRVHRIREAYLPESLPIPGVNVDFIEELKGRIF	959
Db	912	SVDALFVNSQYDLQADTNIAHIAADKRVHSIREAYLPESLPIPGVYNAIFEELEGRIF	971
QY	960	TAFLLYDARNVIRKNGDFNGLSCWNVYKHVDVVEEQNNHRSVLVVPWEAEYSQEVRYCPG	1019
Db	972	TAFSLYDARNVIRKNGDFNGLSCWNVYKHVDVVEEQNNHRSVLVVPWEAEYSQEVRYCPG	1031
QY	1020	RGYILRTAYKEGYGEGCVTHIEINNTDELAFSCNVEEYVYPNNTVTCNDYTAQOEY	1079
Db	1032	RGYILRTAYKEGYGEGCVTHIEINNTDELAFSCNVEEYVYPNNTVTCNDYTAQOEY	1091

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QY   1080 GATYSNRNGDYETGYNSSVPADYASVVEEKSYTGTGRDRNFCESNRNGDYTPLPAGYVT 1139
      I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | |||||
Db   1092 GTYSNRNGDYGAYENSSVPADYASAVEERKAYTGTGRDRNFCESNRNGDYTPLPAGYVT 1151
      I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | |||||
QY   1140 KELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174
      I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | |||||
Db   1152 KELEYPETDKWIEIGETECTFIVDSVELLMEE 1186
      I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | ||||| I | |||||

RESULT 15
US-09-826-660-4
; Sequence 4, Application US/09826660
; Patent No. US20010026940A1
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Steilman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 605
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-4
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QY 481 VVRGPGFTGGDILRETSGPFAYTIVNINGQLPQYRARIYASTTNLRIYVTVAGERIF 540
Db 481 VVRGPGFTGGDILRETSGPFAYTIVNINGQLPQYRARIYASTTNLRIYVTVAGERIF 540
QY 541 AGQFNKTMGTGDPLTFQSFYSATINTAFTFPMQSSTVVGADTFSSGNEVYIDREFELIPV 600
Db 541 AGQFNKTMGTGDPLTFQSFYSATINTAFTFPMQSSTVVGADTFSSGNEVYIDREFELIPV 600
QY 601 TATFE 605
Db 601 TATLE 605

Search completed: November 27, 2002, 20:27:48
Job time : 80 secs

Query Match 100.0%; Score 6244; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNNPEVEILNEERSTGRPLDLSLSLTLSEFVPGVGVAFGLFD 60
DB 1 MENNIONQCVNCLNNPEVEILNEERSTGRPLDLSLSLTLSEFVPGVGVAFGLFD 60

QY 61 LIWGFTPSDWSLFLQIOLIEORITLERNRAITTLRLGLADSYEIIYIETALREWEANPN 120
DB 61 LIWGFTPSDWSLFLQIOLIEORITLERNRAITTLRLGLADSYEIIYIETALREWEANPN 120

QY 121 NACLREDVRIRFANTDDALITAINNFTLTSFEIPLSVVYVQAANLHLSLRDAVSGQGW 180
DB 121 NACLREDVRIRFANTDDALITAINNFTLTSFEIPLSVVYVQAANLHLSLRDAVSGQGW 180

QY 181 GDIAIVNNHYNRLINLHRYTKHCLDYNOGLENLRTGTQWARFNQFRDLTLTVLD 240
DB 181 GDIAIVNNHYNRLINLHRYTKHCLDYNOGLENLRTGTQWARFNQFRDLTLTVLD 240

QY 241 IVALFPNDVRYPIQTSQLTREIYTSVIEDSPVSANIPNGENRAEGVPPHLMDFM 300
DB 241 IVALFPNDVRYPIQTSQLTREIYTSVIEDSPVSANIPNGENRAEGVPPHLMDFM 300

QY 301 NSLFTVETRSQTVMGHLYSSRNAGNINFPYGVFNPGATWIADEDPFRYRILS 360
DB 301 NSLFTVETRSQTVMGHLYSSRNAGNINFPYGVFNPGATWIADEDPFRYRILS 360

QY 361 DPVFRGFGPNHYVLGRVAFQQTGTNHTTFRNSGTISLDEIIPQDNGAPNDYS 420
DB 361 DPVFRGFGPNHYVLGRVAFQQTGTNHTTFRNSGTISLDEIIPQDNGAPNDYS 420

QY 421 HVLNHTVFRWPGESGDSNRAPMFSTHRSATNTIDPERIQIPLVKAHTLQSGTT 480
DB 421 HVLNHTVFRWPGESGDSNRAPMFSTHRSATNTIDPERIQIPLVKAHTLQSGTT 480

QY 481 VVRGFTGGDILRTSGGPFAYTIVNINGQLPQYRARIYASTNLRIVTVAGERIF 540
DB 481 VVRGFTGGDILRTSGGPFAYTIVNINGQLPQYRARIYASTNLRIVTVAGERIF 540

QY 541 AGQNKMTMDGDLTFQSFYATINTATFPMSQSFVVGADTSSGNEVYIDRELIPV 600
DB 541 AGQNKMTMDGDLTFQSFYATINTATFPMSQSFVVGADTSSGNEVYIDRELIPV 600

QY 601 TATFEAEYDLERAOKAVNALFTSINQIGIKTDYDHYDQVSNLVDCSLDEFCDEKREL 660
DB 601 TATFEAEYDLERAOKAVNALFTSINQIGIKTDYDHYDQVSNLVDCSLDEFCDEKREL 660

QY 661 SEKVHAKRLSDERNLLQDPNFKGNQLDRGRWGSTDITIQRGDDVFKENYVTLPGTFD 720
DB 661 SEKVHAKRLSDERNLLQDPNFKGNQLDRGRWGSTDITIQRGDDVFKENYVTLPGTFD 720

QY 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 780
DB 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 780

QY 781 VQSPIRKGGENRCAPHEWNPDLDCSCRDCEKCAHSHHPSLTDVGCCTDLNEDLWVW 840
DB 781 VQSPIRKGGENRCAPHEWNPDLDCSCRDCEKCAHSHHPSLTDVGCCTDLNEDLWVW 840

QY 841 IFKIKTOGHARLGNLFELEKPLVGEALARKVRAEKKWRDKREKLETNIVYKEAKES 900
DB 841 IFKIKTOGHARLGNLFELEKPLVGEALARKVRAEKKWRDKREKLETNIVYKEAKES 900

QY 901 VDALFVNSQDQLQADNIAHIAADKRVHRIEAYLPESVIPGVNVDIPEELKGRIFT 960
DB 901 VDALFVNSQDQLQADNIAHIAADKRVHRIEAYLPESVIPGVNVDIPEELKGRIFT 960

QY 961 AFFLYDARNVTKNGDNGLSCWNVKGVHDVVEEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020
DB 961 AFFLYDARNVTKNGDNGLSCWNVKGVHDVVEEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020

QY 1021 GYLIRVTAYKEGEGCVTIHEIENNTDELKFSNCVEEVEYPPNNTVTCNDYTANQEEYGG 1080
DB 1021 GYLIRVTAYKEGEGCVTIHEIENNTDELKFSNCVEEVEYPPNNTVTCNDYTANQEEYGG 1080

QY 1081 AYTSSNRGYDETYGNSNVPADYASVYEKSYTDGRRDNPCESNRGYGDTPLPAGYVTK 1140
DB 1081 AYTSSNRGYDETYGNSNVPADYASVYEKSYTDGRRDNPCESNRGYGDTPLPAGYVTK 1140

QY 1141 ELEYPETDKVWIEIGETEGTFTIVDSVELLMEE 1174
DB 1141 ELEYPETDKVWIEIGETEGTFTIVDSVELLMEE 1174

RESULT 2

US-08-349-867-25
; Sequence 25, Application US/08349867
; Patent No. 5508264
; GENERAL INFORMATION:
; APPLICANT: Bradfisch, Gregory A.
; APPLICANT: Thompson, Mark E.
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,867
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: XA86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-349-867-25

Query Match 100.0%; Score 6244; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNNPEVEILNEERSTGRPLDLSLSLTLSEFVPGVGVAFGLFD 60
DB 1 MENNIONQCVNCLNNPEVEILNEERSTGRPLDLSLSLTLSEFVPGVGVAFGLFD 60

QY 61 LIWGFTPSDWSLFLQIOLIEORITLERNRAITTLRLGLADSYEIIYIETALREWEANPN 120
DB 61 LIWGFTPSDWSLFLQIOLIEORITLERNRAITTLRLGLADSYEIIYIETALREWEANPN 120

QY 121 NACLREDVRIRFANTDDALITAINNFTLTSFEIPLSVVYVQAANLHLSLRDAVSGQGW 180
DB 121 NACLREDVRIRFANTDDALITAINNFTLTSFEIPLSVVYVQAANLHLSLRDAVSGQGW 180

QY 181 GDIAIVNNHYNRLINLHRYTKHCLDYNOGLENLRTGTQWARFNQFRDLTLTVLD 240
DB 181 GDIAIVNNHYNRLINLHRYTKHCLDYNOGLENLRTGTQWARFNQFRDLTLTVLD 240

Db 181 GLDIATVNNHYNRLNLIHRYTKHCLDVTYNOGLENLRGNTNRQWARFNFQRRDLTLTVLD 240
Qy 241 IVALPNDVTRYPQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
Db 241 IVALPNDVTRYPQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
Qy 301 NSLFTVTAETVRSQTYWGGHLSVSRNAGNINFPSPGVNPGGAIWIADEDPFPYRTLS 360
Db 301 NSLFTVTAETVRSQTYWGGHLSVSRNAGNINFPSPGVNPGGAIWIADEDPFPYRTLS 360
Qy 361 DPVFRGGFGNPHYVYLGVRGVAFOQTGTHRTFRNSGTIDSLDEIPPODNGAPWNDYS 420
Db 361 DPVFRGGFGNPHYVYLGVRGVAFOQTGTHRTFRNSGTIDSLDEIPPODNGAPWNDYS 420
Qy 421 HVLNHTVFRVPGEISGDSWRAPFESWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480
Db 421 HVLNHTVFRVPGEISGDSWRAPFESWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480
Qy 481 VVRGPGFTGGDLRLRTSGGPFAYTIWNINGQLPQRYRARIYASTTNLRIYTVVAGERIF 540
Db 481 VVRGPGFTGGDLRLRTSGGPFAYTIWNINGQLPQRYRARIYASTTNLRIYTVVAGERIF 540
Qy 541 AQOFNKMTGDTGDLTFQSFYSATINTATFPMSQSFTVGADTFSSGNEVYIDRDELIPV 600
Db 541 AQOFNKMTGDTGDLTFQSFYSATINTATFPMSQSFTVGADTFSSGNEVYIDRDELIPV 600
Qy 601 TATFAEYDLERAQAVNALFTSINOIGIKTDVTDYHIDOVNLVDCLSDFCLEKREL 660
Db 601 TATFAEYDLERAQAVNALFTSINOIGIKTDVTDYHIDOVNLVDCLSDFCLEKREL 660
Qy 661 SEKVKHAKRLSDERNLLODPNPKGINROLDRGWRGSTDITIQGGDDVFKENYVTLPGTFD 720
Db 661 SEKVKHAKRLSDERNLLODPNPKGINROLDRGWRGSTDITIQGGDDVFKENYVTLPGTFD 720
Qy 721 ECPYLYLCKIDESKLPKPYRYOLRGYIEDSODLEIYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYLCKIDESKLPKPYRYOLRGYIEDSODLEIYLIRYNAKHETVNVLTGSLWPLS 780
Qy 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHPSLDIDVGCTDLNEDLDVWV 840
Db 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHPSLDIDVGCTDLNEDLDVWV 840
Qy 841 IFKIKTQGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTQGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900
Qy 901 VDALFVNSQYDQLOQADTNIAHAAKRVHRTREAYLPVGVNVDIFPEELKGRIET 960
Db 901 VDALFVNSQYDQLOQADTNIAHAAKRVHRTREAYLPVGVNVDIFPEELKGRIET 960
Qy 961 AFFLYDARNVKNKGNDFNGLSCWNYKGHVDBVEEQNNHRSVLVVPWEAEVSVQEVRCPCR 1020
Db 961 AFFLYDARNVKNKGNDFNGLSCWNYKGHVDBVEEQNNHRSVLVVPWEAEVSVQEVRCPCR 1020
Qy 1021 GYLIVTAYKEGSGGCVTIHEIENNTDELKFSNCVVEEYVNNVTCNDYTPANQEEYGG 1080
Db 1021 GYLIVTAYKEGSGGCVTIHEIENNTDELKFSNCVVEEYVNNVTCNDYTPANQEEYGG 1080
Qy 1081 AYTSSNRGYDETYGNSVSPADYASVYEKSYTDGRONPCSNRGYGDYTPLPAGYVTK 1140
Db 1081 AYTSSNRGYDETYGNSVSPADYASVYEKSYTDGRONPCSNRGYGDYTPLPAGYVTK 1140
Qy 1141 ELEYFPETDKVWIEIGETEGTIFVDSVELLLMEE 1174
Db 1141 ELEYFPETDKVWIEIGETEGTIFVDSVELLLMEE 1174

RESULT 3

US-08-349-867-32
; Sequence 32, Application US/08349867
; Patent No. 5508264
; GENERAL INFORMATION:
; APPLICANT: Bradfisch, Gregory A.

; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: No. 5508264el Pesticidal Compositions
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL USA
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/349,867
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-349-867-32

Query Match 100.0%; Score 6244; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MENNIQNCVPYNCLNNEPEVILNEERSTGRPLDLSLSTRFLSEFVPGVGVAFGLFD 60
Db 1 MENNIQNCVPYNCLNNEPEVILNEERSTGRPLDLSLSTRFLSEFVPGVGVAFGLFD 60
Qy 61 LWGFTIPSDWSLELQLEQLQETLELERNRATTLRLGLADSVETIYLEARWEANEN 120
Db 61 LWGFTIPSDWSLELQLEQLQETLELERNRATTLRLGLADSVETIYLEARWEANEN 120
Qy 121 NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDVAFSGQGW 180
Db 121 NAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDVAFSGQGW 180
Qy 181 GLDIATVNNHYNRLNLIHRYTKHCLDVTYNOGLENLRGNTNRQWARFNFQRRDLTLTVLD 240
Db 181 GLDIATVNNHYNRLNLIHRYTKHCLDVTYNOGLENLRGNTNRQWARFNFQRRDLTLTVLD 240
Qy 241 IVALPNDVTRYPQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
Db 241 IVALPNDVTRYPQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
Qy 301 NSLFTVTAETVRSQTYWGGHLSVSRNAGNINFPSPGVNPGGAIWIADEDPFPYRTLS 360
Db 301 NSLFTVTAETVRSQTYWGGHLSVSRNAGNINFPSPGVNPGGAIWIADEDPFPYRTLS 360
Qy 361 DPVFRGGFGNPHYVYLGVRGVAFOQTGTHRTFRNSGTIDSLDEIPPODNGAPWNDYS 420
Db 361 DPVFRGGFGNPHYVYLGVRGVAFOQTGTHRTFRNSGTIDSLDEIPPODNGAPWNDYS 420
Qy 421 HVLNHTVFRVPGEISGDSWRAPFESWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480
Db 421 HVLNHTVFRVPGEISGDSWRAPFESWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480
Qy 481 VVRGPGFTGGDLRLRTSGGPFAYTIWNINGQLPQRYRARIYASTTNLRIYTVVAGERIF 540

Db 481 VVRGPGFTGGDIIRRTSGGFFAYTIVNINQQLPQRYRARIYASTNLRIVYTVAGERIF 540
QY 541 AGQFNKTMGTGDLTQSSSYATINTAFPPMSQSFVTCADTFSSGNEVYIDRFELIPV 600
Db 541 AGQFNKTMGTGDLTQSSSYATINTAFPPMSQSFVTCADTFSSGNEVYIDRFELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSNLVCLDSDEFCLDEKREL 660
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSNLVCLDSDEFCLDEKREL 660
QY 661 SEKVKAHKLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVKAHKLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
QY 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780
QY 781 VOSPIKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVVV 840
Db 781 VOSPIKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLDVVV 840
QY 841 IFKIKTDQGHARGNLEFTEKPLVGEALARKVRAEKWKDRKREKLELETNIVYKEAKES 900
Db 841 IFKIKTDQGHARGNLEFTEKPLVGEALARKVRAEKWKDRKREKLELETNIVYKEAKES 900
QY 901 VDALFVNSYDQLOADNTAMTHAADKVRHIREAYLPELSVIPGYNVDFEELKGRIFT 960
Db 901 VDALFVNSYDQLOADNTAMTHAADKVRHIREAYLPELSVIPGYNVDFEELKGRIFT 960
QY 961 AFPLXDARNVIKNGDFNGLSCWNVKRGVHDVEBQNNHRSVLVVPWEAEVQSVRVCPCR 1020
Db 961 AFPLXDARNVIKNGDFNGLSCWNVKRGVHDVEBQNNHRSVLVVPWEAEVQSVRVCPCR 1020
QY 1021 GYLIRVATYKEGEGECVTIHEIENNTDELKFSNCVVEEYYPNNVTYCNQDYANQEEYGG 1080
Db 1021 GYLIRVATYKEGEGECVTIHEIENNTDELKFSNCVVEEYYPNNVTYCNQDYANQEEYGG 1080
QY 1081 AYTSNRNGYDEYGNSSVPADYASYEKSXYTDGRDNPCESNRGYGDYTPLPAGYVTK 1140
Db 1081 AYTSNRNGYDEYGNSSVPADYASYEKSXYTDGRDNPCESNRGYGDYTPLPAGYVTK 1140
QY 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174
Db 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174

RESULT 4
US-08-239-476-25
; Sequence 25, Application US/08239476
; Patent No. 552783
; GENERAL INFORMATION:
; APPLICANT: Thompson, Mark
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
; TITLE OF INVENTION: Pseudomonas fluorescens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,476
; FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-239-476-25
Query Match 100.0%; Score 6244; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MENNIOQCVPYCNLANPEVEILNEERSTGRPLDLSLTRELLSEFFVPGVGVAFGLFD 60
Db 1 MENNIOQCVPYCNLANPEVEILNEERSTGRPLDLSLTRELLSEFFVPGVGVAFGLFD 60
QY 61 LWGFTTPSDWSLFLLOIEQLIEQRIETLERNAITTLRGLADSYIYEALREWEANPN 120
Db 61 LWGFTTPSDWSLFLLOIEQLIEQRIETLERNAITTLRGLADSYIYEALREWEANPN 120
QY 121 NQALREDVIRFANTDDALITAINNETLTSFEIPLLSVYQAAHLHLRLDRAVSFGQW 180
Db 121 NQALREDVIRFANTDDALITAINNETLTSFEIPLLSVYQAAHLHLRLDRAVSFGQW 180
QY 181 GLDIATVNNHYNRLINLHRYTKHCLDLYNQGLENLGRNTROWARFNQFRDLTLTVLD 240
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QY 241 IVALFPNDYRVPIOTSSQLTREIYTSVSSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300
Db 241 IVALFPNDYRVPIOTSSQLTREIYTSVSSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300
QY 301 NSLFVTAETVRSQTVWGGHLVSRNTAGNRINFPSPYGVFNPGGAIWIADDPFPYRTLS 360
Db 301 NSLFVTAETVRSQTVWGGHLVSRNTAGNRINFPSPYGVFNPGGAIWIADDPFPYRTLS 360
QY 361 DPFVVRGEGFNHYVLGRGVAFOQTGTNHTFRNSGTIDSLDEIPPODNSGAPWNDYS 420
Db 361 DPFVVRGEGFNHYVLGRGVAFOQTGTNHTFRNSGTIDSLDEIPPODNSGAPWNDYS 420
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Db 421 HVLNHWTFVRWPGETSGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKARTLOSQT 480
QY 481 VVRGPGFTGGDILRRTSGGFFAYTIVNINQQLPQRYRARIYASTNLRIVYTVAGERIF 540
Db 481 VVRGPGFTGGDILRRTSGGFFAYTIVNINQQLPQRYRARIYASTNLRIVYTVAGERIF 540
QY 541 AGQFNKTMGTGDLTQSSSYATINTAFPPMSQSFVTCADTFSSGNEVYIDRFELIPV 600
Db 541 AGQFNKTMGTGDLTQSSSYATINTAFPPMSQSFVTCADTFSSGNEVYIDRFELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSNLVCLDSDEFCLDEKREL 660
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDOVSNLVCLDSDEFCLDEKREL 660
QY 661 SEKVKAHKLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVKAHKLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
QY 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYLYQKIDESKLPYTRYQLRGYIEDSQDLLEYLIRYNAKHETVNVLTGSLWPLS 780

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QY 781 VQSPIKCCGPNRCAPHELEWNPDLDCSCRDGKCAHSHHSHFSLDIDVGCTDLNEDLDVWV 840
Db 781 VQSPIKCCGPNRCAPHELEWNPDLDCSCRDGKCAHSHHSHFSLDIDVGCTDLNEDLDVWV 840
QY 841 IFKIKTDGCHARLGNLEFELEKPLVGEALARYKRAEKKRDRKREKLELETNIVYKEAKES 900
Db 841 IFKIKTDGCHARLGNLEFELEKPLVGEALARYKRAEKKRDRKREKLELETNIVYKEAKES 900
QY 901 VDALFVNSQDQLQADNTIAMIHAADKRVHRIREAYLPESLPIGVNVDFIPELKGRIFT 960
Db 901 VDALFVNSQDQLQADNTIAMIHAADKRVHRIREAYLPESLPIGVNVDFIPELKGRIFT 960
QY 961 AFPLYDARNVWIKNGDNNGLSNWNVGHVDVBQNNHRSVLVVPWEAEVQEVRCPCR 1020
Db 961 AFPLYDARNVWIKNGDNNGLSNWNVGHVDVBQNNHRSVLVVPWEAEVQEVRCPCR 1020
QY 1021 GYILRTAYKEGEGECVTIHEENTNTDELKFSNCVVEEVEYPNNTVTCNDYTANQEEYGG 1080
Db 1021 GYILRTAYKEGEGECVTIHEENTNTDELKFSNCVVEEVEYPNNTVTCNDYTANQEEYGG 1080
QY 1081 AYTSSNRNGYDITYGSSNVPADYASVVEEKSYYDGRDRNPCESNRGYGYDTPLPAGYVTK 1140
Db 1081 AYTSSNRNGYDITYGSSNVPADYASVVEEKSYYDGRDRNPCESNRGYGYDTPLPAGYVTK 1140
QY 1141 ELEVPETDKWIEIGETEGTFIVDSVELLLMEE 1174
Db 1141 ELEVPETDKWIEIGETEGTFIVDSVELLLMEE 1174

RESULT 5
US-08-356-034-8
; Sequence 8, Application US/08356034
; Patent No. 5691308
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Sick, August J.
; TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
; TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
; TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,034
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/210,110
; FILING DATE:
; APPLICATION NUMBER: 07/865,168
; FILING DATE: 09-APR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/451,261
; FILING DATE: 14-DEC-89
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/371,955
; FILING DATE: 27-JUN-89
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, Roman
; REGISTRATION NUMBER: 21,023
; REFERENCE/DOCKET NUMBER: MA43.C1.D1

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904)375-8100
; TELEFAX: (904)372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS81I
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
; CLONE: 811A
; US-08-356-034-8

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Query Match 100.0%; Score 6244; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIQOCVPYCNLNNPEVEILNEERSTGRPLDIDISLTLRFLSSBEPVGVGVAFLGFD 60
Db 1 MENNIQOCVPYCNLNNPEVEILNEERSTGRPLDIDISLTLRFLSSBEPVGVGVAFLGFD 60
QY 61 LIWGFITPSDWSLFLLOEQIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120
Db 61 LIWGFITPSDWSLFLLOEQIEQRIETLERNRAITTLRGLADSYEYIEALREWEANPN 120
QY 121 NAQLREDYRIRFANTDDALITAINNFTLTSEIPLLSVYVOAAMHLHSLDRAYSFGQGW 180
Db 121 NAQLREDYRIRFANTDDALITAINNFTLTSEIPLLSVYVOAAMHLHSLDRAYSFGQGW 180
QY 181 GUDIATVNNHYNRLNLHRYTKHCLDYNQGLENLRGINTQWARFNQFRDLTLVLD 240
Db 181 GUDIATVNNHYNRLNLHRYTKHCLDYNQGLENLRGINTQWARFNQFRDLTLVLD 240
QY 241 IVALEPNYDVRTYPIQTSQSLTREIYTSVIEDSPVSANIPNGFNRAEFVGRPPHLMDFM 300
Db 241 IVALEPNYDVRTYPIQTSQSLTREIYTSVIEDSPVSANIPNGFNRAEFVGRPPHLMDFM 300
QY 301 NSLFTVTAETVRSQTVWGGHLYSSRNNTAGNRRINFPISYGVNFGGAIWADEDPFPFYRLS 360
Db 301 NSLFTVTAETVRSQTVWGGHLYSSRNNTAGNRRINFPISYGVNFGGAIWADEDPFPFYRLS 360
QY 361 DPVFRGGFGNPHYVLGLRGVAFQQTGNHTFRNSGTIDSLDEIPQDNGSGAPWNDYS 420
Db 361 DPVFRGGFGNPHYVLGLRGVAFQQTGNHTFRNSGTIDSLDEIPQDNGSGAPWNDYS 420
QY 421 HVLNHTVFRWPEGEISGSDSNRAPMFSWTHRSATPTNTIDPERITQIPLVKAHLQSGTT 480
Db 421 HVLNHTVFRWPEGEISGSDSNRAPMFSWTHRSATPTNTIDPERITQIPLVKAHLQSGTT 480
QY 481 VVRGPGFTGGDILRRTSGGPAYTTVNINGQLPQYRARIYASTNLRIRYTVVAGERIF 540
Db 481 VVRGPGFTGGDILRRTSGGPAYTTVNINGQLPQYRARIYASTNLRIRYTVVAGERIF 540
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QY 601 TATFEAYDLERAQAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
Db 601 TATFEAYDLERAQAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
QY 661 SEKVHAKRLSDERNLLODPNFKGINRLDRGWRGSTDTTIQRGDDVFKENVTLPGTFD 720
Db 661 SEKVHAKRLSDERNLLODPNFKGINRLDRGWRGSTDTTIQRGDDVFKENVTLPGTFD 720

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QY 961 AFFLYDARNVKNKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCVPCR 1020
DB 961 AFFLYDARNVKNKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCVPCR 1020
QY 1021 GYILRVATYKEGYGEGCVTHIEIENNTDELKPSNCVEEVPNNVTTCNDYTPANOEYGG 1080
DB 1021 GYILRVATYKEGYGEGCVTHIEIENNTDELKPSNCVEEVPNNVTTCNDYTPANOEYGG 1080
QY 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRNPNPCESNRGYGDTPLPAGYVTK 1140
DB 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRNPNPCESNRGYGDTPLPAGYVTK 1140
QY 1141 ELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE 1174
DB 1141 ELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE 1174

RESULT 7

US-08-598-305A-32
; Sequence 32, Application US/08598305A
; Patent No. 5827514
; GENERAL INFORMATION:
; APPLICANT: BRADFISCH, Gregory A.
; APPLICANT: THOMPSON, Mark
; TITLE OF INVENTION: SCHWAB, George E.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606-6669

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,305A
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,867
; FILING DATE: 06-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA86.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-598-305A-32

Query Match 100.0%; Score 6244; DB 2; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIQOCVPYNCLNNPEVILNEERSTGRPLDLSLTRLSEFFVPGVGAGLEFD 60
DB 1 MENNIQOCVPYNCLNNPEVILNEERSTGRPLDLSLTRLSEFFVPGVGAGLEFD 60
QY 61 LINGFITPSWSLFLIQLEQRIETLERNRAITTLRGLADSYEIIYILEARWEANPN 120

DB 61 LINGFITPSWSLFLIQLEQRIETLERNRAITTLRGLADSYEIIYILEARWEANPN 120
QY 121 NAQLREDVRIIRFANTDDALITAINNFTLTSTFEIPLLSVVVQAANLHLSLLRDVAFSGQGW 180
DB 121 NAQLREDVRIIRFANTDDALITAINNFTLTSTFEIPLLSVVVQAANLHLSLLRDVAFSGQGW 180
QY 181 GUDIATVNVNHNRLNLHRYTKHCLDYNQGLENLRGNTQWARFNQFRDRLTLTVLD 240
DB 181 GUDIATVNVNHNRLNLHRYTKHCLDYNQGLENLRGNTQWARFNQFRDRLTLTVLD 240
QY 241 IVALFPNDVRYPIQTSOLTRREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 300
DB 241 IVALFPNDVRYPIQTSOLTRREIYTSVIEDSPSANIPNGFNRAEFGVPPHLMDFM 300
QY 301 NSLFVTAETVRSQTVWVGHLVSSRNTAGNRINFPYGVFNPGGAIWIADEDPFPYRILS 360
DB 301 NSLFVTAETVRSQTVWVGHLVSSRNTAGNRINFPYGVFNPGGAIWIADEDPFPYRILS 360
QY 361 DPVFRGFGFNPHVYGLRGVAFQOTGTNHTRTFNSGTIDSLDEIPQDNGSGAPWNDYS 420
DB 361 DPVFRGFGFNPHVYGLRGVAFQOTGTNHTRTFNSGTIDSLDEIPQDNGSGAPWNDYS 420
QY 421 HVLNHTVFRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
DB 421 HVLNHTVFRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VVRGPGFTGGDILRRTSGGPPFAYTIVNINGQLPQYRARIYASTNLRIVTVAGERIF 540
DB 481 VVRGPGFTGGDILRRTSGGPPFAYTIVNINGQLPQYRARIYASTNLRIVTVAGERIF 540
QY 541 AGQFNKMTDGTDLTFQSFYSATINTAFTFMSQSSFTVGADTFSSGNEVYIDRELIPV 600
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QY 601 TATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
DB 601 TATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVILPGTFD 720
DB 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVILPGTFD 720
QY 721 EYPTLYLYOKIDESKLPYTRYQIRGYIEDSQDLEIYLIRYNAKHETVNVILGTSLWPLS 780
DB 721 EYPTLYLYOKIDESKLPYTRYQIRGYIEDSQDLEIYLIRYNAKHETVNVILGTSLWPLS 780
QY 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLDIDYGCCTDLNEDLDVWV 840
DB 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLDIDYGCCTDLNEDLDVWV 840
QY 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELETNIVYKEAKES 900
DB 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLELETNIVYKEAKES 900
QY 901 VDALFVNSQYDQLQADTNIAHIAADKRVHRIREAYLPESLIPGVNVDIFEELKGRIFT 960
DB 901 VDALFVNSQYDQLQADTNIAHIAADKRVHRIREAYLPESLIPGVNVDIFEELKGRIFT 960
QY 961 AFFLYDARNVKNKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCVPCR 1020
DB 961 AFFLYDARNVKNKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVPWEAEVSQEVRCVPCR 1020
QY 1021 GYILRVATYKEGYGEGCVTHIEIENNTDELKPSNCVEEVPNNVTTCNDYTPANOEYGG 1080
DB 1021 GYILRVATYKEGYGEGCVTHIEIENNTDELKPSNCVEEVPNNVTTCNDYTPANOEYGG 1080
QY 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRNPNPCESNRGYGDTPLPAGYVTK 1140
DB 1081 AYTSRNRGYDITYGSSNVPADYASVYEKSYTDGRRNPNPCESNRGYGDTPLPAGYVTK 1140
QY 1141 ELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE 1174

ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,891
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/356,034
FILING DATE:
APPLICATION NUMBER: US/08/210,110
FILING DATE:
APPLICATION NUMBER: 07/865,168
FILING DATE: 09-APR-92

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,361
FILING DATE: 14-DEC-89
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/371,955
FILING DATE: 27-JUN-89

ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
REGISTRATION NUMBER: 21,023
REFERENCE/DOCKET NUMBER: MA43.C1.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMEDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811a

US-08-933-891-8

Query Match 100.0%; Score 6244; DB 3; Length 1174;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MENNIOQCVPYCLNPNVEILNEERSTGKLPDLSLTLSEFVPGVGVAFLFD 60
Db 1 MENNIOQCVPYCLNPNVEILNEERSTGKLPDLSLTLSEFVPGVGVAFLFD 60
Qy 61 LINGFITPSDWSLLEQLQIETLERNRAITLRLGLADSYETIYIEALREWEANPN 120
Db 61 LINGFITPSDWSLLEQLQIETLERNRAITLRLGLADSYETIYIEALREWEANPN 120
Qy 121 NAQLREDVRIRFANTDALLITAINNFITLSEFIPLLSVYVQAAMHLSLLRDVSRGQGW 180
Db 121 NAQLREDVRIRFANTDALLITAINNFITLSEFIPLLSVYVQAAMHLSLLRDVSRGQGW 180
Qy 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENLRTGTNTROWARNQFRDLTLTVLD 240
Db 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENLRTGTNTROWARNQFRDLTLTVLD 240

Qy 241 IVALFPNDVVRTYPIQTSSQLTREIYTSVSSVIANIENGFNRAEFGVPRPHLMDFM 300
Db 241 IVALFPNDVVRTYPIQTSSQLTREIYTSVSSVIANIENGFNRAEFGVPRPHLMDFM 300
Qy 301 NSLFVTAETVRSQTVWGGHLYSSRNAGNINFFPSYGFNPGGAIWADEDPREFYRTL 360
Db 301 NSLFVTAETVRSQTVWGGHLYSSRNAGNINFFPSYGFNPGGAIWADEDPREFYRTL 360
Qy 361 DPVFRGGFNGPHYVGLRGVAFQQTGTNHTRTFNSGTIDSLDEIPQDSGAPWWDYS 420
Db 361 DPVFRGGFNGPHYVGLRGVAFQQTGTNHTRTFNSGTIDSLDEIPQDSGAPWWDYS 420
Qy 421 HVLNHTVFRWPGELSGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHLQSGTT 480
Db 421 HVLNHTVFRWPGELSGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHLQSGTT 480
Qy 481 VVRGFGTGGDILRTSGGPFAYTIVNINQOLPORIRIYASTTNLRIVTVVAGERIF 540
Db 481 VVRGFGTGGDILRTSGGPFAYTIVNINQOLPORIRIYASTTNLRIVTVVAGERIF 540
Qy 541 AGOFNKMTDGTPLTFQSFYSATINTAFTFPMSSOSTFVGADTFSSGNEVYIDRFELIPV 600
Db 541 AGOFNKMTDGTPLTFQSFYSATINTAFTFPMSSOSTFVGADTFSSGNEVYIDRFELIPV 600
Qy 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHEDQVSNLVDCLSDFCDEKREL 660
Db 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHEDQVSNLVDCLSDFCDEKREL 660
Qy 661 SEKVAKARLSDERNLLODPNFKGINROLDRGWGSTDTITQRGDDVFKENVTLPGTFD 720
Db 661 SEKVAKARLSDERNLLODPNFKGINROLDRGWGSTDTITQRGDDVFKENVTLPGTFD 720
Qy 721 EGYPTLYKQIDESKLPYTRYQLRGYIEDSODLEIYLIRYNAKHETVNLGTGSLWPLS 780
Db 721 EGYPTLYKQIDESKLPYTRYQLRGYIEDSODLEIYLIRYNAKHETVNLGTGSLWPLS 780
Qy 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHFLSDIDVCGTDLNEDLDVWV 840
Db 781 VQSPTRKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHFLSDIDVCGTDLNEDLDVWV 840
Qy 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWKROKREKLELETNIVYKEAKES 900
Db 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWKROKREKLELETNIVYKEAKES 900
Qy 901 VDALFVNSQYDQLOQADTNIAHAAKRVHRIREAYLPBLSVPGVNVVDIFEELKGRIFT 960
Db 901 VDALFVNSQYDQLOQADTNIAHAAKRVHRIREAYLPBLSVPGVNVVDIFEELKGRIFT 960
Qy 961 AFFLYDARNVIRKNGDFNNGLSQWNVKGVHVDVEEQNNHSSVLVWPEWEAEVSQEVRCVGR 1020
Db 961 AFFLYDARNVIRKNGDFNNGLSQWNVKGVHVDVEEQNNHSSVLVWPEWEAEVSQEVRCVGR 1020
Qy 1021 GYLIRVATYKEGYGEGCVTITHEIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080
Db 1021 GYLIRVATYKEGYGEGCVTITHEIENNTDELKFSNCVEEVPNNVTTCNDYTANOEYGG 1080
Qy 1081 AYTSTRNGYDETYGNSVPADYASVYEKSYTDGRRNPNCPESNRGYGDTYPLPAGYTK 1140
Db 1081 AYTSTRNGYDETYGNSVPADYASVYEKSYTDGRRNPNCPESNRGYGDTYPLPAGYTK 1140
Qy 1141 ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174
Db 1141 ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174

RESULT 10
US-09-178-252-6
; Sequence 6, Application US/09178252
; Patent No. 6218188
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Steilman, Steven J.
; APPLICANT: Narva, Kenneth E.

;; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
;; FILE REFERENCE: MA-714X2
;; CURRENT APPLICATION NUMBER: US/09/178,252
;; CURRENT FILING DATE: 1998-10-23
;; EARLIER APPLICATION NUMBER: 60/065,215
;; EARLIER FILING DATE: 1997-11-12
;; EARLIER APPLICATION NUMBER: 60/076,445
;; EARLIER FILING DATE: 1998-03-02
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 1174
;; TYPE: PRT
;; ORGANISM: Bacillus thuringiensis
US-09-178-252-6

Query Match 100.0%; Score 6244; DB 4; Length 1174;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MENNIOQCVPYKCLNPEVEILLNEERSTGRLPLDLSLTRLLSEFVGVGVAFGLFD 60
Db 1 MENNIOQCVPYKCLNPEVEILLNEERSTGRLPLDLSLTRLLSEFVGVGVAFGLFD 60

Qy 61 LIWGFITPDSWSEFLLEQIOLIEORIETLERNRAITLRLGLADSYETIYALREWEANPN 120
Db 61 LIWGFITPDSWSEFLLEQIOLIEORIETLERNRAITLRLGLADSYETIYALREWEANPN 120

Qy 121 NAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDVAVSQGW 180
Db 121 NAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDVAVSQGW 180

Qy 181 GLOIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRTGTROWARNQPRDLTLTVLD 240
Db 181 GLOIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRTGTROWARNQPRDLTLTVLD 240

Qy 241 IVALFPNDVRYPIQTSOLTRIEYTSVIEDSPSANIPNGFNRAEFGVRPPLMDFM 300
Db 241 IVALFPNDVRYPIQTSOLTRIEYTSVIEDSPSANIPNGFNRAEFGVRPPLMDFM 300

Qy 301 NSLFTVTAETVRSQVWGHVSSRNATAGNINFPSSYGVFNPGGAIWADDPFPYRTLS 360
Db 301 NSLFTVTAETVRSQVWGHVSSRNATAGNINFPSSYGVFNPGGAIWADDPFPYRTLS 360

Qy 361 DPVVRGFGFNPHVYLGVRVAFQCTGNTHTFRNSGTDSDLEIPQNSGAPWNDYS 420
Db 361 DPVVRGFGFNPHVYLGVRVAFQCTGNTHTFRNSGTDSDLEIPQNSGAPWNDYS 420

Qy 421 HVLNHTVFRVWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQPLVKAHTLQSGTT 480
Db 421 HVLNHTVFRVWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQPLVKAHTLQSGTT 480

Qy 481 VVRGPGTGGDILARTSGGFPAYTIVNINQOLPORRYARRYASTTNLRYVTVAGERIF 540
Db 481 VVRGPGTGGDILARTSGGFPAYTIVNINQOLPORRYARRYASTTNLRYVTVAGERIF 540

Qy 541 AQQNKMTMDTGLPTFSFSVATINTAFTFPMSSOSTTGVADTFSSGNEVYIDRFELIPV 600
Db 541 AQQNKMTMDTGLPTFSFSVATINTAFTFPMSSOSTTGVADTFSSGNEVYIDRFELIPV 600

Qy 601 TATFEAEYDLERAOKAVNALETNSQIGIKTDVTDYHIDQVSNLVDCSDEFCLDEREL 660
Db 601 TATFEAEYDLERAOKAVNALETNSQIGIKTDVTDYHIDQVSNLVDCSDEFCLDEREL 660

Qy 661 SEKVKHAKRLSDERNLQDPNFKGINQLDRGWSGTDITIQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVKHAKRLSDERNLQDPNFKGINQLDRGWSGTDITIQRGDDVFKENYVTLPGTFD 720

Qy 721 ECPYTYLQKIDESKLPYTRYQLRGYTEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780
Db 721 ECPYTYLQKIDESKLPYTRYQLRGYTEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780

Qy 781 VQSPIRKCGEFPNRCAPHLEWNPDLDCSCROGKCAHSHHFSLDIDVGCYDLDNEDLVWV 840

Db 781 VQSPIRKCGEFPNRCAPHLEWNPDLDCSCROGKCAHSHHFSLDIDVGCYDLDNEDLVWV 840

Qy 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKRAEKWRDKREKLELETNIVYKEAKES 900
Db 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKRAEKWRDKREKLELETNIVYKEAKES 900

Qy 901 VDALFVNSQYDQLQADTNIAHAAADKRVHRIEAYLDELPSLVIGVNVVDIFEELKGRIFT 960
Db 901 VDALFVNSQYDQLQADTNIAHAAADKRVHRIEAYLDELPSLVIGVNVVDIFEELKGRIFT 960

Qy 961 AFFLYDARNVINKGDFNNGLSQWNVKGVHDVEEQNNHSHSVLVVPEWEAEVSQEVRCVPCR 1020
Db 961 AFFLYDARNVINKGDFNNGLSQWNVKGVHDVEEQNNHSHSVLVVPEWEAEVSQEVRCVPCR 1020

Qy 1021 GYLRLVTAIKGYGEGCVTIHEIENNTDELKFSNCVEEVEYPNNVTTCNDYTANQOEYGG 1080
Db 1021 GYLRLVTAIKGYGEGCVTIHEIENNTDELKFSNCVEEVEYPNNVTTCNDYTANQOEYGG 1080

Qy 1081 AYTSNRGYDETYGNSVSPADYASVYEKSYTDGRRDNPCESNRGCGDYTLPAGYVTK 1140
Db 1081 AYTSNRGYDETYGNSVSPADYASVYEKSYTDGRRDNPCESNRGCGDYTLPAGYVTK 1140

Qy 1141 ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174
Db 1141 ELEYPETDKVWIEIGETEGTFIVDSVELLMEE 1174

RESULT 11
PCT-US91-02560-2
; Sequence 2. Application PC/TUS9102560
; GENERAL INFORMATION:
; APPLICANT: Gawron-Burke, Cynthia
; APPLICANT: Chambers, Judith A.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cnyf and cnyx
; TITLE OF INVENTION: GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze et al. c/o A.S. Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02560
; FILING DATE: 19910415
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510327
; FILING DATE: 16-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-27 U1
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02560-2

Query Match 100.0%; Score 6244; DB 5; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONOCVPCNCLNNEPEVILNEERSTGRPLDLSLSTRFLLSSEVPVGVAGFLFD 60
DB 1 MENNIONOCVPCNCLNNEPEVILNEERSTGRPLDLSLSTRFLLSSEVPVGVAGFLFD 60
QY 61 LWGFITPSDWSLFLQIBOLIEQRIETLERNRAITTLRGGLADSYEIVIEALREWEANPN 120
DB 61 LWGFITPSDWSLFLQIBOLIEQRIETLERNRAITTLRGGLADSYEIVIEALREWEANPN 120
QY 121 NAOQLREDVIRFANTDDALITAINFTLSPEIPILLSVYVQAANHLSLRDVAFSGGOW 180
DB 121 NAOQLREDVIRFANTDDALITAINFTLSPEIPILLSVYVQAANHLSLRDVAFSGGOW 180
QY 181 GDIATVNNHYNRLNLIHRYTKHCLDYNQGLNLRGTNTQWARFQNRDLTLTVLD 240
DB 181 GDIATVNNHYNRLNLIHRYTKHCLDYNQGLNLRGTNTQWARFQNRDLTLTVLD 240
QY 241 IVALFPNDVRYPIQTSOLTRREIYTSVIEDSPVSANIPNGFNRAEFGVAPPHLDMFM 300
DB 241 IVALFPNDVRYPIQTSOLTRREIYTSVIEDSPVSANIPNGFNRAEFGVAPPHLDMFM 300
QY 301 NSLFTVTAETVRSQTVWGHVSSRNAGNINFPVGVNPGGATWIADEDPPEYRTLS 360
DB 301 NSLFTVTAETVRSQTVWGHVSSRNAGNINFPVGVNPGGATWIADEDPPEYRTLS 360
QY 361 DPEVVRGGFNGHYVLGRVAFQQTGNHTRFRNSGTIDSLDEIPQDNISGAPWNDYS 420
DB 361 DPEVVRGGFNGHYVLGRVAFQQTGNHTRFRNSGTIDSLDEIPQDNISGAPWNDYS 420
QY 421 HVLNHTVFRVWGEISGDSWAPMPSWTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480
DB 421 HVLNHTVFRVWGEISGDSWAPMPSWTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480
QY 481 VVRGPGTGDILRRTSGGPFAYTIVNINQOLPQRYRARIYASTNRIYVTVAGERIF 540
DB 481 VVRGPGTGDILRRTSGGPFAYTIVNINQOLPQRYRARIYASTNRIYVTVAGERIF 540
QY 541 AQGFNTMTDGLPTQSFYSYATINTAFTFPMSSQSFVGAOTFSSGNEVYIDREFELPV 600
DB 541 AQGFNTMTDGLPTQSFYSYATINTAFTFPMSSQSFVGAOTFSSGNEVYIDREFELPV 600
QY 601 TATFEAYDLERAKKAVNALETSINOIGIKTDVTDVHIDQVNLVDCLEDFCLDEKREL 660
DB 601 TATFEAYDLERAKKAVNALETSINOIGIKTDVTDVHIDQVNLVDCLEDFCLDEKREL 660
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQDRGRGSTDTIQGGDDVFKENYVTLPGTFD 720
DB 661 SEKVKHAKRLSDERNLLQDPNFKGINRQDRGRGSTDTIQGGDDVFKENYVTLPGTFD 720
QY 721 ECVPTVLYOKIDESKLPYTRYQLRGYIEDSODLEIYLIRYNAKHETVNLGTGSLWPLS 780
DB 721 ECVPTVLYOKIDESKLPYTRYQLRGYIEDSODLEIYLIRYNAKHETVNLGTGSLWPLS 780
QY 781 VQSPIRKGCEPNRCAPHEWNPDLDCSRRGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
DB 781 VQSPIRKGCEPNRCAPHEWNPDLDCSRRGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
QY 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARYKRAEKKWRDRKREKLEETNIVYKEAKES 900
DB 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARYKRAEKKWRDRKREKLEETNIVYKEAKES 900
QY 901 VDALFVNSQVQDQADNTAMIHAAKRVHRIREAYLPEISVTPGVNVDIFPELKGRIET 960
DB 901 VDALFVNSQVQDQADNTAMIHAAKRVHRIREAYLPEISVTPGVNVDIFPELKGRIET 960
QY 961 AFFLYDARNYIKNGDFNNGLSKNVKGHVDVEQNNHRSVLYVPEAEVSQEVRCPCR 1020
DB 961 AFFLYDARNYIKNGDFNNGLSKNVKGHVDVEQNNHRSVLYVPEAEVSQEVRCPCR 1020
QY 1021 GYLIRVATYKEGEGCVTTHEIENNTDELKFSNCVDEEYVPPNNTVTCNDYTANQOEYGG 1080
DB 1021 GYLIRVATYKEGEGCVTTHEIENNTDELKFSNCVDEEYVPPNNTVTCNDYTANQOEYGG 1080
QY 1081 AYTSRRNGYDETYGSSNPADYASVYEESYTDGRRDNPCESNRGYGYTTLPGAVYTK 1140

DB 1081 AYTSRRNGYDETYGSSNPADYASVYEESYTDGRRDNPCESNRGYGYTTLPGAVYTK 1140
QY 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLME 1174
DB 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLME 1174

RESULT 12

PCT-US92-11337-10
; Sequence 10, Application PC/TUS9211337
; GENERAL INFORMATION:
; APPLICANT: PAYNE, JEWEL M.
; APPLICANT: HICKLE, LESLIE A.
; TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
; TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 N.W. 41st STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11337
; FILING DATE: 19921231
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 97/828,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA75
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BACILLUS THURINGIENSIS
; STRAIN: AIZAWAI
; INDIVIDUAL ISOLATE: PS811
; IMMEDIATE SOURCE:
; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST STICK
; CLONE: 811A
PCT-US92-11337-10

Query Match 100.0%; Score 6244; DB 5; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MENNIONOCVPCNCLNNEPEVILNEERSTGRPLDLSLSTRFLLSSEVPVGVAGFLFD 60
DB 1 MENNIONOCVPCNCLNNEPEVILNEERSTGRPLDLSLSTRFLLSSEVPVGVAGFLFD 60
QY 61 LWGFITPSDWSLFLQIBOLIEQRIETLERNRAITTLRGGLADSYEIVIEALREWEANPN 120
DB 61 LWGFITPSDWSLFLQIBOLIEQRIETLERNRAITTLRGGLADSYEIVIEALREWEANPN 120

QY 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180
DB 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180
QY 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENRGTNTQWARFNFQFRDLTLTVID 240
DB 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENRGTNTQWARFNFQFRDLTLTVID 240
QY 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
DB 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
QY 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWIAEDDPRTYRLS 360
DB 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWIAEDDPRTYRLS 360
QY 361 DPVFEVGGFNGPHVYVGLRGVAFQQTGNTHTFRNSGTIDSLDETPDQNSGAPWNYX 420
DB 361 DPVFEVGGFNGPHVYVGLRGVAFQQTGNTHTFRNSGTIDSLDETPDQNSGAPWNYX 420
QY 421 HVLNHTVFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480
DB 421 HVLNHTVFRWPGGEISGSDSWRAPMFSWTHRSATPTNTIDPRITQIPLVKAHTLQSGTT 480
QY 481 VVRPGFTGDDILRRTSQGFPAFTVINGQLPQVRARIRASTNRLIYTVAGERIF 540
DB 481 VVRPGFTGDDILRRTSQGFPAFTVINGQLPQVRARIRASTNRLIYTVAGERIF 540
QY 541 AGQFNKMTDGTDLTQSFYSYATINTAFTFPMQSQSFVTCGATFSSGNEVYIDRELIPV 600
DB 541 AGQFNKMTDGTDLTQSFYSYATINTAFTFPMQSQSFVTCGATFSSGNEVYIDRELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDOVNLVDCLDFCLDEKREL 660
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDOVNLVDCLDFCLDEKREL 660
QY 661 SEKVAKRLSDERNLQDPNFKGINKQLDRGWRGSTDITIQGDDVFNKVTLPGTFD 720
DB 661 SEKVAKRLSDERNLQDPNFKGINKQLDRGWRGSTDITIQGDDVFNKVTLPGTFD 720
QY 721 ECPYTLVYQKIDESKLPYTRYOLRGYIEDSQLEIYLYRYNAKHETVNLGTSLWPLS 780
DB 721 ECPYTLVYQKIDESKLPYTRYOLRGYIEDSQLEIYLYRYNAKHETVNLGTSLWPLS 780
QY 781 VQSPIRKCGPNPCAPHLEWNPDLDCSDRGKCAHSHSFSLDIDVCGTDLNEEDLVWV 840
DB 781 VQSPIRKCGPNPCAPHLEWNPDLDCSDRGKCAHSHSFSLDIDVCGTDLNEEDLVWV 840
QY 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900
DB 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900
QY 901 VDALFVNSQYDQLOADNTAMIAADKRVHRIEAYLPELSVTPGVNVDIFELKGRIFT 960
DB 901 VDALFVNSQYDQLOADNTAMIAADKRVHRIEAYLPELSVTPGVNVDIFELKGRIFT 960
QY 961 AFELYDARNYIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLYVPEWAEVSGEVRVCPGR 1020
DB 961 AFELYDARNYIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLYVPEWAEVSGEVRVCPGR 1020
QY 1021 GYLIRVTAKEGEGECVTIHEJNTNDLKTSCNVEEYVYNNVTYNDYTAQOEYGG 1080
DB 1021 GYLIRVTAKEGEGECVTIHEJNTNDLKTSCNVEEYVYNNVTYNDYTAQOEYGG 1080
QY 1081 AYTSSRNGYDETYGSSNVADYASVYEKSYTDGDRDNPCESNRGYGYDTPLPAGYVTK 1140
DB 1081 AYTSSRNGYDETYGSSNVADYASVYEKSYTDGDRDNPCESNRGYGYDTPLPAGYVTK 1140
QY 1141 ELEYFPPTKRWIEIGTEGTFTFVDSVEILLMEE 1174
DB 1141 ELEYFPPTKRWIEIGTEGTFTFVDSVEILLMEE 1174

RESULT 13

PCT-US95-05431-25

: Sequence 25, Application PC/TUS95050431

: GENERAL INFORMATION:

: APPLICANT: Street address: 5501 Oberlin Drive

: APPLICANT: City: San Diego

: APPLICANT: State/Province: California

: APPLICANT: Country: US

: APPLICANT: Postal code/zip: 92121

: APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991

: APPLICANT: Telex number:

: TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in

: NUMBER OF SEQUENCES: 34

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: David R. Saliwanchik

: STREET: 2421 N.W. 41st Street, Suite A-1

: CITY: Gainesville

: STATE: Florida

: COUNTRY: USA

: ZIP: 32606

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: FILING DATE:

: CLASSIFICATION:

: ATTORNEY/AGENT INFORMATION:

: NAME: Saliwanchik, David R.

: REGISTRATION NUMBER: 31,794

: REFERENCE/DOCKET NUMBER: MA83

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (904) 375-8100

: TELEFAX: (904) 372-5800

: INFORMATION FOR SEQ ID NO: 25:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 1174 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: protein

: PCT-US95-05431-25

Query Match 100.0%; Score 6244; DB 5; Length 1174;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MENNIQOCVPYCNLPNPEVILNEERSTGRPLDLSLSTRFLLSEFVPGVGVAFGLFD 60
QY 61 LIWGFITPDSWSLFLQLEIQRITELERNRAITTLRGADSYEYIEALREWEANPN 120
DB 61 LIWGFITPDSWSLFLQLEIQRITELERNRAITTLRGADSYEYIEALREWEANPN 120
QY 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180
DB 121 NAQLREDVIRFANTDDALITAINNNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSGQW 180
QY 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENRGTNTQWARFNFQFRDLTLTVID 240
DB 181 GLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENRGTNTQWARFNFQFRDLTLTVID 240
QY 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
DB 241 IVALFPNDVRYPIOTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVPPHLMDFM 300
QY 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWIAEDDPRTYRLS 360
DB 301 NSLFTVTAETVRSQVWGGHLVSSRNAGNINFPSPYGVNPGGAIWIAEDDPRTYRLS 360

Db 301 NSLFVTAETVRSOTVWGCHLYSSRNTAGNRINFPSYGVNPGGAIWIADDEPRPFYRTLS 360
QY 361 DPVVRGSGFNGPHYVGLRGVAFQGTGTHRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420
Db 361 DPVVRGSGFNGPHYVGLRGVAFQGTGTHRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420
QY 421 HVLNHVTFVRWPGFISGSDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
Db 421 HVLNHVTFVRWPGFISGSDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VVRGPGTGGDILARTSGPPAYITVINGOLPQRYRARIYASTNRIYTVVAGERIF 540
Db 481 VVRGPGTGGDILARTSGPPAYITVINGOLPQRYRARIYASTNRIYTVVAGERIF 540
QY 541 AGQFNKMTDMTGDPLTFQSFYSATINTAFTFPMSSQSFVGDATFSSGNEVYIDREFELPV 600
Db 541 AGQFNKMTDMTGDPLTFQSFYSATINTAFTFPMSSQSFVGDATFSSGNEVYIDREFELPV 600
QY 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
Db 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRWGSDTITIQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRWGSDTITIQRGDDVFKENYVTLPGTFD 720
QY 721 ECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLMPLS 780
Db 721 ECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLMPLS 780
QY 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKAHSHHFSLDIDVGCCTDLNEDLDVWV 840
Db 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKAHSHHFSLDIDVGCCTDLNEDLDVWV 840
QY 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKDRKREKLELETNIVYKAKES 900
Db 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKDRKREKLELETNIVYKAKES 900
QY 901 VDALFVNSQDQLQADNTNAMIHAADKRVHRIREAYLPESLVIPGVNVDIFEELKGRIFT 960
Db 901 VDALFVNSQDQLQADNTNAMIHAADKRVHRIREAYLPESLVIPGVNVDIFEELKGRIFT 960
QY 961 AFELYDARNVKNKGDFNGLSCWNVKGVHDVEQNNHRSVLVPEWEAEVSQEVRCVPCR 1020
Db 961 AFELYDARNVKNKGDFNGLSCWNVKGVHDVEQNNHRSVLVPEWEAEVSQEVRCVPCR 1020
QY 1021 GYLIRVTAKEGYEGGCVTTHEIENNTDELKFSNCVREEVYPNNTVTCNDYTANOEEYGG 1080
Db 1021 GYLIRVTAKEGYEGGCVTTHEIENNTDELKFSNCVREEVYPNNTVTCNDYTANOEEYGG 1080
QY 1081 AVTSRNGYDITYGNSVSPADYASVYEKSYTDGRRDNPCESNRGYGDTPLPAGVYTK 1140
Db 1081 AVTSRNGYDITYGNSVSPADYASVYEKSYTDGRRDNPCESNRGYGDTPLPAGVYTK 1140
QY 1141 ELEYPETDKVWIEIGETGTFIVDSVELLLMEE 1174
Db 1141 ELEYPETDKVWIEIGETGTFIVDSVELLLMEE 1174

RESULT 14

5188960-8

; Patent No. 5188960

; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE

; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL

; LEPIDOPTERAN-ACTIVE TOXINS

; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/451,261

; FILING DATE: 14-DEC-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 371,955

; FILING DATE: 27-JUN-1989

; SEQ ID NO:8:

; LENGTH: 1174

5188960-8

Query Match 100.0%; Score 6244; DB 6; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MENNIONCVYPNCLNPEVEILLNEERSTGRPLDLSLSTRFLLSSEVPVGVAGFLFD 60
QY 61 LIWGFITPSDMSLSFLQLEQRIETLERNRAITTLRGGLADSYEIIYIARLEWEANPN 120
Db 61 LIWGFITPSDMSLSFLQLEQRIETLERNRAITTLRGGLADSYEIIYIARLEWEANPN 120
QY 121 NAQLREDVRIIPANTDDALITAINNFTLTSPFIPLLSYVQAANLHLSLLRDVAVSFGOGW 180
Db 121 NAQLREDVRIIPANTDDALITAINNFTLTSPFIPLLSYVQAANLHLSLLRDVAVSFGOGW 180
QY 181 GLDTATVNNHYNRLINLIHRYTKHCLDTYNOGLENLNRTNROWARFNQFRDLTLTVID 240
Db 181 GLDTATVNNHYNRLINLIHRYTKHCLDTYNOGLENLNRTNROWARFNQFRDLTLTVID 240
QY 241 IVALFPNDVRYTPIQTSSQLTREIYTSSTVEDSPVSNIPNGFNRAEFGVRPPLMDFM 300
Db 241 IVALFPNDVRYTPIQTSSQLTREIYTSSTVEDSPVSNIPNGFNRAEFGVRPPLMDFM 300
QY 301 NSLFVTAETVRSQTVWGCHLYSSRNTAGNRINFPSYGVNPGGAIWIADDEPRPFYRTLS 360
Db 301 NSLFVTAETVRSQTVWGCHLYSSRNTAGNRINFPSYGVNPGGAIWIADDEPRPFYRTLS 360
QY 361 DPVVRGSGFNGPHYVGLRGVAFQGTGTHRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420
Db 361 DPVVRGSGFNGPHYVGLRGVAFQGTGTHRTFRNSGTIDSLDEIPPDNSGAPWNDYS 420
QY 421 HVLNHVTFVRWPGFISGSDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
Db 421 HVLNHVTFVRWPGFISGSDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
QY 481 VVRGPGTGGDILARTSGPPAYITVINGOLPQRYRARIYASTNRIYTVVAGERIF 540
Db 481 VVRGPGTGGDILARTSGPPAYITVINGOLPQRYRARIYASTNRIYTVVAGERIF 540
QY 541 AGQFNKMTDMTGDPLTFQSFYSATINTAFTFPMSSQSFVGDATFSSGNEVYIDREFELPV 600
Db 541 AGQFNKMTDMTGDPLTFQSFYSATINTAFTFPMSSQSFVGDATFSSGNEVYIDREFELPV 600
QY 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
Db 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDEKREL 660
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRWGSDTITIQRGDDVFKENYVTLPGTFD 720
Db 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDGRWGSDTITIQRGDDVFKENYVTLPGTFD 720
QY 721 ECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLMPLS 780
Db 721 ECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLMPLS 780
QY 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKAHSHHFSLDIDVGCCTDLNEDLDVWV 840
Db 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGCEKAHSHHFSLDIDVGCCTDLNEDLDVWV 840
QY 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKDRKREKLELETNIVYKAKES 900
Db 841 IFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKDRKREKLELETNIVYKAKES 900
QY 901 VDALFVNSQDQLQADNTNAMIHAADKRVHRIREAYLPESLVIPGVNVDIFEELKGRIFT 960
Db 901 VDALFVNSQDQLQADNTNAMIHAADKRVHRIREAYLPESLVIPGVNVDIFEELKGRIFT 960
QY 961 AFELYDARNVKNKGDFNGLSCWNVKGVHDVEQNNHRSVLVPEWEAEVSQEVRCVPCR 1020

Db 961 AFFLYDARNVKNKNGDFNGLSCWNRKGVHVDVEBQNNHRSVLVPEAEVQSQVRVCPGR 1020
 Qy 1021 GYLRTVAYKEGEGCVTTHEIENNTDELKPSNCVVEEYVNNVTTCNDYTANQEEYGG 1080
 Db 1021 GYLRTVAYKEGEGCVTTHEIENNTDELKPSNCVVEEYVNNVTTCNDYTANQEEYGG 1080
 Qy 1081 AYTSRNGYDETYGNSVSPADYASVYEKSYTDGRRDNPCESTRNGYGYDTPLPAGYVTK 1140
 Db 1081 AYTSRNGYDETYGNSVSPADYASVYEKSYTDGRRDNPCESTRNGYGYDTPLPAGYVTK 1140
 Qy 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174
 Db 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174

RESULT 15

US-08-239-476-32
 : Sequence 32, Application US/08239476
 : Patent No. 5527883
 : GENERAL INFORMATION:
 : APPLICANT: Thompson, Mark
 : APPLICANT: Schwab, George E.
 : TITLE OF INVENTION: Improvement of Delta-Endotoxin Expression in
 : TITLE OF INVENTION: Pseudomonas fluorescens
 : NUMBER OF SEQUENCES: 34
 : CORRESPONDENCE ADDRESS:
 : STREET: 2421 N.W. 41st Street, Suite A-1
 : CITY: Gainesville
 : STATE: Florida
 : COUNTRY: USA
 : ZIP: 32606
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA: US/08/239,476
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Saliwanchik, David R.
 : REGISTRATION NUMBER: 31,794
 : REFERENCE/DOCKET NUMBER: M83
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (904) 375-8100
 : TELEFAX: (904) 372-5800
 : INFORMATION FOR SEQ ID NO: 32:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1184 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : US-08-239-476-32

Query Match 100.0%; Score 6244; DB 1; Length 1184;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 11 MENNIOQCVNCLNPEVILNEERSTGRPLDLSLSTRLLSFVPGVGFALFLD 70
 Qy 61 LIWGFITPSDWSLFLQIEQIETLRNRAITTLRLGLADSYEYIYALREWEANPN 120
 Db 71 LIWGFITPSDWSLFLQIEQIETLRNRAITTLRLGLADSYEYIYALREWEANPN 130
 Qy 121 NAOLREDVRIRFANTDALTAINNFTLTSPFIPLLSVYVQAANHLSLRLDRAVSFGQW 180
 Db 131 NAOLREDVRIRFANTDALTAINNFTLTSPFIPLLSVYVQAANHLSLRLDRAVSFGQW 190

Qy 181 GLDIATVNNHYNRLNLIHRYTKHCLDTYNOGLNENLRTGTQWARFNQFRDLTIVLD 240
 Db 191 GLDIATVNNHYNRLNLIHRYTKHCLDTYNOGLNENLRTGTQWARFNQFRDLTIVLD 250
 Qy 241 IVALFPNDVRYTPIQSSQLTREIYTSSTVEDSPVANIPNGFNRAEFGVRPPLHMDFM 300
 Db 251 IVALFPNDVRYTPIQSSQLTREIYTSSTVEDSPVANIPNGFNRAEFGVRPPLHMDFM 310
 Qy 301 NSLFTVATVRSQVWVGHLVSSRNTAGNINPFSYGVFNPGGAIWIADDPFPFVTKLS 360
 Db 311 NSLFTVATVRSQVWVGHLVSSRNTAGNINPFSYGVFNPGGAIWIADDPFPFVTKLS 370
 Qy 361 DPVFRGFGNPHYVVLGLRGVAFQQTGTNHTKTRFRNST IDSLEIPPOQNSGAPNDYS 420
 Db 371 DPVFRGFGNPHYVVLGLRGVAFQQTGTNHTKTRFRNST IDSLEIPPOQNSGAPNDYS 430
 Qy 421 HVLNHTVFRWPGELSGSDSHRAPMFSWTHRSATPTTIDPERITOPLKAKHTLOSGET 480
 Db 431 HVLNHTVFRWPGELSGSDSHRAPMFSWTHRSATPTTIDPERITOPLKAKHTLOSGET 490
 Qy 481 VVRGPGFTGGDILRRRTSGGPPAYTIVNINGQLPQRYRARIYASTNLRIVYTVVAGERIF 540
 Db 491 VVRGPGFTGGDILRRRTSGGPPAYTIVNINGQLPQRYRARIYASTNLRIVYTVVAGERIF 550
 Qy 541 AGQPNKTMOTGDTLTFQSFYSATINTAFTPPMSOSSFTVGADTFSSGNEVYIDREFELIPV 600
 Db 551 AGQPNKTMOTGDTLTFQSFYSATINTAFTPPMSOSSFTVGADTFSSGNEVYIDREFELIPV 610
 Qy 601 TATPEAYDLERAOKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDKREL 660
 Db 611 TATPEAYDLERAOKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFCLDKREL 670
 Qy 661 SEKVKHAKRLSDERNLQDPNFKGINQLDRGWRGSDITIIQRGDDVFKENYVTLPGTFD 720
 Db 671 SEKVKHAKRLSDERNLQDPNFKGINQLDRGWRGSDITIIQRGDDVFKENYVTLPGTFD 730
 Qy 721 ECPYPLYOKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 780
 Db 731 ECPYPLYOKIDESKLPYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLWPLS 790
 Qy 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLSDIDVCGCTDLNEDLVWV 840
 Db 791 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLSDIDVCGCTDLNEDLVWV 850
 Qy 841 IFKIKTODGHARLGNLELEKPLVGEALARYKRAEKWRDKREKLELTVNIVYKAKES 900
 Db 851 IFKIKTODGHARLGNLELEKPLVGEALARYKRAEKWRDKREKLELTVNIVYKAKES 910
 Qy 901 VDLEFVNSQYDQLOQADTNIAHAAKRVHRIEAYLPPELSVIGVNVVDIFEELKGRIFT 960
 Db 911 VDLEFVNSQYDQLOQADTNIAHAAKRVHRIEAYLPPELSVIGVNVVDIFEELKGRIFT 970
 Qy 961 AFFLYDARNVKNKNGDFNGLSCWNRKGVHVDVEBQNNHRSVLVPEAEVQSQVRVCPGR 1020
 Db 971 AFFLYDARNVKNKNGDFNGLSCWNRKGVHVDVEBQNNHRSVLVPEAEVQSQVRVCPGR 1030
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 Qy 1081 AYTSRNGYDETYGNSVSPADYASVYEKSYTDGRRDNPCESTRNGYGYDTPLPAGYVTK 1140
 Db 1091 AYTSRNGYDETYGNSVSPADYASVYEKSYTDGRRDNPCESTRNGYGYDTPLPAGYVTK 1150
 Qy 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174
 Db 1151 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1184

Search completed: November 27, 2002, 20:26:20
 Job time : 43 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 27, 2002, 13:01:49 ; Search time 83 Seconds

(without alignments)
1884.774 Million cell updates/sec

Title: US-09-837-961-8

Perfect score: 6244

Sequence: 1 MNNINQVCYPYCLNNPEV.....IGTEGTFIVDSVLLLMEE 1174

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /SID22/qcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/qcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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22: /SID22/qcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/qcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6244	100.0	1174	12 AAR10131	Lepidopteran-activ
2	6244	100.0	1174	12 AAR14856	CryIF protein. Ba
3	6244	100.0	1174	14 AAR39754	Delta endotoxin.
4	6244	100.0	1174	19 AAW76708	Plasmid pMYC2243 B
5	6244	100.0	1174	19 AAW76712	B. thuringiensis c
6	6244	100.0	1174	22 AAU16792	Wild-type B.t cryI
7	6244	100.0	1174	22 AAU00533	B. thuringiensis t
8	6244	100.0	1184	16 AAR84737	Native cryIF toxin
9	6238	99.9	1174	16 AAR84735	CryIF toxin with l
10	6237	99.9	1174	17 AAR94914	CryIF toxin encode

11	6236	99.9	1174	17 AAR94916	Native CryIF/CryIA
12	6049	96.9	1174	16 AAR84732	CryIF/436 chimeric
13	6049	96.9	1174	17 AAR94908	CryIF/436 chimeric
14	6049	96.9	1174	19 AAW76710	Plasmid pMYC2254 c
15	6018.5	96.4	1175	19 AAW76716	Alternative cryIF/
16	5913	94.7	1148	19 AAW76717	Alternative cryIF/
17	5908	94.6	1148	19 AAW76718	Alternative cryIF/
18	5902	94.5	1148	16 AAR84731	CryIF/CryIA(b) chi
19	5902	94.5	1148	16 AAR84733	CryIF/CryIA(b) chi
20	5902	94.5	1148	17 AAR94907	Plasmid pMYC2244 c
21	5902	94.5	1148	19 AAW76709	Plasmid pMYC2253 c
22	5889	94.3	1148	19 AAW76715	Consensus cryIF/cr
23	5889	94.3	1148	19 AAW76715	Plant-optimised cr
24	5879	94.2	1148	20 AAY16790	CryIF/CryIA chimera
25	5879	94.2	1148	22 AAU00531	CryIA(c)/CryIF/cry
26	5674	90.9	1150	16 AAR84734	CryIA(c)/CryIF/cry
27	5674	90.9	1150	17 AAR94913	Plasmid pMYC2239 b
28	5674	90.9	1150	19 AAW76706	Bacillus thuringie
29	5595	89.6	1186	22 AAU00419	CryIF class toxin
30	5409	86.6	1168	17 AAR89493	Generic formula fo
31	5141	82.3	1174	17 AAR89483	Bacillus thuringie
32	4815.5	77.1	1177	19 AAW58558	Bacillus thuringie
33	4815.5	77.1	1177	23 AAU72339	Bacillus thuringie
34	4812.5	77.1	1177	19 AAW58559	Bacillus thuringie
35	4812.5	77.1	1177	23 AAU7240	Bacillus thuringie
36	4804.5	76.9	1177	19 AAW58556	Bacillus thuringie
37	4804.5	76.9	1177	23 AAU7237	Bacillus thuringie
38	4745.5	76.0	1177	19 AAW58560	Bacillus thuringie
39	4745.5	76.0	1177	23 AAU7241	Bacillus thuringie
40	4706.5	75.4	1177	19 AAW58557	Bacillus thuringie
41	4706.5	75.4	1177	23 AAU7238	Bacillus thuringie
42	4647.5	74.4	1177	23 AAU7243	Bacillus thuringie
43	4636.5	74.3	1177	19 AAW58562	Bacillus thuringie
44	4391.5	70.3	1202	10 AAP90717	Bacillus thuringie
45	4380.5	70.2	1180	12 AAR13309	Modified thermosta

ALIGNMENTS

RESULT 1
AAR10131
ID AAR10131 standard; Protein; 1174 AA.
XX AAR10131;
AC AC
XX 20-MAR-1991 (First entry)
DT DT
XX Lepidopteran-active toxin D.
DE Lepidopteran-active toxin D.
XX Lepidopteran-active toxin D; pest control.
XX Lepidopteran-active toxin D; pest control.
XX Bacillus thuringiensis PS8LL (NRRL B-18484).
XX EP405810-A.
XX 02-JAN-1991.
XX 18-JUN-1990; 90EP-0306594.
XX 14-DEC-1989; 89US-0451261.
XX 27-JUN-1989; 89US-0371955.
XX (MYCO-) MYCOGEN CORP.
XX Payne J, Sick AJ;
XX WPI; 1991-009132/02.
XX Q-PSDB; Q10182.

Bacillus thuringiensis contg. DNA encoding lepidopteran-active
PT toxin - use of microorganisms transformed with the toxin gene
PT in pest control

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XX
PS Claim 6; Page 24-27; 28pp; English.
XX
CC Expression of the toxin gene by a host results, directly or
CC indirectly, in the intracellular prodn. and maintenance of the
CC pesticide.
XX See also AAQ10179-82.
XX
SQ Sequence 1174 AA;

Query Match 100.0%; Score 6244; DB 12; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFVPGVGVAFLGFD 60
DB 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFVPGVGVAFLGFD 60
QY 61 LIWGFITPDSWSLFLQIEOLIBORIETLERNAITTLRLGLADSYEYIEALREWEANPN 120
DB 61 LIWGFITPDSWSLFLQIEOLIBORIETLERNAITTLRLGLADSYEYIEALREWEANPN 120
QY 121 NAQLRDVRIRFANTDALLITANNLTLSFEIPLSVVQAAANLHLSLLRDVAVSQGW 180
DB 121 NAQLRDVRIRFANTDALLITANNLTLSFEIPLSVVQAAANLHLSLLRDVAVSQGW 180
QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENGTNTROWARFNQFRDLTLTVLD 240
DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENGTNTROWARFNQFRDLTLTVLD 240
QY 241 IVALFFNYDVRTYPIOTSSOLTEIYTSVIEDSPVSANIPNGFNRAEFGVRPPLHMDFM 300
DB 241 IVALFFNYDVRTYPIOTSSOLTEIYTSVIEDSPVSANIPNGFNRAEFGVRPPLHMDFM 300
QY 301 NSLEFVTAETVRSQTVGGHVLSSRNTAGNINPSPVGNPFGAINTADEDPPEYRTLS 360
DB 301 NSLEFVTAETVRSQTVGGHVLSSRNTAGNINPSPVGNPFGAINTADEDPPEYRTLS 360
QY 361 DPVFRGGFNGPHYVLGLRCVAFQOQTGNTHTFRNSGTIDSLDEIPPOQNSGAPNDYS 420
DB 361 DPVFRGGFNGPHYVLGLRCVAFQOQTGNTHTFRNSGTIDSLDEIPPOQNSGAPNDYS 420
QY 421 HVLNHYTFVRWPGIEISGDSWRAPMFSWTHRSATPNTIDPERITOIPLVKAHTLSGTT 480
DB 421 HVLNHYTFVRWPGIEISGDSWRAPMFSWTHRSATPNTIDPERITOIPLVKAHTLSGTT 480
QY 481 VVRPGFTGDIILRRTSGGPFATYIYVINGQLPQRYRARIYASTNLRIYTVAGERIF 540
DB 481 VVRPGFTGDIILRRTSGGPFATYIYVINGQLPQRYRARIYASTNLRIYTVAGERIF 540
QY 541 AGQFNKMTDGTDLTQSFYSYATINFTAFPMSSQSFYTGADTFSSGNEVIYIDRFELIPV 600
DB 541 AGQFNKMTDGTDLTQSFYSYATINFTAFPMSSQSFYTGADTFSSGNEVIYIDRFELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVSNLVCLSDDEFCLDEKREL 660
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDHIDQVSNLVCLSDDEFCLDEKREL 660
QY 661 SEKVHAKLSBERNLQDPNFKGINRQDRGRGSTDITIQRGDDVFKENYVTLPGTFD 720
DB 661 SEKVHAKLSBERNLQDPNFKGINRQDRGRGSTDITIQRGDDVFKENYVTLPGTFD 720
QY 721 ECVPTLYOKIDESKLPYTRYOLRGYIEDSQDLEIYLYIRNAKHETVNVLTGSLWPLS 780
DB 721 ECVPTLYOKIDESKLPYTRYOLRGYIEDSQDLEIYLYIRNAKHETVNVLTGSLWPLS 780
QY 781 VQSPIRKCEPNRCAPHLWNPDLDCSDEGKCAHSHHFSDDIDVGCTDLNEDLDVVV 840
DB 781 VQSPIRKCEPNRCAPHLWNPDLDCSDEGKCAHSHHFSDDIDVGCTDLNEDLDVVV 840
QY 841 IFKIQTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900
DB 841 IFKIQTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKEAKES 900

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QY 901 VDALFVNSQYDQLOADTNIAIMIHAADKRVHRIRAYILPELSVIPGVNVDIFEELKGRIFT 960
DB 901 VDALFVNSQYDQLOADTNIAIMIHAADKRVHRIRAYILPELSVIPGVNVDIFEELKGRIFT 960
QY 961 AFFLYDARNVIKNGDFNNGLSKNVKGHDVEEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020
DB 961 AFFLYDARNVIKNGDFNNGLSKNVKGHDVEEQNNHRSVLVVPWEAEVSOEVRVCPGR 1020
QY 1021 GYLRTVAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYYPNNTVTCNDYTANQEEYGG 1080
DB 1021 GYLRTVAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYYPNNTVTCNDYTANQEEYGG 1080
QY 1081 AYTSSRNGYDITYGSSSVDPADYASVYEKSYTDGRDNPCESNRGYDITPLPAGVYTK 1140
DB 1081 AYTSSRNGYDITYGSSSVDPADYASVYEKSYTDGRDNPCESNRGYDITPLPAGVYTK 1140
QY 1141 ELEYFFETDKVWIEIGETEGTFIVDSVELLME 1174
DB 1141 ELEYFFETDKVWIEIGETEGTFIVDSVELLME 1174

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RESULT 2
AAR14856
ID AAR14856 standard; Protein; 1174 AA.
XX
AC AAR14856;
XX
DT 31-JAN-1992 (first entry)
XX
DE CryIF protein.
XX
KW Insecticide; Lepidoptera control; ss.
XX
OS Bacillus thuringiensis.
XX
PN WO9116434-A.
XX
PD 31-OCT-1991.
XX
PF 15-APR-1991; 91WO-US02560.
XX
PR 16-APR-1990; 90US-0510327.
XX
PA (ECOG-) ECOGEN INC.
XX
PI Gawron-Burke CM, Chambers JA, Gonzalez JM;
XX
DR WPI: 1991-339822/46.
XX
DR N-PSDB; AAR14848.
XX
PT Purifying and isolating CRY-I type genes - from novel Bacillus
PT thuringiensis strain as insecticides
XX
PS Claim 3; Fig 1A-E; 100pp; English.
XX
CC The sequence is that of the CryIF protein produced by Bacillus
CC thuringiensis strains EG6845 and EG6346 obt'd. from a maize grain
CC dust sample. The CryIF protein is a toxin produced by the cryIF
CC gene can be used in insecticide compns. to control lepidoptera.
CC esp. Ostrinia nubilalis, Spodoptera exigua, and Plutella xylostella.
CC See also AAR14857.
XX
SQ Sequence 1174 AA;

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Query Match 100.0%; Score 6244; DB 12; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFVPGVGVAFLGFD 60
DB 1 MENNIONQCVNCLNNEVEILNEERSTGRPLDLSLSTRLLSEFVPGVGVAFLGFD 60

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QY 61 LMGFTTPSDWSLFLQIQLEQRIETERNPAITTLRGLADSYEIIYIEALREWEANPN 120
DB 61 LMGFTTPSDWSLFLQIQLEQRIETERNPAITTLRGLADSYEIIYIEALREWEANPN 120
QY 121 NAQLEDVIRIRANTDDALITAINNFTLSFEIPILLSVYVQAANHLSSLRDVAFSGQGW 180
DB 121 NAQLEDVIRIRANTDDALITAINNFTLSFEIPILLSVYVQAANHLSSLRDVAFSGQGW 180
QY 181 GUDIAVNNHYNRLNLHRYTKHCLDTYNOGLENLRGTNTROWARFNQFRDLTLTVLD 240
DB 181 GUDIAVNNHYNRLNLHRYTKHCLDTYNOGLENLRGTNTROWARFNQFRDLTLTVLD 240
QY 241 IVALFPNDVIRTYPIQTSQLEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300
DB 241 IVALFPNDVIRTYPIQTSQLEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300
QY 301 NSLFTVTAETVRSQTVMGHVLSSRNAGNINFPSSGVFNPGGAIWIADDEPRFVTL 360
DB 301 NSLFTVTAETVRSQTVMGHVLSSRNAGNINFPSSGVFNPGGAIWIADDEPRFVTL 360
QY 361 DPVFRGGFNGPHYVGLRGVAFQQTGTHRTFRNSGTHIDSLDEIPPODNGAPWNY 420
DB 361 DPVFRGGFNGPHYVGLRGVAFQQTGTHRTFRNSGTHIDSLDEIPPODNGAPWNY 420
QY 421 HVLNHTVFEVRWPCIEISGSDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAKHTLOSQT 480
DB 421 HVLNHTVFEVRWPCIEISGSDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAKHTLOSQT 480
QY 481 VVRGPGFTGDIILRRYSGGFFAYTIWNINGQLPQRYRARIYASTTNLIYVTVAGERIF 540
DB 481 VVRGPGFTGDIILRRYSGGFFAYTIWNINGQLPQRYRARIYASTTNLIYVTVAGERIF 540
QY 541 AGQFNKMTGDPDLTQFSYATINTAFTFPMSSQSFTVGADTFSSGNEVYIDRPELIPV 600
DB 541 AGQFNKMTGDPDLTQFSYATINTAFTFPMSSQSFTVGADTFSSGNEVYIDRPELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINGIKTDVTDHIDOVSNLVDCLDFECLDEKREL 660
DB 601 TATFEAYDLERAQKAVNALFTSINGIKTDVTDHIDOVSNLVDCLDFECLDEKREL 660
QY 661 SEVKHAKRLSDERNLQDQNFNGINRLDQWGRGSTDTIQGDDVFKENYVTLPGTGD 720
DB 661 SEVKHAKRLSDERNLQDQNFNGINRLDQWGRGSTDTIQGDDVFKENYVTLPGTGD 720
QY 721 EGYPTLYQKIDSKLPYTRYOLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLWPLS 780
DB 721 EGYPTLYQKIDSKLPYTRYOLRGYIEDSQDLEIYLIRYNAKHETVNLGTGSLWPLS 780
QY 781 VQSPFKCGEPNRCAPHEWNPDLDCSRRGKCAHSHHFLDIDVGTDLNEDLDVWV 840
DB 781 VQSPFKCGEPNRCAPHEWNPDLDCSRRGKCAHSHHFLDIDVGTDLNEDLDVWV 840
QY 841 IFKIKTDGCHARLGNLEFTEKPLVGEALARVRAKRWKREKLELENTNIVYKEAKES 900
DB 841 IFKIKTDGCHARLGNLEFTEKPLVGEALARVRAKRWKREKLELENTNIVYKEAKES 900
QY 901 VDALFVNSQDQADTNIAHIAAKRVHRIREAYLPESLVPVGNVDIFELKGRIFT 960
DB 901 VDALFVNSQDQADTNIAHIAAKRVHRIREAYLPESLVPVGNVDIFELKGRIFT 960
QY 961 AFFLYDARNVINKGDFNNGLSQWNVKGVHVDVEONNHRSLVVPENAEVSQEVRYCGR 1020
DB 961 AFFLYDARNVINKGDFNNGLSQWNVKGVHVDVEONNHRSLVVPENAEVSQEVRYCGR 1020
QY 1021 GYLIRVTAYKEGEGCVTTHEIENNTDELKFSNCVEEYYPNTVTCNDYTANQBEYGG 1080
DB 1021 GYLIRVTAYKEGEGCVTTHEIENNTDELKFSNCVEEYYPNTVTCNDYTANQBEYGG 1080
QY 1081 AYTSSNRGYDETYGNSSVFADYASVTEKSYTDGRDNPCESNRGYDVTPLPAGYVTK 1140
DB 1081 AYTSSNRGYDETYGNSSVFADYASVTEKSYTDGRDNPCESNRGYDVTPLPAGYVTK 1140
QY 1141 ELEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174

DB 1141 BLEYFPETDKVWIEIGETGTFIVDSVELLMEE 1174
RESULT 3
RAR39754
ID AAR39754 standard; Protein: 1174 AA.
XX AAR39754;
XX AC
XX 28-JAN-1994 (first entry)
XX Delta endotoxin.
XX Endotoxin; Bacillus; lice; insecticide; sheep.
XX OS Bacillus thuringiensis PS81I (Clone 81IA).
XX PN W09314641-A.
XX 05-AUG-1993.
XX 31-DEC-1992; 92WO-US11337.
XX 29-JAN-1992; 92US-0828788.
XX (MYCO) MYCOGEN CORP.
XX Hickle LA, Payne J;
XX WPI; 1993-258266/32.
XX N-PSDB; AAQ47291.
XX Controlling biting lice on sheep - comprises administering
XX Bacillus thuringiensis toxins to host
XX Disclosure; Page 43-46; 64pp; English.
XX Many strains of Bacillus thuringiensis (B.t) produce insecticidal
XX delta endotoxins. A number of these endotoxins have been found to
XX be toxic to Damlinia ovis, the biting louse of sheep. The B.T.
XX isolates which produce these toxins can be grown and the delta
XX endotoxin which is produced can be recovered by standard procedures.
XX The genes encoding these endotoxins can also be transferred to a
XX suitable host via a recombinant vector and the resulting
XX transformants used in methods to control lice.
SQ Sequence 1174 AA;
Query Match 100.0%; Score 6244; DB 14; Length 1174;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MENNTQNCVPCVNCNNPEVELLNEERSTGRPLDLSLSTRFLLSEVPVGVAGFLFD 60
DB 1 MENNTQNCVPCVNCNNPEVELLNEERSTGRPLDLSLSTRFLLSEVPVGVAGFLFD 60
QY 61 LMGFTTPSDWSLFLQIQLEQRIETERNRAITTLRGLADSYEIIYIEALREWEANPN 120
DB 61 LMGFTTPSDWSLFLQIQLEQRIETERNRAITTLRGLADSYEIIYIEALREWEANPN 120
QY 121 NAQLEDVIRIRANTDDALITAINNFTLSFEIPILLSVYVQAANHLSSLRDVAFSGQGW 180
DB 121 NAQLEDVIRIRANTDDALITAINNFTLSFEIPILLSVYVQAANHLSSLRDVAFSGQGW 180
QY 181 GUDIAVNNHYNRLNLHRYTKHCLDTYNOGLENLRGTNTROWARFNQFRDLTLTVLD 240
DB 181 GUDIAVNNHYNRLNLHRYTKHCLDTYNOGLENLRGTNTROWARFNQFRDLTLTVLD 240
QY 241 IVALFPNDVIRTYPIQTSQLEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300
DB 241 IVALFPNDVIRTYPIQTSQLEIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300

301 NSLFVTAETVRSQTVWGCHLVSSRNATAGNRINPFSYGVNPGGAIWIAEDDPRPFYRTLS 360
 301 NSLFVTAETVRSQTVWGCHLVSSRNATAGNRINPFSYGVNPGGAIWIAEDDPRPFYRTLS 360
 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPQDMSGAPWNDYS 420
 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPQDMSGAPWNDYS 420
 421 HVLNHHVTFVRWPGEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480
 421 HVLNHHVTFVRWPGEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480
 481 VVRGPGFTGGDILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYVAGERIF 540
 481 VVRGPGFTGGDILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYVAGERIF 540
 541 AGQFNKMTDGTDLTQSFYSATINTAFTPPMSQSFTVGADTFSSGNEVYIDRFELIPV 600
 541 AGQFNKMTDGTDLTQSFYSATINTAFTPPMSQSFTVGADTFSSGNEVYIDRFELIPV 600
 601 TATFEAYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFECLDEKREL 660
 601 TATFEAYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSDFECLDEKREL 660
 661 SEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQGDDVFKENYVTLPGCTD 720
 661 SEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQGDDVFKENYVTLPGCTD 720
 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSQBLEYLIRYNAKHETVNVLTGSLWPLS 780
 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSQBLEYLIRYNAKHETVNVLTGSLWPLS 780
 781 VOSPIRKCEPNRCAPHLNPNLDSCRDGKCAHSHHFDIDVCGCTDLNEDLDVWV 840
 781 VOSPIRKCEPNRCAPHLNPNLDSCRDGKCAHSHHFDIDVCGCTDLNEDLDVWV 840
 841 IFKIKTDQGHARLGNLEFLEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKAKES 900
 841 IFKIKTDQGHARLGNLEFLEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKAKES 900
 901 VDALFVNSQYDQADNTAMIAHAKRVHRIEAYLPVLPVGVNVDIFEELKGRIFT 960
 901 VDALFVNSQYDQADNTAMIAHAKRVHRIEAYLPVLPVGVNVDIFEELKGRIFT 960
 961 APFLYDARNVKNNGDNLSCWNVKGVHDVEQNNHRSVLLVVPWEAEVQSQRVCPGR 1020
 961 APFLYDARNVKNNGDNLSCWNVKGVHDVEQNNHRSVLLVVPWEAEVQSQRVCPGR 1020
 1021 GYLIRVTAYKEGEGECVTIHEIENNTDELKFSNCVEEVEEYYPNTVTCNDYTANQEYGG 1080
 1021 GYLIRVTAYKEGEGECVTIHEIENNTDELKFSNCVEEVEEYYPNTVTCNDYTANQEYGG 1080
 1081 AYTSNRNGYDETYGNSNPADYASYBEKSYTDGRDNPCESNRGYGYDTPLPAGYVTK 1140
 1081 AYTSNRNGYDETYGNSNPADYASYBEKSYTDGRDNPCESNRGYGYDTPLPAGYVTK 1140
 1141 ELEYFPETDKVWEIGETEGTFTVDSVELLMEE 1174
 1141 ELEYFPETDKVWEIGETEGTFTVDSVELLMEE 1174

RESULT 4
 AA76708
 ID AA76708 standard; Protein; 1174 AA.
 AC AA76708;
 XX
 XX
 DT 13-JAN-1999 (first entry)
 DE Plasmid pMYC2243 Bt endotoxin protein fragment.
 XX Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);
 KW synergism; plant; primer; endotoxin.
 QW

Synthetic.
 US5827514-A.
 27-OCT-1998.
 08-FEB-1996; 96US-0598305.
 06-DEC-1994; 94US-0349867.
 08-FEB-1996; 96US-0598305.
 (MYCO) MYCOGEN CORP.
 Bradfisch GA, Schwab GE, Thompson M;
 WPI; 1998-593944/50.
 N-PSDB; AAV62081.
 Composition for biological control of lepidopteran pests -
 comprising cells expressing two chimeric Bacillus thuringiensis
 crystal proteins
 Example 5; Column 57-64; 75pp; English.
 This sequence represents a Bt endotoxin which is used in a method for
 controlling lepidopteran pests. The method involves the use of cells
 that express the Bacillus thuringiensis delta-endotoxin cryIF chimeric
 core toxin-containing protein and CryIA(c) chimeric core toxin-containing
 protein in a combination that have synergistically enhanced activity.
 against e.g. corn earworm (Heliothis zea).
 Sequence 1174 AA;
 Query Match 100.0%; Score 6244; DB 19; Length 1174;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MENNIOQCVPVNCNNPEVILNEERSTGRPLDLSLSLTRELLSEFVPGVGVAFGLFD 60
 1 MENNIOQCVPVNCNNPEVILNEERSTGRPLDLSLSLTRELLSEFVPGVGVAFGLFD 60
 61 LWGFTTPSDWSLFLQIEQLTEORITLERNRAITTLRGLADSYEIIYEALEWEANPN 120
 61 LWGFTTPSDWSLFLQIEQLTEORITLERNRAITTLRGLADSYEIIYEALEWEANPN 120
 121 NQALREDVIRFANTDDALITAINNFTLTSFEIPLSVVQVQANLHLSLLRDVAVSGQW 180
 121 NQALREDVIRFANTDDALITAINNFTLTSFEIPLSVVQVQANLHLSLLRDVAVSGQW 180
 181 GLDIATVNNHYNRLINLHRYTKHCLDLYNQGLNLRGTNRQWARFNQFRDLTLTVLD 240
 181 GLDIATVNNHYNRLINLHRYTKHCLDLYNQGLNLRGTNRQWARFNQFRDLTLTVLD 240
 241 IVALPNYDVRYPYQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVAPPHLMDPM 300
 241 IVALPNYDVRYPYQTSQTLREIYTSVIEDSPVSANIPNGFNRAEFGVAPPHLMDPM 300
 301 NSLFTVTAETVRSQTVWGCHLVSSRNATAGNRINPFSYGVNPGGAIWIAEDDPRPFYRTLS 360
 301 NSLFTVTAETVRSQTVWGCHLVSSRNATAGNRINPFSYGVNPGGAIWIAEDDPRPFYRTLS 360
 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPQDMSGAPWNDYS 420
 361 DPVFRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPQDMSGAPWNDYS 420
 421 HVLNHHVTFVRWPGEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480
 421 HVLNHHVTFVRWPGEISGSDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLQSGTT 480
 481 VVRGPGFTGGDILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYVAGERIF 540
 481 VVRGPGFTGGDILRRSTSGGPFATIVNINGQLPQRYARIRYASTNLRIVYVAGERIF 540

QY 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600
 DB 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600
 QY 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLDSDFCLDEKREL 660
 DB 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLDSDFCLDEKREL 660
 QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTIIQRGDDVFKENYVTLGTFD 720
 DB 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTIIQRGDDVFKENYVTLGTFD 720
 QY 721 EGYPTLYQKIDESKLPKPYTRVQLRGYIEDSQDLLEYLYRYNAKHETVNVLTGSLWPLS 780
 DB 721 EGYPTLYQKIDESKLPKPYTRVQLRGYIEDSQDLLEYLYRYNAKHETVNVLTGSLWPLS 780
 QY 781 VQSPIKCGEPNRCAPHELPWNPDLDCSRDGEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
 DB 781 VQSPIKCGEPNRCAPHELPWNPDLDCSRDGEKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
 QY 841 IPKIKTODGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIYVKEAKES 900
 DB 841 IPKIKTODGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIYVKEAKES 900
 QY 901 VDALFYNSOYDQLOADNTIAMIHAADKRVHRIREAYLPESLVIPGVNVDIFFEELKGRIFT 960
 DB 901 VDALFYNSOYDQLOADNTIAMIHAADKRVHRIREAYLPESLVIPGVNVDIFFEELKGRIFT 960
 QY 961 AFPLYDARNVKNKNGDNNGLSKNVKGHDVBEQNNHRSVLVVPWEAEVYQEVRYCPGR 1020
 DB 961 AFPLYDARNVKNKNGDNNGLSKNVKGHDVBEQNNHRSVLVVPWEAEVYQEVRYCPGR 1020
 QY 1021 GYLRYTAYKEGEGECVTIHEIENNTDELKFSNOCVEEYYPNNTVTCNDYTANQOEYGG 1080
 DB 1021 GYLRYTAYKEGEGECVTIHEIENNTDELKFSNOCVEEYYPNNTVTCNDYTANQOEYGG 1080
 QY 1081 AYTSRNRGYDEYTGSSNPADYASVYEKSYDGRDRNPCESTRNGYGDYTPLPAGYVTK 1140
 DB 1081 AYTSRNRGYDEYTGSSNPADYASVYEKSYDGRDRNPCESTRNGYGDYTPLPAGYVTK 1140
 QY 1141 ELEYFPTDKVMEIGETGTFTVDSVELLMEE 1174
 DB 1141 ELEYFPTDKVMEIGETGTFTVDSVELLMEE 1174

RESULT 5

AAW76712
 ID AAW76712 standard; Protein; 1174 AA.
 AC AAW76712;
 XX
 DT 13-JAN-1999 (first entry)
 XX
 DE B. thuringiensis cryIF/cryIA(b) endotoxin protein.
 XX
 KW Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);
 KW synergism; plant; primer; endotoxin.
 XX
 OS Bacillus thuringiensis.
 XX
 PN US5827514-A.
 XX
 PD 27-OCT-1998.
 XX
 PF 08-FEB-1996; 96US-0598305.
 XX
 PR 06-DEC-1994; 94US-0349867.
 PR 08-FEB-1996; 96US-0598305.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Bradfisch GA, Schwab GE, Thompson M;

XX WPI; 1998-593944/50.
 XX
 PT Composition for biological control of lepidopteran pests -
 PT comprising cells expressing two chimeric Bacillus thuringiensis
 PT crystal proteins
 XX
 PS Disclosure; Column 81-88; 75pp; English.
 XX
 CC This sequence represents a Bt endotoxin which is used in a method for
 CC controlling lepidopteran pests. The method involves the use of cells
 CC that express the Bacillus thuringiensis delta-endotoxin cryIF chimeric
 CC core toxin-containing protein and CryIA(c) chimeric core toxin-containing
 CC protein in a combination that have synergistically enhanced activity,
 CC against e.g. corn earworm (Heliothis zea).
 XX
 SQ Sequence 1174 AA;
 Query Match 100.0%; Score 6244; DB 19; Length 1174;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MENNIQOCVPYNCLANPEVEILNEERSTGRPLDLSLTRELLSEFVGVGVAFLFD 60
 DB 1 MENNIQOCVPYNCLANPEVEILNEERSTGRPLDLSLTRELLSEFVGVGVAFLFD 60
 QY 61 LIWGFPTPSDWSLFIQIEQLIEQRIETLERNAITTLGLADSYEIIYI EALREWEANPN 120
 DB 61 LIWGFPTPSDWSLFIQIEQLIEQRIETLERNAITTLGLADSYEIIYI EALREWEANPN 120
 QY 121 NAQREDVRIRFANTDALLITANNFTLSFEIPLSVYVQAAANLHLSLLRDVSVFGQW 180
 DB 121 NAQREDVRIRFANTDALLITANNFTLSFEIPLSVYVQAAANLHLSLLRDVSVFGQW 180
 QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENRGTNTROWARNQFRDLTLTVLD 240
 DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENRGTNTROWARNQFRDLTLTVLD 240
 QY 241 IVAFPNYDVRTPIOTSSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300
 DB 241 IVAFPNYDVRTPIOTSSQLTREIYTSVIEDSPYSANIPNGFNRAEFGVRPHLMDFM 300
 QY 301 NSLFTVAETVRSQTVMGHLYSSRNAGNINFPSPGVNPGGAIWADDDPPFRTLS 360
 DB 301 NSLFTVAETVRSQTVMGHLYSSRNAGNINFPSPGVNPGGAIWADDDPPFRTLS 360
 QY 361 DPVVRGGFGNPHYVLGLRGVAFQQTGTNTRFRNSGTTIDSLDEIPPDQNSGAPNDYS 420
 DB 361 DPVVRGGFGNPHYVLGLRGVAFQQTGTNTRFRNSGTTIDSLDEIPPDQNSGAPNDYS 420
 QY 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
 DB 421 HVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
 QY 481 VVRGPGTGGDILRRISGGPFAYTIIVNINGQLPQRYRARIYASTNLRIYVTVAGERIF 540
 DB 481 VVRGPGTGGDILRRISGGPFAYTIIVNINGQLPQRYRARIYASTNLRIYVTVAGERIF 540
 QY 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600
 DB 541 AGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSFYAGDFFSSGNEVYIDRFELIPV 600
 QY 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLDSDFCLDEKREL 660
 DB 601 TATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNLVCLDSDFCLDEKREL 660
 QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTIIQRGDDVFKENYVTLGTFD 720
 DB 661 SEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTIIQRGDDVFKENYVTLGTFD 720
 QY 721 EGYPTLYQKIDESKLPKPYTRVQLRGYIEDSQDLLEYLYRYNAKHETVNVLTGSLWPLS 780
 DB 721 EGYPTLYQKIDESKLPKPYTRVQLRGYIEDSQDLLEYLYRYNAKHETVNVLTGSLWPLS 780

Qy 781 VQSPIKCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840
 Db 781 VQSPIKCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840
 Qy 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900
 Db 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900
 Qy 901 VDALFVNSQYDQLOADTNIAHAAKRVHRIREAYLPFLSVIPGVNVDIPEELKGRIFT 960
 Db 901 VDALFVNSQYDQLOADTNIAHAAKRVHRIREAYLPFLSVIPGVNVDIPEELKGRIFT 960
 Qy 961 AFPLDARNVKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSOEVRVCPGR 1020
 Db 961 AFPLDARNVKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVPEWEAEVSOEVRVCPGR 1020
 Qy 1021 GYLAVTAYKEGEGGVYIHEIENNTDELKFSNCEVEEVPNTVTCNDYTANOEEYGG 1080
 Db 1021 GYLAVTAYKEGEGGVYIHEIENNTDELKFSNCEVEEVPNTVTCNDYTANOEEYGG 1080
 Qy 1081 AYTSNRGYDETYGNSVVPADYASVYEKSYTDGRRDNPCESNRGYGDYTPPLPAGYVTK 1140
 Db 1081 AYTSNRGYDETYGNSVVPADYASVYEKSYTDGRRDNPCESNRGYGDYTPPLPAGYVTK 1140
 Qy 1141 ELEYFETDKVWIEGEGTGFIVDSVELLME 1174
 Db 1141 ELEYFETDKVWIEGEGTGFIVDSVELLME 1174
 RESULT 6
 AA16792
 ID AA16792 standard; Protein; 1174 AA.
 XX AA16792;
 AC AA16792;
 DT 27-JUL-1999 (first entry)
 DE Wild-type B.t cryIF toxin 81IA.
 XX
 KW Plant-optimised gene; pesticidal toxin; CryIF; CryIaC; CryIc; 158C2c;
 XX 3IGla; CryIaB prototoxin; insect control; chimeric.
 OS Bacillus thuringiensis.
 XX WO9324581-A2.
 XX 20-MAY-1999.
 XX 04-NOV-1998; 98WO-US23457.
 XX 23-OCT-1998; 98US-0178252.
 XX 12-NOV-1997; 97US-0065215.
 XX 02-MAR-1998; 98US-0076443.
 XX (MYCO) MYCOGEN CORP.
 XX
 XX Cardineau GA, Narva KE, Stelman SJ;
 XX WPI: 1999-327409/27.
 XX N-PSDB; AAX60606.
 XX
 PT Nucleic acids encoding pesticidal proteins, optimized for plant
 PT expression
 XX
 XX Disclosure; Page 30-34; 67pp; English.
 XX
 CC The invention relates to nucleic acid sequences, optimised for
 CC expression in plants, that encode: (i) one of the pesticidal toxins
 CC CryIF, CryIaC, CryIc, 158C2c or 3IGla, or (ii) a portion of the CryIaB
 CC prototoxin. The pesticidal toxins (AA16790, AA16792, AA16798) are used for
 CC pest, especially insect control, particularly on plants. The nucleic acid
 CC sequences are used to produce (truncated or chimeric) toxins, and related

CC fusion genes or proteins, particularly they are used to generate
 CC transgenic plants that show increased resistance to pests. Compared with
 CC wild-type Bacillus thuringiensis sequences, the optimised sequences are
 CC better suited to expression in plants. The present sequence represents
 CC the amino acid sequence for a wild-type, full-length B.t toxin designated
 CC 81IA.
 XX
 SQ Sequence 1174 AA;
 Query Match 100.0%; Score 6244; DB 20; Length 1174;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MENNIOQCVPYCNLANPEVEILNEERSTGRPLDLSLTLRFLSEFVPGVGVAFLGD 60
 Db 1 MENNIOQCVPYCNLANPEVEILNEERSTGRPLDLSLTLRFLSEFVPGVGVAFLGD 60
 Qy 61 LIWGFITPDSWLSFLQIEQLIEQRIETLERNAITTLRGLADSYEIIYIETALREWEANFN 120
 Db 61 LIWGFITPDSWLSFLQIEQLIEQRIETLERNAITTLRGLADSYEIIYIETALREWEANFN 120
 Qy 121 NAOLREDVIRFANTDDALITAINNFTLSFEIPLSVVQAAHLSLLRDVAVSFGQGW 180
 Db 121 NAOLREDVIRFANTDDALITAINNFTLSFEIPLSVVQAAHLSLLRDVAVSFGQGW 180
 Qy 181 GLDIATVNNHYNRLNLIHRYTKHCLDVTNQGLENLGRNTQWARFNQFRDLTLTVLD 240
 Db 181 GLDIATVNNHYNRLNLIHRYTKHCLDVTNQGLENLGRNTQWARFNQFRDLTLTVLD 240
 Qy 241 IVALFPNDVRYPIQTSOLTRIEYTSVIEDSPYSANIPNGFNRAEFGVPPHLMDFM 300
 Db 241 IVALFPNDVRYPIQTSOLTRIEYTSVIEDSPYSANIPNGFNRAEFGVPPHLMDFM 300
 Qy 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINPPSYGVNPGCAIWIADDPFPYRTLS 360
 Db 301 NSLFVTAETVRSQTVWGGHLVSSRNTAGNRINPPSYGVNPGCAIWIADDPFPYRTLS 360
 Qy 361 DPVVRGGFGNPHYVLGRVAFQQTGNHTRFRNSGTIDSLDEIPPDNSCAPNDYS 420
 Db 361 DPVVRGGFGNPHYVLGRVAFQQTGNHTRFRNSGTIDSLDEIPPDNSCAPNDYS 420
 Qy 421 HVLNHTVFWRPGEISGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLOSGET 480
 Db 421 HVLNHTVFWRPGEISGDSWRAPMFSWTHRSATPNTIDPERITQIPLVKAHTLOSGET 480
 Qy 481 VVRGPGFTGDIILRRYSGGPFATYIVNINGQLPQRIARIRASTNLRIYTVAGERIF 540
 Db 481 VVRGPGFTGDIILRRYSGGPFATYIVNINGQLPQRIARIRASTNLRIYTVAGERIF 540
 Qy 541 AGOFNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSFYVGAOTFSSGNEVYIDRFELIPV 600
 Db 541 AGOFNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSFYVGAOTFSSGNEVYIDRFELIPV 600
 Qy 601 TATFEAEYDLERAQKAVNALFTSINGIGIKTDVTDYHIDQVSNLVDCLDEKREL 660
 Db 601 TATFEAEYDLERAQKAVNALFTSINGIGIKTDVTDYHIDQVSNLVDCLDEKREL 660
 Qy 661 SEVKHAKRLSDERNLLQDPNFENGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
 Db 661 SEVKHAKRLSDERNLLQDPNFENGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
 Qy 721 ECTPTLYQKIDESKLPYTRYOLRGYIEDSQDLEYLYLRYNAKHETVNLGTSWLPVS 780
 Db 721 ECTPTLYQKIDESKLPYTRYOLRGYIEDSQDLEYLYLRYNAKHETVNLGTSWLPVS 780
 Qy 781 VQSPIKCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840
 Db 781 VQSPIKCGEPNRCAPHLEWNPDLDCSCRDGCEKCAHSHHFLSLDIDVGCTDLNEDLDVWV 840
 Qy 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900
 Db 841 IFKIKTQGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLELETNIVYKEAKES 900

QY 901 VDALFVNSQVDQLQADNTNMIHAADKRVHRIREAYLPESLVIPGVNVDIFEEELKGRIFT 960
 Db 901 VDALFVNSQVDQLQADNTNMIHAADKRVHRIREAYLPESLVIPGVNVDIFEEELKGRIFT 960
 QY 961 AFPLYDARVWIKNGDFNGLSCNWNVGHVDVBEQNNHRSVLVVPWEAEVSVQEVRCVPCR 1020
 Db 961 AFPLYDARVWIKNGDFNGLSCNWNVGHVDVBEQNNHRSVLVVPWEAEVSVQEVRCVPCR 1020
 QY 1021 GYLIRVTAKEGEGECVTHETENNTDELKFSNCVEEVEEYPNNTVTCNDYTANQBEYGG 1080
 Db 1021 GYLIRVTAKEGEGECVTHETENNTDELKFSNCVEEVEEYPNNTVTCNDYTANQBEYGG 1080
 QY 1081 AYTSNRGDETYGSSNPADYASVEEKSYPDGRDRDNPCESNRGVDYTPLPAGVYTK 1140
 Db 1081 AYTSNRGDETYGSSNPADYASVEEKSYPDGRDRDNPCESNRGVDYTPLPAGVYTK 1140
 QY 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174
 Db 1141 ELEYFPETDKVWIEIGETEGTFIVDSVELLMEE 1174

RESULT 7

AAU00533

ID AAU00533 standard; Protein; 1174 AA.

XX AAU00533;

XX 14-MAY-2001 (first entry)

XX B. thuringiensis toxin 8IIA (CryIIa).

XX Toxin 8IIA; cryIIa; cutworm; pesticide; corn; soybean; canola; cotton;

KW Agrotis ipsilon; Agrotis malefida; Porasagrotis gypaetiana; sunflower;

KW Xylomyges curialis; Tribe Agrotini; Feltia jaculifera; Euxoa sp.

XX Bacillus thuringiensis.

XX WO200113731-A1.

XX 01-MAR-2001.

XX 23-AUG-2000; 2000WO-US23156.

XX 23-AUG-1999; 99US-0150319.

XX (MYCO) MYCOGEN CORP.

XX Stockhoff BA, Conlan C;

XX WPI; 2001-211270/21.

XX N-PSDB; AAS00565.

XX Controlling cutworm pests especially black cutworm comprises contacting

PT the pest with crystal protein CryIIa toxin

XX Example 5; Page 44-48; 52pp; English.

XX The sequence represents the wild-type, full length Bacillus thuringiensis

CC toxin 8IIA (CryIIa). Full-length, truncated and chimeric CryIIa genes and

CC proteins can be used for controlling cutworm pests, by contacting the

CC pest with a Bacillus thuringiensis toxin comprising a pesticidal portion

CC of a CryIIa toxin. These genes and proteins are useful for controlling

CC cutworm pests such as Agrotis ipsilon, Agrotis malefida, Porasagrotis

CC gypaetiana, Xylomyges curialis, members of the Tribe Agrotini, Feltia

CC jaculifera, Euxoa messoria, Euxoa scandens, Euxoa auxiliaris, Euxoa

CC detersa, Euxoa tessellata, Euxoa ochragaster and Peridroma saucia in

CC plants such as corn, sunflower, soybean, canola and cotton. The plants

CC are transformed with a polynucleotide encoding a Cry II protein such that

CC the transformed plant cells express pesticidal proteins in tissues

CC consumed by the target pests.

XX Sequence 1174 AA;

Query Match 100.0%; Score 6244; DB 22; Length 1174;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MENNIQOCVPYNNCLNPEVEILNEERSTGRPLDLSLSTRFLLSEFVGVGVAFLGD 60
 Db 1 MENNIQOCVPYNNCLNPEVEILNEERSTGRPLDLSLSTRFLLSEFVGVGVAFLGD 60
 QY 61 LIWGFTIPSDWSLFLQIEOLIEQRIETELERNRAITTLRGLADSYEYIEALREWEANPN 120
 Db 61 LIWGFTIPSDWSLFLQIEOLIEQRIETELERNRAITTLRGLADSYEYIEALREWEANPN 120
 QY 121 NAOLREDVRIRFANTDDALITANNFTLTSEFPLSLVVOAANLHLSLRDVAVSFGQW 180
 Db 121 NAOLREDVRIRFANTDDALITANNFTLTSEFPLSLVVOAANLHLSLRDVAVSFGQW 180
 QY 181 GLDIATVNNHYNLNLHRYTKHCLDYNQGLENLKGTNTROWARENQFRDLTLVLD 240
 Db 181 GLDIATVNNHYNLNLHRYTKHCLDYNQGLENLKGTNTROWARENQFRDLTLVLD 240
 QY 241 IVALFPNYDVRTPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRPPLMDFM 300
 Db 241 IVALFPNYDVRTPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRPPLMDFM 300
 QY 301 NSLFTVTAETVRSQTVWGGHUVSSRNAGNINFPSPGVNPGGAIWTADEDPFFYRTLS 360
 Db 301 NSLFTVTAETVRSQTVWGGHUVSSRNAGNINFPSPGVNPGGAIWTADEDPFFYRTLS 360
 QY 361 DPVFRGGFNGPHYVLGLRGVAFQGTGNHTRTFRNSGTTDSLSDEIPPODSNAGPNDYS 420
 Db 361 DPVFRGGFNGPHYVLGLRGVAFQGTGNHTRTFRNSGTTDSLSDEIPPODSNAGPNDYS 420
 QY 421 HVLNHYTFVWPGEISGDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
 Db 421 HVLNHYTFVWPGEISGDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAHTLQSGTT 480
 QY 481 VVRGPGFTGGDILRRTSGGPFATYIVNINQOLPORVRRARYASTNLRIYTVVAGBRIF 540
 Db 481 VVRGPGFTGGDILRRTSGGPFATYIVNINQOLPORVRRARYASTNLRIYTVVAGBRIF 540
 QY 541 AGQFNKTMGTDPDLTQSFSTYATINTAFTPPMSQSSFTVGADTFSSGNEYVIDRFELIPV 600
 Db 541 AGQFNKTMGTDPDLTQSFSTYATINTAFTPPMSQSSFTVGADTFSSGNEYVIDRFELIPV 600
 QY 601 TATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDHIDQVSNLVDCLSDPCLDEKREL 660
 Db 601 TATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDHIDQVSNLVDCLSDPCLDEKREL 660
 QY 661 SEKVHAKRLSDERNLLQDPNFKGINRQDLDRGWSGTDITIQRGDDVFKENYVTLPGTFD 720
 Db 661 SEKVHAKRLSDERNLLQDPNFKGINRQDLDRGWSGTDITIQRGDDVFKENYVTLPGTFD 720
 QY 721 ECVPTLYOKIDSKLKPTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780
 Db 721 ECVPTLYOKIDSKLKPTRYQLRGYIEDSQDLEIYLIRYNAKHETVNVLTGSLWPLS 780
 QY 781 VQSPIRKCEPNKCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
 Db 781 VQSPIRKCEPNKCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
 QY 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLEFNIYVKEAKES 900
 Db 841 IFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLEFNIYVKEAKES 900
 QY 901 VDALFVNSQVDQLQADNTNMIHAADKRVHRIREAYLPESLVIPGVNVDIFEEELKGRIFT 960
 Db 901 VDALFVNSQVDQLQADNTNMIHAADKRVHRIREAYLPESLVIPGVNVDIFEEELKGRIFT 960
 QY 961 AFPLYDARVWIKNGDFNGLSCNWNVGHVDVBEQNNHRSVLVVPWEAEVSVQEVRCVPCR 1020
 Db 961 AFPLYDARVWIKNGDFNGLSCNWNVGHVDVBEQNNHRSVLVVPWEAEVSVQEVRCVPCR 1020
 QY 1021 GYLIRVTAKEGEGECVTHETENNTDELKFSNCVEEVEEYPNNTVTCNDYTANQBEYGG 1080

AAR84735
ID AAR84735 standard; Protein: 1174 AA.
XX AC AAR84735;
XX AC AAR84735;
DT 23-JUN-1996 (first entry)
XX XX CryIF toxin with limited codon rework.
XX XX Delta endotoxin; crystal protein; chimeric toxin; codon rework;
KW insecticide; pesticide; Pseudomonas fluorescens;
KW biological control agent; transgenic plant; insect resistance;
KW disease resistance; crop improvement; protein engineering.
XX XX Bacillus thuringiensis.
OS OS
XX XX WO9530753-A1.
XX PD 16-NOV-1995.
XX XX 05-MAY-1995; 95WO-US05431.
XX PF 06-MAY-1994; 94US-0239476.
XX PR (MYCO) MYCOGEN CORP.
XX PA
XX PI Schwab GE, Thompson M;
XX DR WPI: 1995-404120/51.
XX DR N-PSDB; AAT05270.
XX XX Nucleic acid encoding chimeric Bacillus thuringiensis
PT delta-endotoxin - providing increased expression in Pseudomonas,
PT esp. for control of lepidoptera pests.
XX XX
PS Example 5; Page 47-50; 91pp; English.
XX XX
CC The sequence represents the CryIF toxin sequence with codon rework.
CC DNA encoding this sequence can be used in the construction of
CC chimeric toxins, which are expressed in Pseudomonas fluorescens
CC better than native delta endotoxins. Host cells expressing the
CC chimeric gene and producing chimeric toxin may be used in insecticide
CC compositions, where the host cells are plant cells, the gene confers
XX insect resistance to the transformed plant.
XX XX
SQ Sequence 1174 AA;
Query Match 99.9%; Score 6238; DB 16; Length 1174;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MENNIONQCPVNCNLPNPEVEILNEERSTGRPLDLSLRFLLSEFVPGVAFGLFD 60
DB 1 MENNIONQCPVNCNLPNPEVEILNEERSTGRPLDLSLRFLLSEFVPGVAFGLFD 60
QY 61 LWGFTTPSDWSLFLQIQEQLIEQRIETLERNRAITLRLGLADSYEIEALREWEANPN 120
DB 61 LWGFTTPSDWSLFLQIQEQLIEQRIETLERNRAITLRLGLADSYEIEALREWEANPN 120
QY 121 NAOLREDVIRFANTDAILITNFTLTSFEIPLLSVVQAANLHLSLLRDVAVSGOGW 180
DB 121 NAOLREDVIRFANTDAILITNFTLTSFEIPLLSVVQAANLHLSLLRDVAVSGOGW 180
QY 181 GLDIATVNNHYNFLNLIHRYTKHCLDVTYNOGLENLGRNTROWARFNQFRDLTLTVD 240
DB 181 GLDIATVNNHYNFLNLIHRYTKHCLDVTYNOGLENLGRNTROWARFNQFRDLTLTVD 240
QY 241 IVALFPNDVRYPIQTSQLTREIYTSSTVEDSPYSANIPNGFNRAEFGVRPPLMDFM 300
DB 241 IVALFPNDVRYPIQTSQLTREIYTSSTVEDSPYSANIPNGFNRAEFGVRPPLMDFM 300
QY 301 NSLFTVTAETVRSQTVWGGHLVSSRNINFPSPGVNPGCAIWIADDEPRPYRTLS 360
DB 301 NSLFTVTAETVRSQTVWGGHLVSSRNINFPSPGVNPGCAIWIADDEPRPYRTLS 360
QY 361 DPVFRGGFNGPHYVILGRGVAFOQTGTNHTFRNSGTIDSLDEIPFDNSGAPWNDYS 420
DB 361 DPVFRGGFNGPHYVILGRGVAFOQTGTNHTFRNSGTIDSLDEIPFDNSGAPWNDYS 420
QY 421 HVLNHTVFRWPEGEISGSDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480
DB 421 HVLNHTVFRWPEGEISGSDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHTLOSITT 480
QY 481 VVRGPGFTGSDILRRFSGGPFATVINGQLPQRYRARIYASTNRIYVTVAGERIF 540
DB 481 VVRGPGFTGSDILRRFSGGPFATVINGQLPQRYRARIYASTNRIYVTVAGERIF 540
QY 541 AGQFNKMTDGTPLTFQSFYSATINTAFTFPMQSQSFTVGADTFSSGNEVYIDRPELIPV 600
DB 541 AGQFNKMTDGTPLTFQSFYSATINTAFTFPMQSQSFTVGADTFSSGNEVYIDRPELIPV 600
QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTVDYTHIDQVSNLVDCLSDEFCLOEKREL 660
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTVDYTHIDQVSNLVDCLSDEFCLOEKREL 660
QY 661 SEKVKHAKRLSDERNLLQDPNFKGINRQDLDRGWRGSTDITIQGDDVFRENVTLPGTED 720
DB 661 SEKVKHAKRLSDERNLLQDPNFKGINRQDLDRGWRGSTDITIQGDDVFRENVTLPGTED 720
QY 721 EGYPTLYQKIDESKLPKPYTRYOLRGYIEDSQLEIYLYRYNAKHETVNVLTGSLWPLS 780
DB 721 EGYPTLYQKIDESKLPKPYTRYOLRGYIEDSQLEIYLYRYNAKHETVNVLTGSLWPLS 780
QY 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
DB 781 VQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
QY 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKWKREKLELETNIVYKAKES 900
DB 841 IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKWKREKLELETNIVYKAKES 900
QY 901 VDALFVNSQYDQLOADTNIAHIAADKRVHRIREAYLPESLVIPGVNVDIFELKGRIFT 960
DB 901 VDALFVNSQYDQLOADTNIAHIAADKRVHRIREAYLPESLVIPGVNVDIFELKGRIFT 960
QY 961 AFFLYDARNYKNGDFNGLSCNWNKGVHDVEQNNHRSVLVVPWEAEVYQSVRYCPGR 1020
DB 961 AFFLYDARNYKNGDFNGLSCNWNKGVHDVEQNNHRSVLVVPWEAEVYQSVRYCPGR 1020
QY 1021 GYLRTVYAYKEGEGCVTTHEIENNTDELKFSNCVEEYVPNTVTCNDYTANQEEYGG 1080
DB 1021 GYLRTVYAYKEGEGCVTTHEIENNTDELKFSNCVEEYVPNTVTCNDYTANQEEYGG 1080
QY 1081 AYTSRNRYDETYGSSSVFADYASVVEEKSYSYDGRDNPCESNRGYGYDTPLPAGVYTK 1140
DB 1081 AYTSRNRYDETYGSSSVFADYASVVEEKSYSYDGRDNPCESNRGYGYDTPLPAGVYTK 1140
QY 1141 ELEYFPTDKWIEIGETEGTFIVDSVELLMBE 1174
DB 1141 ELEYFPTDKWIEIGETEGTFIVDSVELLMBE 1174
RESULT 10
AAR94914
ID AAR94914 standard; Protein: 1174 AA.
XX AC AAR94914;
XX AC AAR94914;
DT 18-AUG-1996 (first entry)
XX XX CryIF toxin encoded by pMYC2243.
XX XX CryIF; crystal protein; chimeric toxin; protoxin; pMYC2243;
KW delta-endotoxin; chimeric gene; fusion protein;
KW Pseudomonas fluorescens; CryIA(b); CryI(c); synerg; Lepidoptera;
KW insect; biological control agent; transgenic plant;

insect resistance; crop improvement.

Bacillus thuringiensis.

Key Location/Qualifiers
590..601

Peptide
/note= "Core toxin-prototoxin junction marker (AAR94909);"
1061..1068

Peptide
/note= "Marker (AAR94910) for start of critical
hypervariable region in protoxin"

US5508264-A.

16-APR-1996.

06-DEC-1994; 94US-0349867.

06-DEC-1994; 94US-0349867.

(MYCO) MYCOGEN CORP.

Bradffisch GA, Schwab GE, Thompson M;
WPI; 1996-208745/21.
N-PSDB; AAT18722.

Compsn. for controlling lepidopteran pests - comprises CryIF and
CryIA(c) chimeric core toxin-contg. proteins.

Example 5; Column 55-62; 59pp; English.

This sequence represents a Bacillus thuringiensis CryIF delta-
endotoxin. A gene from pMW2047 has been subjected to splice-
overlap extension to alter codons in a limited region in the cryIF
fragment to favor G or C in the wobble position, to improve
expression in *Pseudomonas* spp. The resulting cryIF clone is
pMW2243. The cryIF fragment may be fused with cryIA(b) and/or
cryIA(c) fragments to give fusion proteins by recombinant DNA
methods. The core toxin sequence ends with peptide AAR94909,
which marks the start of the protoxin sequence, and the preferred
heterologous region is the hypervariable fragment beyond peptide
AAR94910. The resulting chimeric genes may be cloned in a
Pseudomonas fluorescens lactose-inducible strain to produce
chimeric toxins. The toxins, when combined in synergy, have
unexpectedly enhanced toxicity to lepidopteran pests. P.
fluorescens or *B. thuringiensis* cells expressing the genes may be
used as insect biological control agents, or transgenic plants
expressing the genes may become resistant to insect attack.

Query Match 99.9%; Score 6237; DB 17; Length 1174;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENNQNCVPYNCLNPEVEILNEERSTGRPLDISLFRLLSEFVPGVGAFGLFD 60
DB 1 MENNQNCVPYNCLNPEVEILNEERSTGRPLDISLFRLLSEFVPGVGAFGLFD 60

QY 61 LIWGFTTPSDWSLFLQIQEQLTEQLERNAITTLGLADSYEIVIEALREWEANPN 120
DB 61 LIWGFTTPSDWSLFLQIQEQLTEQLERNAITTLGLADSYEIVIEALREWEANPN 120

QY 121 NAQLREDVRIRFANTDDALITAINNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSFGOGW 180
DB 121 NAQLREDVRIRFANTDDALITAINNFTLSFEIPLLSVYVQAANLHLSLLRDVAVSFGOGW 180

QY 181 GLDIATVNNHYNRLINLHRYTKHCLDITVNGLENLRGNTQWARFNQPRDLTLTVLD 240
DB 181 GLDIATVNNHYNRLINLHRYTKHCLDITVNGLENLRGNTQWARFNQPRDLTLTVLD 240

QY 241 IVALFPNDVRYPIQTSQSLTREIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300
DB 241 IVALFPNDVRYPIQTSQSLTREIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300

Db 241 IVALFPNDVRYPIQTSQSLTREIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300

QY 301 NSLFTVTAETVRSQTVMGHLYSSRNTAGNRINFPSPYGVNPGGAIWIADDEDPFPYRTLS 360
DB 301 NSLFTVTAETVRSQTVMGHLYSSRNTAGNRINFPSPYGVNPGGAIWIADDEDPFPYRTLS 360

QY 361 DPVFFRGFGNPHYVGLRGVAFPOQTGTHRTFRNSGTIDSLDEIPPODNGAPANDYS 420
DB 361 DPVFFRGFGNPHYVGLRGVAFPOQTGTHRTFRNSGTIDSLDEIPPODNGAPANDYS 420

QY 421 HVLNHYTEVRWPGCEISGSDSWRAPMFSWTHRSATPNTIDPBRITQIPLVKAHTLQSGT 480
DB 421 HVLNHYTEVRWPGCEISGSDSWRAPMFSWTHRSATPNTIDPBRITQIPLVKAHTLQSGT 480

QY 481 VVRGPGTGGDILRRRTSGGPFAYTIIVNINGQLPQRYRARIYASTNLIYVTVAGERIF 540
DB 481 VVRGPGTGGDILRRRTSGGPFAYTIIVNINGQLPQRYRARIYASTNLIYVTVAGERIF 540

QY 541 AGQFNKMTDGTDLTFQSFYSATINTAFIPMSQSFVGCADTFSSGNEVYIDRPELIPV 600
DB 541 AGQFNKMTDGTDLTFQSFYSATINTAFIPMSQSFVGCADTFSSGNEVYIDRPELIPV 600

QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTQVTDYHIDQVSNLVCLSDFCCLDEKREL 660
DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTQVTDYHIDQVSNLVCLSDFCCLDEKREL 660

QY 661 SEKVKAHRLSDERNLLQDPNFKGINRQDRGWRGSTDITIQGDDVDFKENVYTLPGTFD 720
DB 661 SEKVKAHRLSDERNLLQDPNFKGINRQDRGWRGSTDITIQGDDVDFKENVYTLPGTFD 720

QY 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSQDLEYLYIRYNAKHETVNVLTGSLWPLS 780
DB 721 ECPYTYLYQKIDESKLPYTRYOLRGYIEDSQDLEYLYIRYNAKHETVNVLTGSLWPLS 780

QY 781 VQSPIKCGEPNRCAPHELNWPLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840
DB 781 VQSPIKCGEPNRCAPHELNWPLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLDVWV 840

QY 841 IFKIKTQDCHARLGNLEFLEEKPLVGENLARVKAEEKKQEDKLELETINIVYKEAKES 900
DB 841 IFKIKTQDCHARLGNLEFLEEKPLVGENLARVKAEEKKQEDKLELETINIVYKEAKES 900

QY 901 VDALFVNSOYDQLQADNTNIAHAAKRVHRIREAYLPELSVIPGVNVDIFEELKGRIFT 960
DB 901 VDALFVNSOYDQLQADNTNIAHAAKRVHRIREAYLPELSVIPGVNVDIFEELKGRIFT 960

QY 961 AFLYDARNVIKNGDFNGLSCHWVKGHDVBERQNHRSVLVYVPEWAEVYQEVRYCPGR 1020
DB 961 AFLYDARNVIKNGDFNGLSCHWVKGHDVBERQNHRSVLVYVPEWAEVYQEVRYCPGR 1020

QY 1021 GYLIRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVDEEYVNNVTTCNDYTANQBEYGG 1080
DB 1021 GYLIRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVDEEYVNNVTTCNDYTANQBEYGG 1080

QY 1081 AYTSTRNGYDETYGSSNSVPADYASVYEKSYTGDGRDNDPCESNRGYGYDTPLPAGYVTK 1140
DB 1081 AYTSTRNGYDETYGSSNSVPADYASVYEKSYTGDGRDNDPCESNRGYGYDTPLPAGYVTK 1140

QY 1141 ELEFYEPETDKVWEIETEGTEGTFIVDSVELLMEE 1174
DB 1141 ELEFYEPETDKVWEIETEGTEGTFIVDSVELLMEE 1174

RESULT 11
AAR94916
ID AAR94916 standard; Protein; 1174 AA.
XX AAR94916;
XX
DT 18-AUG-1996 (first entry)
XX
DE Native CryIF/CryIA(b) toxin.
XX

KW CryIF; CryIA(b); crystal protein; chimeric toxin;
 KW protoxin; delta-endotoxin; fusion protein; CryIA(C);
 KW Pseudomonas fluorescens; synergy; Lepidoptera; insect;
 KW biological control agent; transgenic plant; insect resistance;
 KW crop improvement.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 590...601
 FT /note= "Core toxin-prototoxin junction marker (AAR94909)"
 FT 1061..1068
 FT /note= "Marker (AAR94910) for start of critical
 FT hypervariable region in protoxin"
 XX
 PN US5508264-A.
 XX
 PD 16-APR-1996.
 XX
 PF 06-DEC-1994; 94US-0349867.
 XX
 PR 06-DEC-1994; 94US-0349867.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Bradfisch GA, Schwab GE, Thompson M;
 XX
 DR WPI; 1996-208745/21.
 XX
 PT Compsn. for controlling lepidopteran pests - comprises CryIF and
 PT CryIA(c) chimeric core toxin-contg. proteins.
 XX
 PS Disclosure; Column 79-86; 59pp; English.
 CC This sequence represents a Bacillus thuringiensis delta-endotoxin
 CC native CryIF/CryIA(b) toxin sequence. The core toxin sequence ends
 CC with peptide AAR94909, which marks the start of the protoxin
 CC sequence, and the critical hypervariable fragment beyond peptide
 CC AAR94910 may be used for insertion of heterologous fragments to give
 CC chimeric toxins with altered activity by recombinant DNA methods.
 CC The resulting chimeric genes may be cloned in a Pseudomonas
 CC fluorescens lactose-inducible strain. The chimeric toxins, when
 CC combined in synergy, have unexpectedly enhanced toxicity to
 CC lepidopteran pests. P. fluorescens or B. thuringiensis cells
 CC expressing the chimeric genes may be used as insect biological
 CC control agents, or transgenic plants expressing the genes may
 CC become resistant to insect attack.
 XX
 SQ Sequence 1174 AA;
 Query Match 99.9%; Score 6236; DB 17; Length 1174;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MENNTONOCVPYNCLNNEVEILNEERSTGRPLDLSLTLSEFVPGVGAFLGFD 60
 DB 1 MENNTONOCVPYNCLNNEVEILNEERSTGRPLDLSLTLSEFVPGVGAFLGFD 60
 QY 61 LIWGPIITSDWSLFLLOEQLEQRIETLERNRAITTLRLGLADSYEITYEALREWEANPN 120
 DB 61 LIWGPIITSDWSLFLLOEQLEQRIETLERNRAITTLRLGLADSYEITYEALREWEANPN 120
 QY 121 NAOLEDVRIRFANTDDALITAINFTLTSFEIPLSVVQAAHLHLSLRDAVSPGOGW 180
 DB 121 NAOLEDVRIRFANTDDALITAINFTLTSFEIPLSVVQAAHLHLSLRDAVSPGOGW 180
 QY 181 GLDIATVNNHYNRLINLHRYTKHCLDITYNQGLNRLRGNTNQWARFNQFRDLTLTVLD 240
 DB 181 GLDIATVNNHYNRLINLHRYTKHCLDITYNQGLNRLRGNTNQWARFNQFRDLTLTVLD 240
 QY 241 IVALFPNDVRYPIQTSSQLTREITYTSSVIEDSPVSANIPNGFRAEFGVPPHLMDFM 300
 DB 241 IVALFPNDVRYPIQTSSQLTREITYTSSVIEDSPVSANIPNGFRAEFGVPPHLMDFM 300

QY 301 NSLFTVTAETVRSQTVWGGHLVSRNTAGNRINPSPSYGVNPGGAIWIADDEPPFYETLS 360
 DB 301 NSLFTVTAETVRSQTVWGGHLVSRNTAGNRINPSPSYGVNPGGAIWIADDEPPFYETLS 360
 QY 361 DPVFRGGFCNPNHYVLGLRGVAFQQTGTNFTFRNSGTIDSLDEIPPODNGSAPNDYS 420
 DB 361 DPVFRGGFCNPNHYVLGLRGVAFQQTGTNFTFRNSGTIDSLDEIPPODNGSAPNDYS 420
 QY 421 HVLNHNVTFFVRPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSQT 480
 DB 421 HVLNHNVTFFVRPGEISGDSWRAPMFSWTHRSATPTNTIDPERITQIPLVKAHTLOSQT 480
 QY 481 VVRGPGFTGGDILRLRTSGGPFAYTIVNINGQLPQRYRARIRYASTNLRIRYTVAGERIF 540
 DB 481 VVRGPGFTGGDILRLRTSGGPFAYTIVNINGQLPQRYRARIRYASTNLRIRYTVAGERIF 540
 QY 541 AGQFNKTMGTGDLPTFQSFYSATINTAFTFPMQSSFTVGADTFSSGNEVYIDRPELIPV 600
 DB 541 AGQFNKTMGTGDLPTFQSFYSATINTAFTFPMQSSFTVGADTFSSGNEVYIDRPELIPV 600
 QY 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLDSEFCLEKREL 660
 DB 601 TATFEAYDLERAQKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLDSEFCLEKREL 660
 QY 661 SEKVKHAKLSDERNLLQDPNFKGINRQLDRGRWGSTDITIQRGDDVFKENVTPLGTED 720
 DB 661 SEKVKHAKLSDERNLLQDPNFKGINRQLDRGRWGSTDITIQRGDDVFKENVTPLGTED 720
 QY 721 EGYPTLYQKIDESKLKPYTRYOLRGYIEDSDLEIYLIRYNAKHTVNVLTGSLWPLS 780
 DB 721 EGYPTLYQKIDESKLKPYTRYOLRGYIEDSDLEIYLIRYNAKHTVNVLTGSLWPLS 780
 QY 781 VQSPIRKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
 DB 781 VQSPIRKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLDVWV 840
 QY 841 IFKIKTDQGHARLGNLFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKAKES 900
 DB 841 IFKIKTDQGHARLGNLFLEEKPLVGEALARYKRAEKKWRDKREKLELETNIVYKAKES 900
 QY 901 VDALFVNSOYDQLOADNTIAMHAADKRVHREAYLPESLVPVGVNDFIFELKGRIFT 960
 DB 901 VDALFVNSOYDQLOADNTIAMHAADKRVHREAYLPESLVPVGVNDFIFELKGRIFT 960
 QY 961 AFPLDARNVIRKNGDFNGLSCWNVKGHVDBEQNNHRSVLVVPWEAEVSVQVRCPCR 1020
 DB 961 AFPLDARNVIRKNGDFNGLSCWNVKGHVDBEQNNHRSVLVVPWEAEVSVQVRCPCR 1020
 QY 1021 GYLIRVATYKEGYGEGCVTHIEIENNTDELKFSNCVEEVEVYNTVTCNDYTANOEYGG 1080
 DB 1021 GYLIRVATYKEGYGEGCVTHIEIENNTDELKFSNCVEEVEVYNTVTCNDYTANOEYGG 1080
 QY 1081 AYTSNRGYDETYGSNSVPADYASYIEEKSYTDGRRDNPCESNRGSGYDTPLPAGYVTK 1140
 DB 1081 AYTSNRGYDETYGSNSVPADYASYIEEKSYTDGRRDNPCESNRGSGYDTPLPAGYVTK 1140
 QY 1141 ELEYFPETDKVWIEIGETEGTTFIVDSVELLMEE 1174
 DB 1141 ELEYFPETDKVWIEIGETEGTTFIVDSVELLMEE 1174
 RESULT 12
 AAR84732
 ID AAR84732 standard; Protein; 1174 AA.
 XX
 AC AAR84732;
 XX
 DT 27-MAY-1996 (first entry)
 XX
 DE CryIF/436 chimeric toxin.
 XX
 KW Delta endotoxin; crystal protein; chimeric toxin; insecticide;

KW pesticide; Pseudomonas fluorescens; biological control agent;
 KW transgenic plant; insect resistance; disease resistance;
 XX crop improvement; protein engineering.

OS Bacillus thuringiensis.

XX Key Location/Qualifiers

FT Misc-difference 619 /note= "E to A substitution"

FT Misc-difference 624 /note= "S to I substitution"

FT Misc-difference 646 /note= "E to T substitution"

FT Misc-difference 658 /note= "K to R substitution"

FT Misc-difference 680 /note= "P to S substitution"

FT Misc-difference 684 /note= "G to D substitution"

FT Misc-difference 689 /note= "L to P substitution"

FT Misc-difference 694 /note= "R to G substitution"

FT Misc-difference 698 /note= "D to G substitution"

FT Misc-difference 716 /note= "L to S substitution"

FT Misc-difference 782 /note= "P to Q substitution"

FT Misc-difference 912 /note= "R to Q substitution"

FT W09530753-A1.

PN 16-NOV-1995.

XX 05-MAY-1995; 95WO-US05431.

XX 06-MAY-1994; 94US-0239476.

XX (MYCO) MYCOGEN CORP.

XX Schwab GE, Thompson M;

XX WPI; 1995-404120/51.

XX N-PSDB; AAT05250.

XX Nucleic acid encoding chimeric Bacillus thuringiensis
 PT delta-endotoxin - providing increased expression in Pseudomonas,
 PT esp. for control of lepidoptera pests.

XX Claim 10; Page 58-61; 91pp; English.

XX The sequence represents the cryIF/436 chimeric toxin encoded by
 CC plasmid pMYC2254. The chimeric toxin is expressed in Pseudomonas
 CC fluorescens better than native delta endotoxins. Host cells
 CC expressing the chimeric gene and producing chimeric toxin may be
 CC used in insecticide compositions. Where the host cells are plant
 CC cells, the gene confers insect resistance to the transformed
 CC plant.

XX Sequence 1174 AA;

Query Match 96.9%; Score 6049; DB 16; Length 1174;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1143; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 1 MENNIONQCVNCLNPNVEILNEERSTGRPLDLSLTRLFLSEFPVGVGVAFLPD 50
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1 MENNIONQCVNCLNPNVEILNEERSTGRPLDLSLTRLFLSEFPVGVGVAFLPD 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 LIWGFITPDSWLSFLIQIEQLIEQRIETLERNRAITTLRGLADSYEITYEALREWEANPN 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 61 LIWGFITPDSWLSFLIQIEQLIEQRIETLERNRAITTLRGLADSYEITYEALREWEANPN 120
 QY 121 NAQREDVRIRFANTDDALITAINNETLTLSFEIPLLSVYQAAANLHLSLRDVSFGQGW 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 NAQREDVRIRFANTDDALITAINNETLTLSFEIPLLSVYQAAANLHLSLRDVSFGQGW 180
 QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNOGLENLGNTROWARFNFRDLTLTVLD 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 GLDIATVNNHYNRLINLIHRYTKHCLDLYNOGLENLGNTROWARFNFRDLTLTVLD 240
 QY 241 IVALFPNDVRYPIOTSSOLTREIYTSVIEDSPYSANIPNGFNRAEFGVRPHLDFM 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 241 IVALFPNDVRYPIOTSSOLTREIYTSVIEDSPYSANIPNGFNRAEFGVRPHLDFM 300
 QY 301 NSLFTVTAETVRSQTVWGGHLVSSRNTAGRNIPPSYGVFNPGGAIWIADDPFPFYRTLS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 NSLFTVTAETVRSQTVWGGHLVSSRNTAGRNIPPSYGVFNPGGAIWIADDPFPFYRTLS 360
 QY 361 DPVVRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLEIPPODNGAPWNDYS 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 DPVVRGGFGNPHYVGLRGVAFQQTGNTNTRFRNSGTIDSLEIPPODNGAPWNDYS 420
 QY 421 HVLNHTVFRWPGCEISGSDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAHTLQSGT 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 421 HVLNHTVFRWPGCEISGSDSWRAPMSWTHRSATPTNTIDPERITQIPLVKAHTLQSGT 480
 QY 481 VVRPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTNLRIRYIVVAGERIF 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 481 VVRPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTNLRIRYIVVAGERIF 540
 QY 541 AGQFNKMTDGTPLTFQSFYSYATINTAFTFMSQSSTFVGADTFSSGNEVYIDRFELIPV 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 541 AGQFNKMTDGTPLTFQSFYSYATINTAFTFMSQSSTFVGADTFSSGNEVYIDRFELIPV 600
 QY 601 TATFEAEYDLERAQKAVNALFTSINOIGIKTDVTDVHDQVSNLVCLSDEFCCLDEKREL 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 601 TATFEAEYDLERAQKAVNALFTSINOIGIKTDVTDVHDQVSNLVCLSDEFCCLDEKREL 660
 QY 661 SEKVHAKRLSDERNLLODPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 661 SEKVHAKRLSDERNLLODPNFKGINRQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD 720
 QY 721 ECPYLYQKIDESKLKPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTSWLPLS 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 721 ECPYLYQKIDESKLKPYTRYQLRGYIEDSQDLEIYLIRYNAKHETVNLGTSWLPLS 780
 QY 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCITDLEDLDVWV 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 781 VQSPKRCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCITDLEDLDVWV 840
 QY 841 IFKIKTQDGHARLGNLEFLLEKPLVGEALARYKRAEKKWRDKREKLELETNTIYVKEAKES 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 841 IFKIKTQDGHARLGNLEFLLEKPLVGEALARYKRAEKKWRDKREKLELETNTIYVKEAKES 900
 QY 901 VDALLFVNSOYDLOADNTIAMTHAADKRVHRTREAYLPSELVPGVNDVDFELKGRIFT 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 901 VDALLFVNSOYDLOADNTIAMTHAADKRVHRTREAYLPSELVPGVNDVDFELKGRIFT 960
 QY 961 AFPLDYDARNVKNQDNGLSCWNVKGHVDEEONNHRSLVVPWEAEVSOEVRVCPGR 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 961 AFPLDYDARNVKNQDNGLSCWNVKGHVDEEONNHRSLVVPWEAEVSOEVRVCPGR 1020
 QY 1021 GYLIRVATYKEGYGECVYTHIEINNTDELKFSNCVEEVEYNNVTTCNDYTANOEEYGG 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1021 GYLIRVATYKEGYGECVYTHIEINNTDELKFSNCVEEVEYNNVTTCNDYTANOEEYGG 1080
 QY 1081 ATYSNRNGYDETYGNSNSVPADYASVYBEKSYTDGRRONPCSNRGYGDYTPLPAGYVTK 1140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1081 ATYSNRNGYDETYGNSNSVPADYASVYBEKSYTDGRRONPCSNRGYGDYTPLPAGYVTK 1140
 QY 1141 ELEYFPETDKVWIEGTETEGTFIVDSVELLMEE 1174
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1141 ELEYFPETDKVWIEGTETEGTFIVDSVELLMEE 1174

RESULT 13
 AAR94908
 ID AAR94908 standard; Protein; 1174 AA.
 XX AAR94908:
 AC
 DT 18-AUG-1996 (first entry)
 XX
 XX
 DE CryIF/436 chimeric toxin encoded by pMYC2254.
 DE
 KW CryIF; CryIA(c); CryIA(b); crystal protein; chimeric toxin;
 KW protoxin; pMYC2244; delta-endotoxin; fusion protein;
 KW Pseudomonas fluorescens; synergy; Lepidoptera; insect;
 KW biological control agent; transgenic plant; insect resistance;
 KW crop improvement.
 XX
 OS Bacillus thuringiensis.
 XX
 FH Key
 FH Region 1..601
 FT /note= "CryIF toxin region"
 FT Peptide 590..601
 FT /note= "Core toxin-prototoxin junction marker (AAR94909)"
 FT Region 602..1148
 FT /note= "CryIA(c)/CryIA(b) 436 protoxin region"
 FT Peptide 1061..1068
 FT /note= "Marker (AAR94910) for start of critical
 FT hypervariable region in protoxin"
 XX
 XX US508264-A.
 XX
 XX 16-APR-1996.
 XX
 XX 06-DEC-1994; 94US-0349867.
 XX
 XX 06-DEC-1994; 94US-0349867.
 XX
 XX (MYCO) MYCOGEN CORP.
 XX
 PI Bradfisch GA, Schwab GE, Thompson M;
 XX
 XX WPI; 1996-208745/21.
 DR N-PSDB; AAT18702.
 XX
 XX Compn. for controlling lepidopteran pests - comprises CryIF and
 PT CryIA(c) chimeric core toxin-contg. proteins.
 XX
 PS Claim 7; Column 73-80; 59pp; English.
 XX
 CC This sequence represents a Bacillus thuringiensis chimeric
 CC CryIF/436 delta-endotoxin. The sequence is constructed by
 CC substitution of a CryIA(c)-CryIA(b) 436 (AAR94911) fragment for a
 CC CryIA(b) fragment encoded by pMYC2523 (AAR94907). The 436 protoxin
 CC sequence consists of CryIA(c) sequence except at the very
 CC C-terminus. The product contains CryIF up to the toxin-prototoxin
 CC junction, followed by a CryIA(c) protoxin sequence with a small
 CC C-terminal fragment of CryIA(b). The core toxin sequence ends
 CC with peptide AAR94909, which marks the start of the protoxin
 CC sequence, and the preferred heterologous region is the
 CC hypervariable fragment beyond peptide AAR94910. The resulting
 CC chimeric gene may be cloned in a Pseudomonas fluorescens
 CC lactose-inducible strain to produce a chimeric toxin. The toxin,
 CC when combined with another chimeric toxin in synergy, has
 CC unexpectedly enhanced toxicity to lepidopteran pests. P.
 CC fluorescens or B. thuringiensis cells expressing the gene may be
 CC used as an insect biological control agent, or a transgenic plant
 CC expressing the gene may become resistant to insect attack.
 XX
 XX Sequence 1174 AA;

Query Match 96.9%; Score 6049; DB 17; Length 1174:

		Best Local Similarity 97.4%; Pred. No. 0;			
		Matches 1143; Conservative 5; Mismatches 26; Indels 0; Gaps 0;			
QY	1	MENNIONQCVYPCNPNPEYLLNEERSTGRPLDLSLTRFLLSFVGVGVAFGLFD	60		
DB	1	MENNIONQCVYPCNPNPEYLLNEERSTGRPLDLSLTRFLLSFVGVGVAFGLFD	60		
QY	61	LIWGFITPDSWLSFLLOIEOLIEORIETLERNRAITTLRGLADSYEYIEALREWEANPN	120		
DB	61	LIWGFITPDSWLSFLLOIEOLIEORIETLERNRAITTLRGLADSYEYIEALREWEANPN	120		
QY	121	NAOLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDVAFSGGW	180		
DB	121	NAOLREDVRIRFANTDDALITAINNFTLTSTFEIPLLSVYVQAANLHLSLLRDVAFSGGW	180		
QY	181	GLDIATVNNHYNLNLHRYTKHCLDTYNOGLENLKGTNRQWARFNQFRDLTLVLD	240		
DB	181	GLDIATVNNHYNLNLHRYTKHCLDTYNOGLENLKGTNRQWARFNQFRDLTLVLD	240		
QY	241	IVALFPNYDVRTYPIOTSSOLTREIYTSVLEDSVPSANIPNGFNRAEFGVRPPLHDEM	300		
DB	241	IVALFPNYDVRTYPIOTSSOLTREIYTSVLEDSVPSANIPNGFNRAEFGVRPPLHDEM	300		
QY	301	NSLFVTAETVRSQTVMGCHLVSSRNTAGNINFPISYGVNPGGAIWIADEDPREFYRTLS	360		
DB	301	NSLFVTAETVRSQTVMGCHLVSSRNTAGNINFPISYGVNPGGAIWIADEDPREFYRTLS	360		
QY	361	DPVVRGFGFNPHVYGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPQDNGSGAPNDYS	420		
DB	361	DPVVRGFGFNPHVYGLRGVAFQQTGNTNTRFRNSGTIDSLDEIPQDNGSGAPNDYS	420		
QY	421	HVLNHVTFVRWPGEISGDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHFLQSGTT	480		
DB	421	HVLNHVTFVRWPGEISGDSWRAPMFSTHRSATPTNTIDPERITQIPLVKAHFLQSGTT	480		
QY	481	VVRGPGFTGGDILERTSGGPFAYTIVNINGOLPQRYRARIYASTTNLRIYVTVAGERIF	540		
DB	481	VVRGPGFTGGDILERTSGGPFAYTIVNINGOLPQRYRARIYASTTNLRIYVTVAGERIF	540		
QY	541	AGQFNKTMDTGDLPTFQSFYATINTAFTPMQSSSTVGADTFSSGNEVYIDREFELIPV	600		
DB	541	AGQFNKTMDTGDLPTFQSFYATINTAFTPMQSSSTVGADTFSSGNEVYIDREFELIPV	600		
QY	601	TATFEAYDLERAKAVNALFTSINQIGIKTDVTDYHIDOVSNLVDCLSDEFCDEKREL	660		
DB	601	TATFEAYDLERAKAVNALFTSINQIGIKTDVTDYHIDOVSNLVDCLSDEFCDEKREL	660		
QY	661	SEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD	720		
DB	661	SEKVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDITIQRGDDVFKENYVTLPGTFD	720		
QY	721	ECYPTLYQKIDSKLKPYYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLAPLS	780		
DB	721	ECYPTLYQKIDSKLKPYYTRYQLRGYIEDSDLEIYLIRYNAKHETVNVLTGSLAPLS	780		
QY	781	VQSPIKCGPNPCAPHELEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLVWV	840		
DB	781	VQSPIKCGPNPCAPHELEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTDLNEDLVWV	840		
QY	841	IFKIKTDGCHARLGNLEFLEEKPLVGEALARKRAKKWRDKREKLEETNIYVKEAKES	900		
DB	841	IFKIKTDGCHARLGNLEFLEEKPLVGEALARKRAKKWRDKREKLEETNIYVKEAKES	900		
QY	901	VDALFVNSQYDQLOADTNIAHIAADKRVHRIEAYLPESLPIGVNVDIFEBELKGRIFT	960		
DB	901	VDALFVNSQYDQLOADTNIAHIAADKRVHRIEAYLPESLPIGVNVDIFEBELKGRIFT	960		
QY	961	AFELYDARNVKNKGNDFNNGLSCNWKVGHVDVEQNNHRSVLVVPWEAEYSQEVRCPCR	1020		
DB	961	AFELYDARNVKNKGNDFNNGLSCNWKVGHVDVEQNNHRSVLVVPWEAEYSQEVRCPCR	1020		
QY	1021	GYTLRTAYKEGYGEGCVTTIETENNTDELKFSNCEVEEYVNNVTVCNDYTAQNEBYGG	1080		

Db 1021 GYLLRVATAYKEGEGCVTHIEIENNTDELKFSNCVEEVEYFNNTVTCNDYATATQEEYEG 1080
 QY 1081 AYTSRNGYDEYSGNSVADYASVYEEKSVYDGRDRNPCESSNGYGDYTPLPAGYVTK 1140
 Db 1081 TYTSRNGYDAYSNSVADYASVYEEKSVYDGRDRNPCESSNGYGDYTPLPAGYVTK 1140
 QY 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174
 Db 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174

RESULT 14
 AAW76710
 ID AAW76710 standard; Protein; 1174 AA.
 XX
 AC AAW76710;
 XX
 DT 13-JAN-1999 (first entry)
 DE
 XX Plasmid pMYC2254 cryIF/436 chimeric toxin protein fragment.
 XX
 KW Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);
 KW synergism; plant; primer; endotoxin.
 XX
 OS Synthetic.
 XX
 PN US5827514-A.
 XX
 PD 27-OCT-1998.
 XX
 PF 08-FEB-1996; 96US-0598305.
 XX
 PR 06-DEC-1994; 94US-0349867.
 PR 08-FEB-1996; 96US-0598305.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Bradfisch GA, Schwab GE, Thompson M;
 XX
 DR WPI; 1998-593944/50.
 DR N-PSDB; AAV62083.
 XX
 PT Composition for biological control of lepidopteran pests -
 PT comprising cells expressing two chimeric Bacillus thuringiensis
 PT crystal proteins
 XX
 PS Claim 9; Column 75-82; 75pp; English.
 XX
 CC This sequence represents a Bt endotoxin which is used in a method for
 CC controlling lepidopteran pests. The method involves the use of cells
 CC that express the Bacillus thuringiensis delta-endotoxins cryIF chimeric
 CC core toxin-containing protein and cryIA(c) chimeric core toxin-containing
 CC protein in a combination that have synergistically enhanced activity,
 CC against e.g. corn earworm (Heliothis zea).
 XX
 SQ Sequence 1174 AA;

Query Match 96.9%; Score 6049; DB 19; Length 1174;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1143; Conservative 5; Mismatches 26; Indels 0; Gaps 0;

QY 1 MENNIQCVPYCNLNNPEYILNEERSTGRPLDLSLSTRFLLSFVPGVGVAFLFD 60
 Db 1 MENNIQCVPYCNLNNPEYILNEERSTGRPLDLSLSTRFLLSFVPGVGVAFLFD 60
 QY 61 LINGFTPPDSWSLFLQIEQLIEQRIETLERNRAITTLRLGLADSYEYIIEALREWEANPN 120
 Db 61 LINGFTPPDSWSLFLQIEQLIEQRIETLERNRAITTLRLGLADSYEYIIEALREWEANPN 120
 QY 121 NAQLREDVIRFANTDDALITANNFTLTSFEITPLISVYVQAAANLHLSLRDAVSFGQW 180
 Db 121 NAQLREDVIRFANTDDALITANNFTLTSFEITPLISVYVQAAANLHLSLRDAVSFGQW 180

QY 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGCTNTQWARFNQFRDLTLTVLD 240
 Db 181 GLDIATVNNHYNRLINLIHRYTKHCLDTYNOGLENLRGCTNTQWARFNQFRDLTLTVLD 240
 QY 241 IVALFPNDVDTYPIQTSSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300
 Db 241 IVALFPNDVDTYPIQTSSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVPPHLMDFM 300
 QY 301 NSLFTVTAETVRSQTVWGGHLYSSRNTAGNRIFFSYGVFNPGGAIWIADDEPRFYRTL 360
 Db 301 NSLFTVTAETVRSQTVWGGHLYSSRNTAGNRIFFSYGVFNPGGAIWIADDEPRFYRTL 360
 QY 361 DPVEVRGFGNPHYVGLGRGVAFOQTGTHNTRTFNSGTDLSLDEIPPODNGAPWNDYS 420
 Db 361 DPVEVRGFGNPHYVGLGRGVAFOQTGTHNTRTFNSGTDLSLDEIPPODNGAPWNDYS 420
 QY 421 HVLNHTVFRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITOPLVKAHTLQSGTT 480
 Db 421 HVLNHTVFRWPGEISGDSWRAPMFSWTHRSATPTNTIDPERITOPLVKAHTLQSGTT 480
 QY 481 VVRPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYASTTNLRIYTVVAGERIF 540
 Db 481 VVRPGTGGDILRRTSGGPFAYTIVNINGOLPORYRARIYASTTNLRIYTVVAGERIF 540
 QY 541 AGQFNKTMGTGDLTFOSESYATINTAFTPMSSOSSTVGADTFSSGNEVYIDREFELIPV 600
 Db 541 AGQFNKTMGTGDLTFOSESYATINTAFTPMSSOSSTVGADTFSSGNEVYIDREFELIPV 600
 QY 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSOBFCDEKREL 660
 Db 601 TATFEAEYDLERAKAVNALFTSINOIGIKTDVTDYHIDQVSNLVDCLSOBFCDEKREL 660
 QY 661 SEVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDTIQRGDDVFKENYVLTGTFD 720
 Db 661 SEVKHAKRLSDERNLLQDPNFKGINQLDRGWRGSTDTIQRGDDVFKENYVLTGTFD 720
 QY 721 EGYPTYLYQKIDSKLPYTRYQLRGVIEDSODLEIYLIRYNAKHETVNVLTGSLAPLS 780
 Db 721 EGYPTYLYQKIDSKLPYTRYQLRGVIEDSODLEIYLIRYNAKHETVNVLTGSLAPLS 780
 QY 781 VQSPIRKCGEPNRCAPHLWNPDLCSCRDGCKCAHSHHFLSDIDYGCCTDLNEDLDVWV 840
 Db 781 VQSPIRKCGEPNRCAPHLWNPDLCSCRDGCKCAHSHHFLSDIDYGCCTDLNEDLDVWV 840
 QY 841 IFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKKRDKREKLEETNIVYKEAKES 900
 Db 841 IFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKKRDKREKLEETNIVYKEAKES 900
 QY 901 VDALFVNSQYDQLOADFNIAHAAKRVHIREAYLPELSVPGVVDVFEELKGRIFT 960
 Db 901 VDALFVNSQYDQLOADFNIAHAAKRVHIREAYLPELSVPGVVDVFEELKGRIFT 960
 QY 961 AFFLYDARNVIKNGDFNNGLSCHWNKGVHVDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020
 Db 961 AFFLYDARNVIKNGDFNNGLSCHWNKGVHVDVEEQNNHRSVLVVPWEAEVSQEVRCPCR 1020
 QY 1021 GYLIRVATAYKEGEGCVTHIEIENNTDELKFSNCVEEVEYFNNTVTCNDYATQEEYEG 1080
 Db 1021 GYLIRVATAYKEGEGCVTHIEIENNTDELKFSNCVEEVEYFNNTVTCNDYATQEEYEG 1080
 QY 1081 AYTSRNGYDEYSGNSVADYASVYEEKSVYDGRDRNPCESSNGYGDYTPLPAGYVTK 1140
 Db 1081 AYTSRNGYDEYSGNSVADYASVYEEKSVYDGRDRNPCESSNGYGDYTPLPAGYVTK 1140
 QY 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174
 Db 1141 ELEYPETDKWIEIGETEGTFIVDSVELLMEE 1174

RESULT 15
 AAW76716
 ID AAW76716 standard; Protein; 1175 AA.
 XX

AC	AAW76716;
XX	
XX	13-JAN-1999 (first entry)
XX	
DE	Alternative cryIF/cryIA(b) chimeric endotoxin protein #1.
XX	
XX	Bt toxin; lepidoptera; pest; cryIF; chimeric; core toxin; cryIA(c);
KW	synergism; plant; primer; endotoxin.
XX	
XX	Synthetic.
XX	
XX	US5827514-A.
PN	
XX	27-OCT-1998.
XX	
XX	08-FEB-1996; 96US-0598305.
PF	
XX	
PR	06-DEC-1994; 94US-0349867.
PR	08-FEB-1996; 96US-0598305.
XX	
XX	(MYCO) MYCOGEN CORP.
PA	
XX	
PI	Braafisch GA, Schwab GE, Thompson M;
XX	
XX	WPI; 1998-593944/50.
DR	
XX	
PT	Composition for biological control of lepidopteran pests -
PT	comprising cells expressing two chimeric Bacillus thuringiensis
PT	crystal proteins
XX	
PS	Claim 10; Column 105-112; 75pp; English.
XX	
CC	This sequence represents a Bt endotoxin which is used in a method for
CC	controlling lepidopteran pests. The method involves the use of cells
CC	that express the Bacillus thuringiensis delta-endotoxins cryIF chimeric
CC	core toxin-containing protein and CryIA(c) chimeric core toxin-containing
CC	protein in a combination that have synergistically enhanced activity,
CC	against e.g. corn earworm (Heliothis zea).
XX	
SQ	Sequence 1175 AA;
	Query Watch 96.4%; Score 6018.5; DB 19; Length 1175;
	Best Local Similarity 96.9%; Pred No. 0;
	Matches 1138; Conservative 11; Mismatches 25; Indels 1; Gaps 1
QY	1 MENNIQCVPVNCNLNPEVEILNEERSTGRPLDLSLSTRFLSEFVGCVGVAFLFD 60
Db	1 MENNIQCVPVNCNLNPEVEILNEERSTGRPLDLSLSTRFLSEFVGCVGVAFLFD 60
QY	61 LINGFTTPSDWSLFLLQIEQLLEQRLETERRNAITTLRGADSYEIIYEALREWEANPN 120
Db	61 LINGFTTPSDWSLFLLQIEQLLEQRLETERRNAITTLRGADSYEIIYEALREWEANPN 120
QY	121 NAOLREDVRIRFANTDDALITAINNFITTSFEIPLLVSVVQAANLHLSLRDAYSFQGW 180
Db	121 NAOLREDVRIRFANTDDALITAINNFITTSFEIPLLVSVVQAANLHLSLRDAYSFQGW 180
QY	181 GLDIATVNHNHYNLINLIHRYKHKCLDTYNQGLENLRTNTROWARFNQFRDLTFLVL 240
Db	181 GLDIATVNHNHYNLINLIHRYKHKCLDTYNQGLENLRTNTROWARFNQFRDLTFLVL 240
QY	241 IVALFPNVDRVTPIDTSSOLTREIYTSSVIDSPVSANIPNGFNRAEFVGPPLHMDFM 300
Db	241 IVALFPNVDRVTPIDTSSOLTREIYTSSVIDSPVSANIPNGFNRAEFVGPPLHMDFM 300
QY	301 NSLFTVAETVRSOTVMGGHLVSSRNTAGNRINFPPSYGVNFGGAIWAIDEDEPRFYRTL 360
Db	301 NSLFTVAETVRSOTVMGGHLVSSRNTAGNRINFPPSYGVNFGGAIWAIDEDEPRFYRTL 360
QY	361 DPVFVRGFGGNPHVILGRGVAPOQTGTNHTTFRNSTGIDSLEDPIDQNSGAPWNDS 420
Db	361 DPVFVRGFGGNPHVILGRGVAPOQTGTNHTTFRNSTGIDSLEDPIDQNSGAPWNDS 420

Qy	421	HVLNVHVFVRVPGCEISGSDSNRAPMFSWTHSRSAPTNTIDPERITQIPLVKAHTLOSQT	480
Db	421	HVLNVHVFVRVPGCEISGSDSNRAPMFSWTHSRSAPTNTIDPERITQIPLVKAHTLOSQT	480
Qy	481	VVRGPGFTGDDILRRTSGGPPAYTIVNLNGOLPORYRARIRYASTTNLRIYVTVAGERIF	540
Db	481	VVRGPGFTGDDILRRTSGGPPAYTIVNLNGOLPORYRARIRYASTTNLRIYVTVAGERIF	540
Qy	541	AGOFNKMTDGPLTFQSFYSYATINTAFTFMSQSSFTVGADTFSSGNEVYIDRFELIPV	600
Db	541	AGOFNKMTDGPLTFQSFYSYATINTAFTFMSQSSFTVGADTFSSGNEVYIDRFELIPV	600
Qy	601	TATFEAEYDLERAQAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSEDFCLDEKREL	660
Db	601	TATFEAEYDLERAQAVNALFTSINQIGIKTDVTDYHIDQVSNLVDCLSEDFCLDEKREL	660
Qy	661	SEKVKIAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDVFKNYVTLPGTFD	720
Db	661	SEKVKIAKRLSDERNLLODPNFKGINROLDRGWRGSTDITIQRGDDVFKNYVTLPGTFD	720
Qy	721	ECYPTLYQKIDESKLPYTRYOLRGYTEDSODLEIYLIRYNAKHETVNVLTGSLWPLS	780
Db	721	ECYPTLYQKIDESKLPYTRYELRGYTEDSODLEIYLIRYNAKHETVNVLTGSLWRLS	780
Qy	781	VQSPIRKCGEPNRCAPHLEWNPDLDCSDRGDEKCAHGHSHFSLDIDYGCCTDLNEDLDVVV	840
Db	781	FESSIRKCGEPNRCAPHLEWNPDLDCSDRGDEKCAHGHSHFSLDIDYGCCTDLNEDLDVVV	840
Qy	841	IFKIKTQDGHARGLNLEFLEEK - PLVGEALARVKAEEKKWKREKLELEFINIYVKEAKE	899
Db	841	IFKIKTQDGHARGLNLEFLEGRAPLVGEALARVKAEEKKWKREKLELEFINIYVKEAKE	900
Qy	900	SVDA\FVNSQYDOLQADNTMIAMHAADRVRHRIREAYIPELSVTPGVNVDIFELKGRIF	959
Db	901	SVDA\FVNSQYDOLQADNTMIAMHATKRVHRIQZAYIPELSVTPGVNVDIFELKGRIF	960
Qy	960	TAFFLXDARNVINKGDFNNGLSWNVKGHDVDEEQNNHRSVLVWPWEAEVQSQVRVCPG	1019
Db	961	TAFFLXDARNVINKGDFNNGLSWNVKGHDVDEEQNNQRSVLVWPWEAEVQSQVRVCPG	1020
Qy	1020	RGYILRVTAYKEGYGCGCVTHIEINNTDELKFSNCVVEEYVPNNTVTCNDYTANQOEYG	1079
Db	1021	RGYILRVTAYKEGYGCGCVTHIEINNTDELKFSNCFVEEYVPNNTVTCNDYTANQOEYG	1080
Qy	1080	GAYTSNRNGYDEYTGNSNSVPADYASVYEKSYTQGRDNPCESNRGYGDYTPLPAGYVT	1139
Db	1081	GAYTSNRNGYDEYTGNSYVPADYASVYEKAYTQGRDNPCESNRGYGDYTPLPAGYVT	1140
Qy	1140	KELEYFPETDKWIEIGETEGTFIVDSVELLAMEE 1174	
Db	1141	KOLRYFPETDKWIEIGETEGTFIVDSVELLAMEE 1175	

Search completed: November 27, 2002, 18:38:03
Job time : 87 secs